STIC Search Report
Biotech-Chem Library

USPTO

TO: Anne-Marie ~~Baker~~ *Falk*
Location: rem/2A45/2C18
Art Unit: 1632
Thursday, March 09, 2006
Case Serial Number: 10/607712

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner ~~Baker,~~ *Falk*.

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

*Please note - the pending files were not searched.
If you need these please contact me.*

Toby

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SEARCH REQUEST FORM

Scientific and Technical Information Center

CRFE

Requester's Full Name: _Anne-Marie Falk_ Examiner #: _74977_ Date: _2/28/06_

Art Unit: _1632_ Phone Number ~~#0~~ x 20728 Serial Number: _10/607,712_

Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): (PAPER) DISK E-MAIL

L→ 2C18 L→ 2A45 ME

If more than one search is submitted, please prioritize searches in order of need.

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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _Human Methionine Synthase_

Inventors (please provide full names): _Roy A. Gravel_

Earliest Priority Filing Date: _11/27/96_

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

- Please search SEQ ID NO: 1 (3919 nucleotides)

and _RA 3919_

- also a size limited search to cover probes of at least 18, 40, 50, or 60 nucleotides. (see attached claims) (although the claims cover a nucleic acid molecule of any length, I would like to see hits that are 100 nucleotides or smaller, in addition to hits that cover the full-length sequence).

- Please search commercial/patents and pre-grant pubs databases.

RECEIVED MAR - 2006

ME

Thanks!

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Claims

1. A substantially pure human nucleic acid comprising at least 40 nucleotides that hybridizes under high stringency conditions to a sequence found within the nucleic acid of SEQ ID NO:1.

2. The nucleic acid of claim 1, wherein said sequence has a sequence complementary to at least 50% of at least 60 contiguous nucleotides of the nucleic acid encoding the methionine synthase polypeptide, said sequence sufficient to allow nucleic acid hybridization under high stringency conditions.

3. The nucleic acid of claim 1, wherein said nucleic acid comprises a mutation or a polymorphism, wherein said nucleic acid probe detects a mutation or polymorphism selected from the group consisting of D919G, H920D, and ΔIle881.

4. The nucleic acid of claim 3, wherein said sequence of said nucleic acid comprises the cobalamin binding domain of the human methionine synthase gene.

5. The nucleic acid of claim 2, wherein at least 18 contiguous nucleotides of said sequence are complementary to at least 90% of the corresponding nucleotides of the nucleic acid encoding the methionine synthase polypeptide.

6. The nucleic acid of claim 1, wherein said high stringency conditions comprise hybridization in 2X SSC at 40°C.

7. A substantially pure human nucleic acid, wherein the sequence of said nucleic acid is at least 75% identical to the corresponding region of at least 50 contiguous base pairs of the nucleic acid of SEQ ID NO:1.

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8. A substantially pure human nucleic acid, wherein the sequence of said nucleic acid is at least 35% identical to the corresponding region of at least 50 contiguous base pairs of the nucleic acid of SEQ ID NO:1.

5

9. A kit for the analysis of a human methionine synthase nucleic acid, said kit comprising a nucleic acid probe useful for detecting in the nucleic acids of a human a mutation or polymorphism in said methionine synthase nucleic acid, wherein said mutation or polymorphism is selected from the group consisting of D919G, H920D, and

10   ΔIle881.

10. The kit of claim 9, wherein said probe comprises at least 40 nucleotides that hybridizes at high stringency to a sequence found within the nucleic acid of SEQ ID NO:1.

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                    GenCore version 5.1.7
           Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    March  6, 2006, 14:48:16 ; Search time 19267 Seconds
                              (without alignments)
                              11562.230 Million cell updates/sec

Title:           US-10-607-712-1
Perfect score:   3919
Sequence:        1 ggtcacctgtggagagcacg........ctcaaggaaatacaacctag 3919

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5883141 seqs, 2842172653 residues

Total number of hits satisfying chosen parameters:      11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                  1: gb_ba:*
                  2: gb_in:*
                  3: gb_env:*
                  4: gb_om:*
                  5: gb_ov:*
                  6: gb_pat:*
                  7: gb_ph:*
                  8: gb_pr:*
                  9: gb_ro:*
                 10: gb_sts:*
                 11: gb_sy:*
                 12: gb_un:*
                 13: gb_vi:*
                 14: gb_htg:*
                 15: gb_pl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	3919	100.0	3919	6	AR482278	AR482278 Sequence
2	3894.4	99.4	3917	8	HSU71285	U71285 Human 5-met
3	3884.8	99.1	7122	6	AR144957	AR144957 Sequence
4	3884.8	99.1	7122	6	AR367907	AR367907 Sequence
5	3884.8	99.1	7122	6	AX050442	AX050442 Sequence
6	3884.8	99.1	7122	8	AX069340	AX069340 Sequence
7	3884.8	99.1	7122	6	HSU75743	U75743 Human methi
8	3883.2	99.1	7224	6	AR367908	AR367908 Sequence
9	3883.2	99.1	7224	8	AX069342	AX069342 Sequence
10	3883.2	99.1	7224	8	HSU73338	U73338 Human methi
11	3876.2	98.9	7224	6	AR300095	AR300095 Sequence
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15	3785.2	96.6	3798	6	AX930571	AX930571 Sequence
16	3179.6	81.1	3832	4	DQ084519	DQ084519 Bos tauru
17	3069.4	78.3	4498	9	AF034214	AF034214 Rattus no
18	2417	61.7	5168	5	AJ720857	AJ720857 Gallus ga

19	2380.2	60.7	5240	8	HSM807075	BX641132 Homo sapi
20	2003.4	51.1	4537	5	BC045477	BC045477 Danio rer
21	2003.4	51.1	4570	5	AF506733	AF506733 Danio rer
22	1015.6	25.9	110000	14	CR954203_07	Continuation (8 of
23	986.2	25.2	110000	14	CT005246_0	CT005246 Leishmani
24	928.8	23.7	10099	1	AB011599	AB011599 Leptospir
25	926.8	23.6	3780	6	AX930575	AX930575 Sequence
26	926.8	23.6	11311	1	AE008131	AE008131 Agrobacte
27	926.8	23.6	12416	1	AE009165	AE009165 Agrobacte
28	926.8	23.6	43461	2	CER03D7	Z46828 Caenorhabdi
29	925.6	23.6	110000	1	AE016824_0	AE016824 Leptospir
30	915	23.3	110000	1	CP000075_42	Continuation (43 o
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35	903.4	23.1	110000	1	BA000040_15	Continuation (16 o
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41	896.8	22.9	3771	6	AY509252	AY509252 Sinorhizo
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43	895	22.8	304742	1	AE016770	AE016770 Escherich
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45	894	22.8	300620	1	AE016782	AE016782 Pseudomon

ALIGNMENTS

RESULT 1
AR482278
LOCUS   AR482278   3919 bp   DNA   linear   PAT 14-MAY-2004
DEFINITION Sequence 1 from patent US 6703197.
ACCESSION   AR482278
VERSION   AR482278.1 GI:47244567
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 3919)
  AUTHORS   Gravel,R.A., Rozen,R., LeClerc,D., Goyette,P. and Campeau,E.
  TITLE   Human methionine synthase: cloning, and methods for evaluating risk
            of neural tube defects, cardiovascular disease, and cancer
  JOURNAL   Patent: US 6703197-A 1 09-MAR-2004;
            Martinex R&D, Inc.; Montreal;
            CAX;
FEATURES   Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match   100.0%; Score 3919; DB 6; Length 3919;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 3919; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 GGTCACCTGTGGAGAGCACGCAGTCTTCTCTGCGCCGCCCCTCTGCGCCAAGGAGAGACTCGAC 60
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Db          1 GGTCACCTGTGGAGAGCACGCAGTCTTCTCTGCGCCGCCCCTCTGCGCCAAGGAGAGACTCGAC 60

Qy         61 AACATGTCACCCGCGCTCCAAGACCGTGCGCAACCCGAAGGTCTGAAGAAAACCCTGCGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTCGAGATGGGATGGGGGACC 180
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Qy        181 ATGATCCAGCGGGAGAGCTAAACGAAGAAGAACACTTCCGAGACATTTAAAGATCAT 240
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Qy   361 AGCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATG 420
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Qy   721 CGGCCTATCTTATTCAGGGACGATCGTGATAAAGTGGGCGGACTCTTTCCGGACAG 780
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Db   781 ACAGGAGAGGGATTTGTCATCAGCGTGTCTGTCTCATGGAGAAGCCACTCTGATTAAAT 840

Qy   841 TGTGCTTTGGGTGCAGTGAGATGAGACCTTTTATTGAAATAATAATGGAAAATGTACAACA 900
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Qy   901 GCCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAA 960
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Db   901 GCCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAA 960

Qy   961 ACGCCCTTCTATGATGATGCCAAGCACCTAAAGATTTTGCTGTATGGCTTGGTGCAATATA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1021 GTTGCAGGATGATGCTGTGGGTCAACACCAGTACACCACCTTGTGAAGCTGTGAAA 1080
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Db  1021 GTTGCAGGATGATGCTGTGGGTCAACACCAGTACACCACCTTGTGAAGCTGTGAAA 1080

Qy  1081 AATTGTAAGCCTAGAGTTTGCTAAACTGCAGGAAACTATCATCATGCGAGGAACTATGGAGAGCGCTTG 1140
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Qy  1141 CTAGAGCCCTTCAGGATTGGACCGTACACCAGTACACCACCTTGTTAACATTGTAACTGTCTCGGT 1200
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Qy  1201 GTTGCAGGATCAAGGAAGTTTGCTAAACTATCATCATGGCAGGAAACTATGAAGAAGCCTTG 1260
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Qy  1261 TGTGTTGCCAAAGTGCAGTGAAATGGAGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGAT 1320
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Db  1321 GGATGCGCTAGATGGTTCCAAGTGCAATGACCACCAGATTTTTGCAACTTAATTGCTTCCGAGCCA 1380
                                                                                
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Qy  1441 TTAAAGTGCTGCCAAGGAAGTGCATTGCATTGCATTGTCAATAGCATTAGTGTGAAGGAAGGAGAGGAC 1500
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Qy  1561 TTTGATGAAGAAGACAGGCCAACAGCAACACAAAATCAGAGTGTGCACCCGGGCC 1620
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Qy  1621 TACCATCTGTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAAT 1680
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Qy  1981 CCTGAGGCCACTGAGAGTCTTCTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAA 2040
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Qy  2041 GTCATTCAGACTGATGAGTGGAGAAATGGCCTGTGAAGAACGCCTTGAGTATGCCCTT 2100
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Qy  2221 GGTGATCTTTTGGAGCTGGCCACCTTCTACCTCAGGTTATAAAGTCAGCCCGGGGTT 2280
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Qy  2281 ATGAAGAAGGCTGTTGGCCACCTTCATGGAAAAAGAGAAGAGAAGAACCAGA 2340
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Qy  2341 GTGCTTAACGGCACAGTAGAAGAGAGAGAGAAGAACATCGTGCTGCCACT 2400
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Db  3841 TTGGGATATGATACAGACTAACTTTTTTTTTTTTTTGCCTTTTATCTTGATGATCC 3900

Qy  3901 TCAAGGAAATACAACCTAG 3919
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Db  3901 TCAAGGAAATACAACCTAG 3919
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RESULT 2
HSU71285
LOCUS   HSU71285   3917 bp   mRNA   linear   PRI 03-APR-1997
DEFINITION Human 5-methyltetrahydrofolate-homocysteine methyltransferase mRNA,
            complete cds.
ACCESSION   U71285
VERSION   U71285.1 GI:1923220
KEYWORDS   vitamin B12; cobalamin binding site; methionine synthase.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 3917)
  AUTHORS   Leclerc,D., Campeau,E., Goyette,P., Adjalla,C.E., Christensen,B.,
            Ross,M., Eydoux,P., Rosenblatt,D.S., Rozen,R. and Gravel,R.A.
  TITLE   Human methionine synthase: cDNA cloning and identification of
            mutations in patients of the cblG complementation group of
            folate/cobalamin disorders
  JOURNAL   Hum. Mol. Genet. 5 (12), 1867-1874 (1996)
   PUBMED   8968737
REFERENCE   2 (bases 1 to 3917)
  AUTHORS   Leclerc,D.
  TITLE   Direct Submission
  JOURNAL   Submitted (19-SEP-1996) Human Genetics, McGill University, Montreal
            Children's Hospital - Research Institute, Place Toulon, Room 222,
            4060 Ste-Catherine West, Montreal H3Z 2Z3, Canada
COMMENT   On Apr 3, 1997 this sequence version replaced gi:1731672.
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ORIGIN

Query Match         99.4%;    Score 3894.4;    DB 8;    Length 3917;
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Matches 3910;   Conservative 0;   Mismatches 0;   Indels 2;   Gaps 1;
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Qy  2762 ATCTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAAGATATTAGACAGGACC 2821
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Qy  2822 ATTATGAGTCTTCTCAAGGAGGAGAGAGATACTACCCTTAAGTCAAGTCAAGCCAGAAAAAGTGGTT 2881
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Qy  2882 TCCAAATGATTGGCTGTCTGAACCTCACCCAGTGAAGCCTTCACCCAGTGAAGCCCAGG 2941
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2942 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGTGACTACATTGACTGGAAGCCTTTCTTTG 3001
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Db  2942 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGTGACTACATTGACTGGAAGCCTTTCTTTG 3001

Qy  3002 ATGTCTGGCAGCTCCCGGGGCAAGTGACCTACCCCAAGATATTTAACGACA 3061
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Qy  3062 AAACAGTAGGTGGAGAGGCCAGGAAGTTCACGATGATGCCCACAATATGCTGAACACAC 3121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3062 AAACAGTAGGTGGAGAGGCCAGGAAGTTCACGATGATGCCCACAATATGCTGAACACAC 3121

Qy  3122 TGATTAGTCAAAAGAAACTCCGGGCCGGGTGTGGTGGGTGGTTCTCGGCCAGCACAGAGTA 3181
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Qy  3182 TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGCCCCAGGCTGCAGAGGCCCATAG 3241
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Db  3182 TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGCCCCAGGCTGCAGAGGCCCATAG 3241

Qy  3242 CCACTTTCTATGGGTTAAGGCAACAGGCTCTGCGCACGGAGCCATACT 3301
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Qy  3302 ACTGCCCTCTCAGACTTCATCGCTCTGCATCCGGACTTCTGGGCCTGT 3361
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Qy  3362 TTGCCGTTGCCTGCTTTGGGTAGAAGCAACAGGCCTGAGCGAGGATGAGATGGTGACG 3421
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Db  3362 TTGCCGTTGCCTGCTTTGGGTAGAAGCAACAGGCCTGAGCGAGGATGAGATGGTGACG 3421

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Qy  3542 TCGCAGACCTGCCGGAAGGTTGCGGTACAAGGGCATCCGCCGGCTTCCTGGCTACCCCGGCC 3601
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Qy  3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACTCGCTTCAGCAGTTCTCACT 3721
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Qy    482 GGTTTGTTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG  541
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Db    705 GGTTTGTTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG  764

Qy    542 AAAGGCCGGATTATAGGAACATCATCATTGATGAGCTTGTTGTGAAGCATACCAAGAGCAGG  601
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Qy    602 CCAAAGGACTTCTGGATGGCGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG  661
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Db    825 CCAAAGGACTTCTGGATGGCGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG  884

Qy    662 CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC  721
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Qy    722 GGCCTATCTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGCCGGACTCTTTCCGGACAGA  781
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Qy    782 CAGGAGAGGATTTGTCATCAGCGTGTCTCATCGGGAACCACCTCTGCATTGGATTAAATT  841
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Db   1005 CAGGAGAGGATTTGTCATCAGCGTGTCTCATCGGGAACCACCTCTGCATTGGATTAAATT 1064

Qy    842 GTGCTTTGGGTGCAGCTGAAGTGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG  901
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Db   1065 GTGCTTTGGGTGCAGCTGAAGTGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG 1124

Qy    902 CCTATGTCCTCTGTTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAA  961
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Db   1125 CCTATGTCCTCTGTTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAA 1184

Qy    962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAG 1021
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Qy   1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGTGTGAAA 1081
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Db   1245 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGTGTGAAA 1304

Qy   1082 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCTGTC 1141
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Db   1305 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCTGTC 1364

Qy   1142 TAGAGCCCTTCAGGATTGACCGTACACCAACTTGTTAACATTGGAGCGCGCTAATG 1201
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Db   1365 TAGAGCCCTTCAGGATTGACCGTACACCAACTTGTTAACATTGGAGCGCGCTAATG 1424

Qy   1202 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGGCAGGAAACTATGGAAGAGCCTTGT 1261
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Qy   1322 GCATGCTAGATGGTCAAGTGCAATGACCTGACTCCTCCAATTTGCTGTGATTGAAGCTGGGT 1381
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Db   1545 GCATGCTAGATGGTCAAGTGCAATGACCTGACTCCTCCAATTTGCTGTGATTGAAGCTGGGT 1604

Qy   1382 ACATCGCAAAGGTACCTTTGTGCATCGACTGACTCCTCCAATTTAGCA 1441
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Db   1605 ACATCGCAAAGGTACCTTTGTGCATCGACTGACTCCTCCAATTTAGCA 1664

Qy   1442 TAAAGTGCTGCCAAGGAAGGAGTGCATTGTCAATAGCATTAGTCTGAAGGAGGAGGAGACG 1501
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Db   1665 TAAAGTGCTGCCAAGGAAGGAGTGCATTGTCAATAGCATTAGTCTGAAGGAGGAGGAGACG 1724

Qy   1502 ACTTCTTGGAGAAGGCCCAGGAAGAGTTAAAAAGTATGGAGCGTGCTATGGTTGGTCATGGGCTT 1561
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Db   1725 ACTTCTTGGAGAAGGCCCAGGAAGAGTTAAAAAGTATGGAGCGTGCTATGGTTGGTCATGGGCTT 1784
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RESULT 3
AR144957

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LOCUS       AR144957                7122 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6210950.
ACCESSION   AR144957
VERSION     AR144957.1  GI:15106824
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7122)
  AUTHORS   Johnson,W.G. and Stenroos,E.Scott.
  TITLE     Methods for diagnosing, preventing, and treating developmental
            disorders due to a combination of genetic and environmental factors
  JOURNAL   Patent: US 6210950-A 2 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1..7122
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match       99.1%;  Score 3884.8;  DB 6;   Length 7122;
Best Local Similarity  99.6%;
Matches 3904;  Conservative   0;  Mismatches  12;  Indels   2;  Gaps   1;

Qy      2 GTCACCCTGTGGAGAGCACGTCTTCTCTGCGCCCCTCTGCGCAAGGAGGAGACTCGACA   61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 GTCACCCTGTGGAGAGCACGTCTTCTCTGCGCCCCTCTGCGCAAGGAGGAGACTCGACA  284

Qy     62 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAACCCTGCGGG  121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAACCCTGCGGG  344

Qy    122 ATGAGATCAATGCCATTCGCAGAAGAGGATTATGGTGCTGAGGATGGGATGGGGACCA  181
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Db    345 ATGAGATCAATGCCATTCGCAGAAGAGGATTATGGTGCTGAGGATGGGATGGGGACCA  404

Qy    182 TGATCCAGCGGGAGAAGGCTAAACGAAGACACTTCCGAGGTCAGGAGAATTAAAGATCATG  241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 TGATCCAGCGGGAGAAGGCTAAACGAAGACACTTCCGAGGTCAGGAGAATTAAAGATCATG  464

Qy    242 CCAGGCCGCTGAAAGGCTAAACGAAGACACTTTAAGTATAACTCAGCCTGATGTCATTTACC  301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 CCAGGCCGCTGAAAGGCTAAACGAAGACACTTTAAGTATAACTCAGCCTGATGTCATTTACC  524

Qy    302 AAATCCATAAGGAATACTTGCTGCTGGGCAGATCATTGAAACAAATACTTTTAGCA  361
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Db    525 AAATCCATAAGGAATACTTGCTGCTGGGCAGATCATTGAAACAAATACTTTTAGCA  584

Qy    362 GCACTAGTATTGCCCAAGTCGACTATGCCGATGCCTTGAACACTTGGCCTACCCGATGAACATGT  421
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Db    585 GCACTAGTATTGCCCAAGTCGACTATGCCGATGCCTTGAACACTTGGCCTACCCGATGAACATGT  644

Qy    422 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGAAGGTAACTCTCCAGACAGGAATTAAGA  481
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Db    645 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGAAGGTAACTCTCCAGACAGGAATTAAGA  704
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Qy   1562  TTGATGAAGAAGGACAGGCAACAGAAACAGACACAAAAATCAGAGTGTGACCCGGGCCT  1621
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Db   1785  TTGATGAAGAAGGACAGGCAACAGAAACAGACACAAAAATCAGAGTGTGACCCGGGCCT  1844

Qy   1622  ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAATA  1681
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Db   1845  ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAATA  1904

Qy   1682  TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTTATCCATG  1741
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Db   1905  TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTTATCCATG  1964

Qy   1742  CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTTCCAACT  1801
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Db   1965  CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTTCCAACT  2024

Qy   1802  TGTCCTTCCTCCGGAATGGAAGCCATTCGAGAGCAATGCAATGCATGGGGTTTTCCTTT  1861
           |||||| | |  ||||||||||||||||||||||||||||||||||||||||||||||
Db   2025  TGTCCTTCTCTCCCTCCGGAATGGAAGCCATTCGAGAGCAATGCAATGCATGGGGTTTTCCTTT  2084

Qy   1862  ACCATGCAATCAAGTCTCGGCATGGACATGACTGGCATGGTGAATGCTGGAAACCTCCCTGTGT  1921
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Db   2085  ACCATGCAATCAAGTCTCGGCATGGACATGACTGGCATGGTGAATGCTGGAAACCTCCCTGTGT  2144

Qy   1922  ATGATGATATCATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGTGAATAAAGACC  1981
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Db   2145  ATGATGATATCATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGTGAATAAAGACC  2204

Qy   1982  CTGAGGCCACTCAGAAGCTCTTACGTTGAGAGTGGAGAAAATGGCCCTGTCGAAGAACGCCTTG  2041
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Db   2205  CTGAGGCCACTCAGAAGCTCTTACGTTGAGAGTGGAGAAAATGGCCCTGTCGAAGAACGCCTTG  2264

Qy   2042  TCATTCAGACTGATGAGTGGAGAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA  2101
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2265  TCATTCAGACTGATGAGTGGAGAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA  2324

Qy   2102  TGAAGGGCATTGAAATACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA  2161
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Db   2325  TGAAGGGCATTGAAATACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA  2384

Qy   2162  AATATCCCCGGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAATGAAAATTGTTG  2221
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Db   2385  AATATCCCCGGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAATGAAAATTGTTG  2444

Qy   2222  GTGATCTTTTGGAGCTGGAAAAATGTTCTTACCTCAGGTTATAAAGTCAGCCCGGGTTA  2281
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Db   2445  GTGATCTTTTGGAGCTGGAAAAATGTTCTTACCTCAGGTTATAAAGTCAGCCCGGGTTA  2504

Qy   2282  TGAAGAAGGCTGTTGCACCACCCTTATCCCTTTCATGGAAAAAAGAAGAGAAACCAGAG  2341
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Db   2505  TGAAGAAGGCTGTTGCACCACCCTTATCCCTTTCATGGAAAAAAGAAGAGAAACCAGAG  2564

Qy   2342  TGCTTAACGGCACAGTAGAGAAGAAGAGACATAGGTGGAGTCCATTGATACTGATAAGTGCTC  2401
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Db   2565  TGCTTAACGGCACAGTAGAGAAGAAGAGACATAGGTGGAGTCCATTGATACTGATAAGTGCTC  2624

Qy   2402  TTAAAGCCAGCGTCACGCACGACACGTCCAAGGACAAGACATAGTTGGAGTCCTGCTGCAATA  2461
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Db   2625  TTAAAGCCAGCGTCACGCACGACACGTCCAAGGACAAGACATAGTTGGAGTCCTGCTGCAATA  2684

Qy   2462  ATTTCCGAGTTATTGATTTAGGAGTCCATGTGATTGATAAGTACTGAAAGCTGCTC  2521
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Db   2685  ATTTCCGAGTTATTGATTTAGGAGTCCATGTGATTGATAAGTACTGAAAGCTGCTC  2744

Qy   2522  TTGACCACACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCGGATGAAA  2581
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Db   2745  TTGACCACACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCGGATGAAA  2804

Qy   2582  TGATTTTTGTTGCCAAGGAGTTAGCTATTAAGGAGATTCCATTGTTGATTGGAG  2641
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Db   2805  TGATTTTTGTTGCCAAGGAGTTAGCTATTAAGGAGATTCCATTGTTGATTGGAG  2864

Qy   2642  GAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGTCCGAGATACAGTGCACCTG  2701


Qy   2865  GAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGTCCGAGATACAGTGCACCTG  2924
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Db   2865  GAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGTCCGAGATACAGTGCACCTG  2924

Qy   2702  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTTCCCAGCTGTTAGATGAAA  2761
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Db   2702  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTTCCCAGCTGTTAGATGAAA  2761

Qy   2925  ATCTAAAGGATGAATACTTTGAGGAAATCATCGGAAGAATATGAAGATATTAGACAGGACC  2984
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Db   2925  ATCTAAAGGATGAATACTTTGAGGAAATCATCGGAAGAATATGAAGATATTAGACAGGACC  2984

Qy   2762  ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAAGTGGTT  2821
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Db   2762  ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAAGTGGTT  2821

Qy   2985  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAGCCACCACGTTTATTGGGACCCAGG  3044
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Db   3045  ATGTCTGCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCAAAGATATTTAACGACA  3104

Qy   2882  AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGATGATGCCCACAACATGCTGAACACAC  2941
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Qy   2942  CTGAGGCCACTCAGAAGCTCGGCATGGACATGACTGGCATGGTGGTTCTCGGCCTGCTGCCCAGGAGTCA  3001
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Qy   3165  TCCAAGACACATTCACCTGTAGCGTGAGAGGCTGCTGTCGGCCTGCCCAGCACAGAGTA  3224
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Db   3165  TCCAAGACACATTCACCTGTAGCGTGAGAGGCTGCTGTCGGCCTGCCCAGCACAGAGTA  3224

Qy   3002  TCCAAGACGCATTCACCTGTAGCGTGAGAGGCTGCTGTCGGCCTGCCCAGCACAGAGTA  3061
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Db   3002  TCCAAGACGCATTCACCTGTAGCGTGAGAGGCTGCTGTCGGCCTGCCCAGCACAGAGTA  3061

Qy   3225  AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGATGATGCCCACAACATGCTGAACACAC  3284
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Db   3225  AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGATGATGCCCACAACATGCTGAACACAC  3284

Qy   3062  AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGATGATGCCCACAACATGCTGAACACAC  3121
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Db   3062  AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGATGATGCCCACAACATGCTGAACACAC  3121

Qy   3285  TGATTAGTCAAAAGAAACTCACCTGTTAAGGCAACAGCGTGAGAAGCACTCGCCAGCACTACT  3344
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Db   3285  TGATTAGTCAAAAGAAACTCACCTGTTAAGGCAACAGCGTGAGAAGCACTCGCCAGCACTACT  3344

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Qy   3525  ACTGCCTCTCAGACTTCATCGCTTCATTCTCAGACTTCATTCTCGGCCTCGTGACTACTTCGGGCCTCGT  3584
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Qy   3705  AGCTCCATGAAGAGTTCGCGGAAGTTGCGTGCAGGCCGCCATCCGGGGCATCCCGGCCGCCGAGACTGGACG  3764
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Qy   3722  TCTCCAATTTGAAGTCCAAATATTTTGTCGTGTGGGGAGAATTTCGTGTGGGGAGAATCAGGTTGAGG  3781
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RESULT 4
AR367907
LOCUS       AR367907        7122 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 4 from patent US 6376210.
ACCESSION   AR367907
VERSION     AR367907.1  GI:34601378
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7122)
  AUTHORS   Yuan,C.-S.
  TITLE     Methods and compositions for assaying analytes
  JOURNAL   Patent: US 6376210-A 4 23-APR-2002;
            General Atomics; San Diego, CA
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match         99.1%;  Score 3884.8;  DB 6;  Length 7122;
Best Local Similarity   99.6%;  Pred. No. 0;
Matches 3904;  Conservative 0;  Mismatches 12;  Indels 2;  Gaps 1;
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Qy     2 GTCACCTGTGGAGGAGCAGCACGTCTTCTTCTGCGCCCCTGCGCCAAGGAGGAGGACTCGACA   61
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Db   225 GTCACCTGTGGAGGAGCACGTCTTCTTCTGCGCCCCTGCGCCAAGGAGGAGGACTCGACA    284
Qy    62 ACATGTCACCCGGCTCCAAGACCTGTCCAACCTGTCGAAGTCTGAAGAAAAACCCTGCGGG    121
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Db   285 ACATGTCACCCGGCTCCAAGACCTGTCCAACCTGTCGAAGTCTGAAGAAAAACCCTGCGGG    344
Qy   122 ATGAGATCAATGCCATTCTGCAGAAGGATTATGTGCTGGATGGGDATGGGGACCA    181
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Db   345 ATGAGATCAATGCCATTCTGCAGAAGGATTATGTGCTGGATGGGDATGGGGGGGACCA    404
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Db   405 TGATCCAGGCGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAAGTTAAAGATCATG    464
Qy   242 CCAGGCCGCCGAAAGGCAACAATGACATTTAAGTATAAACTCAGCCTGATGTCATTACC    301
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Db   465 CCAGGCCGCCGAAAGGCAACAATGACATTTAAGTATAAACTCAGCCTGATGTCATTTACC    524
Qy   302 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA    361
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Qy   362 GCACTAGTATTGCCCAAGCTGCCGAGAAAAGTGCCGAGGAGTAACTCTCCAGACAGGTT    421
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Qy   422 GCTCTGCGAGAGTGGCCAGAAAAGTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGA    481
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Qy   482 GGTTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG    541
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Qy   722 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA    781
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Qy   782 CAGGAGAGGGATTTGTCATCAGGTGTCTCATGGAGACCACTCTGCATTGGATTAAATT    841
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Qy   842 GTGCTTTGGGTGGTCAGCTGAGATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG    901
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Db  1125 CCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA   1184
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Qy  1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAA   1081
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Qy  1142 TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCTGTAATG   1201
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Qy  1202 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGAAGAGCATATGAAGAAGCCTTGT   1261
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Qy  1322 GCATGCTAGATGGTCCAAGTGCAATGACCTGAGACTTTCGAACTTAATTGCTTCCGAGCCAG   1381
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Qy  1682 TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTATCCATG 1741
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Db  1905 TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTATCCATG 1964

Qy  1742 CAACAAAAGTCATTAAAGAACATTACCTGGAGCCGAATAAGTGAGGTCTTTCCAACT 1801
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Db  1965 CAACAAAAGTCATTAAAGAACATTACCTGGAGCCGAATAAGTGAGGTCTTTCCAACT 2024

Qy  1802 TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTT 1861
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Qy  2582 GAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 2641
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Db  4123 CAAGGAAATACAACCTAG 4140
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RESULT 5
AX050442

LOCUS   AX050442   7122 bp   DNA   linear   PAT 12-JAN-2001
DEFINITION Sequence 2 from Patent WO0071754.
ACCESSION   AX050442
VERSION   AX050442.1 GI:12226649
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS   Johnson,W.G. and Stenroos,E.S.
TITLE   Methods for diagnosing, preventing, and treating developmental
            disorders due to a combination of genetic and environmental factors
JOURNAL   Patent: WO 0071754-A 2 30-NOV-2000;
            University of Medicine and Dentistry of New Jersey (US)
FEATURES   Location/Qualifiers
source   1..7122
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN

Query Match   99.1%; Score 3884.8; DB 6; Length 7122;
Best Local Similarity   99.6%; Pred. No. 0;
Matches 3904; Conservative   0; Mismatches 12; Indels   2; Gaps   1;

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Db   225 GTCACCCTGTGGAGGACGACGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACA 284

Qy    62 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGGAGGTCTGAAGAAAACCCTGCGGG 121
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Db   285 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGGAGGTCTGAAGAAAACCCTGCGGG 344

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Qy   242 CCAGGCCGCTGAAAGGCAACAATGACAATTGCTCGGCTGCGCTGGGGCAGATATCATTTTAGCA 301
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Qy   962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAG 1021
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Qy  1562  TTGATGAAGAAGGACAGGCAACAGAACAGACACAACAAAATCAGAGTGTGCACCCGGCCT  1621
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Db  1905  TCCTAACCATTGGGACTGGAATGGAGAACACAACTTGTATGCCATTAATTTATCCATG  1964

Qy  1742  CAACAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTTCCAACT  1801
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Db  3045  ATTATGAGTCTCTCAAGGAGGAGAGAGAGATACTTAACCCTTAAGTCAAGCCAGAAAAAGTGGTT 3104

Qy  2882  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAGACCTCACCCAGTTTATTGGACCCAGG 2941
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RESULT 6
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DEFINITION  Sequence 4 from Patent WO0102600.
ACCESSION   AX069340
VERSION     AX069340.1  GI:12579203
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Yuan,C.S.
  TITLE     Detection of analytes using attenuated enzymes
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Qy   782 CAGGAGAGGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACCTCGCATTGGATTAAATT 841
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                     ORIGIN

                     Query Match   99.1%;   Score 3884.8;   DB 8;   Length 7122;
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Qy   2   GTCACCTGTGGAGGACACGTCTTCTCTGCGCCGCCCTCGCCAAGGAGGAGACTCGACA   61
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HSU75743
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DEFINITION   Human methionine synthase mRNA, complete cds.
ACCESSION   U75743
VERSION   U75743.1 GI:1763339
KEYWORDS   .
SOURCE   Homo sapiens (human)
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REFERENCE   1 (bases 1 to 7122)
  AUTHORS   Li,Y.N., Gulati,S., Baker,P.J., Brody,L.C., Banerjee,R. and
              Kruger,W.D.
  TITLE   Cloning, mapping, and RNA analysis of the human methionine synthase
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  JOURNAL   Hum. Mol. Genet. (1996) In press
REFERENCE   2 (bases 1 to 7122)
  AUTHORS   Li,Y.N., Gulati,S., Baker,P.J., Brody,L.C., Banerjee,R. and
              Kruger,W.D.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-OCT-1996) Population Science, Fox Chase Cancer
              Center, 7701 Burholme Ave., Philadelphia, PA 19111, USA
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Qy   1562 TTGATGAAGAAGGACAGGCAGCCAACAGAGAAACAGAGAAACAGACACAACAAAAATCAGAGTGTGCACCCGGGGGCCT 1621
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Db   3585 TTGCCGGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCATGAGAGATGGTGACG 3644

Qy   3422 ACTACAGCAGCATCATGGTCAAGGCGCTCAGGGCATCCGCCGGCTCCTGGCTACCCCAGCC 3481
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Db   3645 ACTACAGCAGCATCATGGTCAAGGCGCTCAGGGCATCCGCCGGCTCCTGGCTACCCCAGCC 3704

Qy   3482 AGCTCCATGAAAGAAGTTCGCCGGAAGAGTTGGGCCTACTGTGGGCAGCTGGACG 3541
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Db   3705 AGCTCCATGAAAGAAGTTCGCCGGAAGAGTTGGGCCTACTGTGGGCAGCTGGACG 3764

Qy   3542 TCGCAGACCTGCGAAGGTTGCGCGGTACAAGGGCATCCGGCTCCTGGCTACCCCAGCC 3601
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Db   3765 TCGCAGACCTGCGAAGGTTGCGCGGTACAAGGGCATCCGGCTCCTGGCTACCCCAGCC 3824

Qy   3602 AGCCCGACCGACCACACCGAGAAGCTCACCATGTGCAGATCGCAGACAGTCAGTCTACAG 3661
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Db   3825 AGCCCGACCGACCACACCGAGAAGCTCACCATGTGCAGATCGCAGACAGTCAGTCTACAG 3884

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGCACATGGCTCTCAGCAGTCTCACT 3721
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Db   3885 GCATTAGGTTAACAGAATCATTAGCAATGCACATGGCTCTCAGCAGTCTCACT 3944

Qy   3722 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGGAAGATTTCCAAGGATCAGGTTGAGG 3781
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Db   3945 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGGAAGATTTCCAAGGATCAGGTTGAGG 4004
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Db   3782 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATT 3841

Qy   4005 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATT 4064

Qy   3842 TGGGATATGATACGACTAACTTTTTTTTGGCCTTTTTATCTTGATGATCCT 3901
          |||||||||||||||||||||||||||||||      ||||| ||||||||||||||
Db   4065 TGGGATATGATACAGACTAAC--TTTTTTTTTTTGGCCTTTTTATTCTTGATGATCCT 4122

Qy   3902 CAAGGAAATACAACCTAG 3919
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Db   4123 CAAGGAAATACAACCTAG 4140
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RESULT 8
AR367908
LOCUS   AR367908   7224 bp   DNA   linear   PAT 12-SEP-2003
DEFINITION   Sequence 6 from patent US 6376210.
ACCESSION   AR367908
VERSION   AR367908.1 GI:34601379
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 7224)
  AUTHORS   Yuan,C.-S.
  TITLE   Methods and compositions for assaying analytes
  JOURNAL   Patent: US 6376210-A 6 23-APR-2002;
                General Atomics; San Diego, CA
FEATURES   Location/Qualifiers
     source   1..7224
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match   99.1%; Score 3883.2; DB 6; Length 7224;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3903; Conservative   0; Mismatches   13; Indels   2; Gaps   1;

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Qy      2 GTCACCTGTGGAGAGCACGTCTTCTCGCCGCCCTCTGCGCAAGGAGGAGGAGACTCGACA 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    333 GTCACCTGTGGAGAGCACGTCTTCTCGCCGCCCTCTGCGCAAGGAGGAGGAGACTCGACA 392

Qy     62 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCGAAGAAACCCTGCGGG 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCGAAGAAACCCTGCGGG 452

Qy    122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGGATGGGGACCA 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGGATGGGGACCA 512

Qy    182 TGATCCAGCGGGAGAAGCTAAACGAAGGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513 TGATCCAGCGGGAGAAGCTAAACGAAGGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 572

Qy    242 CCAGGCCGCTGAAAGGCAACAATGACATTTAGTATAACTCAGCCTGATGTCATTACC 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    573 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTACC 632

Qy    302 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA 361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    633 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA 692

Qy    362 GCACTAGTATTGCCCAAGCTGACTATGGCCTACAGCTTGGCCTTCGGCCTACCGGATGAACATGT 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693 GCACTAGTATTGCCCAAGCTGACTATGGCCTACAGCTTGGCCTTCGGCCTACCGGATGAACATGT 752

Qy    422 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGAAAGCTAACTCTCCAGACAGGAATTAAGA 481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGAAAGCTAACTCTCCAGACAGGAATTAAGA 812

Qy    482 GGTTTGTGGCGGAGGGCTCTGGGTCTGGTGGCTGCAATAAGACACTTCTCGTGTCCCATCGTGTG 541
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Right-hand alignment blocks:

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Qy  1622 ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATA 1681
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Db  1953 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATATTTTTGACCCTAATA 2012

Qy  1682 TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATG 1741
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Db  2013 TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATG 2072

Qy  1742 CAACAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 1801
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2073 CAACAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 2132

Qy  1802 TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAGAAGCAATGCATGGGGTTTCTTT 1861
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2133 TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAGAAGCAATGCATGGGGTTTCTTT 2192

Qy  1862 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGGAAATGCTGGAAACCTCCCTGT 1921
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2193 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGGAAATGCTGGAAACCTCCCTGT 2252

Qy  1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 1981
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2253 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 2312

Qy  1982 CTGAGGCCACTGACTGAGAGCTCTTACGTACGTTGGTGACTATGATGAAAG 2041
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2313 CTGAGGCCACTGACTGAGAGCTCTTACGTACGTTGGTGACTATGATGAAAG 2372

Qy  2042 TCATTCAGACTGATGAGTGGAGAAATGGCCCCTGTCGAAGAACGCCTTGAGTATGCCCCTG 2101
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2373 TCATTCAGACTGATGAGTGGAGAAATGGCCCCTGTCGAAGAACGCCTTGAGTATGCCCCTG 2432

Qy  2102 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGCCAGGTTAAACCAAAAAA 2161
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2433 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGCCAGGTTAAACCAAAAAA 2492

Qy  2162 AATATCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAATGAAAATTGTTG 2221
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Db  2493 AATATCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAATGAAAATTGTTG 2552

Qy  2222 GTGATCTTTTTGGAGCTGGAAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2553 GTGATCTTTTTGGAGCTGGAAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2612

Qy  2282 TGAAGAGGCGTGTTGGCCACCTTATCCCTTCATGGAAAAAGAGAAGAAACCAGAG 2341
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2613 TGAAGAGGCGTGTTGGCCACCTTATCCCTTCATGGAAAAAGAGAAGAAACCAGAG 2672

Qy  2342 TGCTTAACGGACAGTGGCACAGTAGAGAGAGACCTTACCAGGGCACCATCGTGCTGGCCACTG 2401
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2673 TGCTTAACGGACAGTGGCACAGTAGAGAGAGACCTTACCAGGGCACCATCGTGCTGGCCACTG 2732

Qy  2402 TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGCAATA 2461
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2733 TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGCAATA 2792

Qy  2462 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGACTCGAAAGCTGCTC 2521
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2793 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGACTCGAAAGCTGCTC 2852

Qy  2522 TTGACCACAAAGCAGATATAATTGGCCGTGTCTGTCAGGACTCATCATCCCTTCCCTGGATGAAA 2581
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Db  2853 TTGACCACAAAGCAGATATAATTGGCCGTGTCTGTCAGGACTCATCATCCCTTCCCTGGATGAAA 2912

Qy  2582 TGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG 2641
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Db  2913 TGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG 2972

Qy  2642 GAGCAACCACTTCAAAAACCCACAACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 2701
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Db  2973 GAGCAACCACTTCAAAAACCCACAACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 3032
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Left-hand alignment blocks:

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Db   813 GGTTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG 872

Qy   542 AAAGGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 601
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   873 AAAGGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 932

Qy   602 CCAAAGGACTTCTGGATGCGGGGGTTGATATCTCATTGAAACTATTTTGATACTG 661
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   933 CCAAAGGACTTCTGGATGCGGGGGTTGATATCTCATTGAAACTATTTTGATACTG 992

Qy   662 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTGAGGAGAAATATGCTCCCC 721
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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1113 CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT 1172

Qy   842 GTGCTTTGGGTGCAGTGAGATGAGACCTTTATTGAAAATAATTGAAAAATGTACAACAG 901
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Db  1173 GTGCTTTGGGTGCAGTGAGATGAGACCTTTATTGAAAATAATTGAAAAATGTACAACAG 1232

Qy   902 CCTATGTCCCTGTTATCCCATGCAGTCTTCCCAACACCTTGGTGACTATGATGAAA 961
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Qy   962 CGCCTTCTATGATGGCCAAGCACCTAAAGAGATTTGCTATGGATGGCTTGGTCAATATAG 1021
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Db  1293 CGCCTTCTATGATGGCCAAGCACCTAAAGAGATTTGCTATGGATGGCTTGGTCAATATAG 1352

Qy  1022 TTGGAGGATGCGTGTGGGTCAACACCAGATCATATCAGGGGAAATTGCTGAAGCGTGTGAAAA 1081
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1082 ATTGTAAGCCTAGAGTTCCACCTGCCCACTGCTTTGAAGGACATATGTTACTGTCTGGTC 1141
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Qy  1142 TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCGCTGTAATG 1201
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Db  1473 TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCGCTGTAATG 1532

Qy  1202 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATCAGCGAGAAACTATGAGAAGAAGCCTTGT 1261
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1533 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATCAGCGAGAAACTATGAGAAGAAGCCTTGT 1592

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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1593 GTGTTGCCAAAGTCAGTGAAATGGAGCCCAGGTGTTGATGTCAACATGGATGATG 1652

Qy  1322 GCATGCTAGATGGTCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCAG 1381
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Qy  1382 ACATCCAAAGTACCTTTGTTGCATCGACTCCCAATTTTGCTGTGATGATTGCTGTGGGT 1441
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Qy  1502 ACTTCTTGGAGAGGACAGGACTGCTATGGTGCTGCTATGGTCGTCATGGCTT 1561
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1833 ACTTCTTGGAGAGGACAGGACTGCTATGGTGCTGCTATGGTCGTCATGGCTT 1892

Qy  1562 TTGATGAAGAAGGAGCAGCAGGCCAACAGACAACAGAGAAAATCAGAGTGTGCACCCGGCCT 1621
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Db  1893 TTGATGAAGAAGGAGCAGCAGGCCAACAGACAACAGAGAAAATCAGAGTGTGCACCCGGCCT 1952
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Left margin row labels (top to bottom): Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db, Qy, Db

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Db   3033 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTGTTCCCAGCTGTTAGATGAAA 3092

Qy   2762 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAATATTAGACAGGACC 2821
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Db   3093 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAATATTAGACAGGACC 3152

Qy   2822 ATTATGAGTCTCTCAAGAGAGAGAGATACTTACCCTTAAGTCAAGCCAGAGAAAAGTGTT 2881
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Db   3153 ATTATGAGTCTCTCAAGAGAGAGAGATACTTACCCTTAAGTCAAGCCAGAGAAAAGTGTT 3212

Qy   2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG 2941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3213 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG 3272

Qy   2942 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGACTACATTGACTGAAGCCTTTCTTTTG 3001
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Db   3273 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGACTACATTGACTGAAGCCTTTCTTTTG 3332

Qy   3002 ATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACA 3061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3333 ATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACA 3392

Qy   3062 AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACAC 3121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3393 AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACAC 3452

Qy   3122 TGATTAGTCAAAGAAACTCCGGGCCCGGGGTGTGGTTCTGGCCAGCACAGAGTA 3181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3182 TCCAAGACGACATTCACCTGTACGACGAGGCTGCTGGACGCTGCAGAGCCCATAG 3241
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Db   3513 TCCAAGACGACATTCACCTGTACGACGAGGCTGCTGGACGCTGCAGAGCCCATAG 3572

Qy   3242 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACT 3301
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Qy   3302 ACTGCCTCTCAGACTTCATCGCTCCCCTTGCATTCTGGCACCTCGGACTACCTGGGCCTGT 3361
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Db   3633 ACTGCCTCTCAGACTTCATCGCTCCCCTTGCATTCTGGCACCTCGGACTACCTGGGCCTGT 3692

Qy   3362 TTGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG 3421
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Db   3693 TTGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG 3752

Qy   3422 ACTACAGCAGCATCATGTCAAGGCGCTGGGGGACCCGGCTGGCAGAGGCCTTTGCAGAAG 3481
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Qy   3482 AGTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGTGACG 3541
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Db   3813 AGTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGTGACG 3872

Qy   3542 TCGGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCGGCTCCTGCTACCCCAGCC 3601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3873 TCGGCAGACCTGCGCGGCAGGTTGCGGTACAAGGGCATCCGCCGGCTCCTGCTACCCCAGCC 3932

Qy   3602 AGCCCGACCACCACCCGAGAAGCTCACCATGTGGAGACTCGCAGACATCGAGCAGTCTACAG 3661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3933 AGCCCGACCACCACCCGAGAAGCTCACCATGTGGAGACTCGCAGACATCGAGCAGTCTACAG 3992

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCGTCTCAGGCCTCTACT 3721
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Qy   3722 TCTCCAATTTGAAGTCCAAATATTTTGTCTGTGGGAAGAATTTCCAAGGATCAGGTTGAGG 3781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4113 ATTATGCATTGAGGAAGAACATATCTGTGCGGAGGTTGAGAAATGGCTTGGACCCATTT 4172

Qy   3842 TGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTTGCCTTTTTATCTTGATGATCCT 3901
          |||||||||||||||||||||||||        ||||||||||||||||||||||||||
Db   4173 TGGGATATGATACAGACTAAC--TTTTTTTTTTTTTTTTTTGCCTTTTTATCTTGATGATCCT 4230

Qy   3902 CAAGGAAATACAACCTAG 3919
          ||||||||||||||||||
Db   4231 CAAGGAAATACAACCTAG 4248
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RESULT 9
AX069342
LOCUS   AX069342   7224 bp   DNA   linear   PAT 25-JAN-2001
DEFINITION   Sequence 6 from Patent WO0102600.
ACCESSION   AX069342
VERSION   AX069342.1   GI:12579205
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yuan,C.S.
  TITLE   Detection of analytes using attenuated enzymes
  JOURNAL   Patent: WO 0102600-A 6 11-JAN-2001;
              GENERAL ATOMICS (US)
FEATURES   Location/Qualifiers
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                     /db_xref="GI:12579206"
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Query Match          99.1%;  Score 3883.2;  DB 6;  Length 7224;
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Qy   482 GGTTTGTGTCGCAGGGGCTCTCGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGG 541

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Qy   842 GTGCTTTGGGTGCAGCTGAGATGAAAATTGAAAATAATTGAAATGTTATTGGAAAATGTACAACAG 901

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Db  2733  TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA  2792

Qy  2462  ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTC  2521
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Qy  2522  TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTTCATCACTCCTTCCCTGGATGAAA  2581
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Db  2853  TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTTCATCACTCCTTCCCTGGATGAAA  2912

Qy  2582  TGATTTTTGTTGCCAAGGAAATGAGAGATTAGCTATATAAGGATTCCATTGTTGATTGGAG  2641
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Qy  2642  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  2701
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Qy  2882  TCCAAATGGATTGGCTGTCTGACCTCACCCAGTGAAGCCCAGTTTATTGGGACCCAGG  2941
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Qy  3362  TTGCCGTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG  3421
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Db  4053  TCTCCAATTGAAGTCCAAATATTTTGCGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG  4112

Qy  3782  ATTATGCATTGAGGAAGAACACATATCTGTGGCTGAGAAATGGCTTGAGACCCATTT  3841
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Qy  3902  CAAGGAAATACAACCTAG  3919
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RESULT 10
HSU73338

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LOCUS       HSU73338                7224 bp    mRNA    linear   PRI 02-JAN-1997
DEFINITION  Human methionine synthase mRNA, complete cds.
ACCESSION   U73338
VERSION     U73338.1  GI:1763268
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 7224)
  AUTHORS   Chen,L.H., Liu,M.-L., Hwang,H.-Y., Chen,L.-S., Korenberg,J. and
            Shane,B.
  TITLE     Human methionine synthase: cDNA cloning, gene localization and
            expression
  JOURNAL   J. Biol. Chem. (1996) In press
REFERENCE   2  (bases 1 to 7224)
  AUTHORS   Chen,L.H., Liu,M.-L., Hwang,H.-Y., Chen,L.-S., Korenberg,J. and
            Shane,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-OCT-1996) Nutritional Sciences, University of
            California, 117 Morgan Hall, Berkeley, CA 94720-3104, USA
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RESULT 11

AR300095

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VERSION   AR300095.1 GI:31687382
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REFERENCE   1 (bases 1 to 7224)
  AUTHORS   Stanton,V.P. Jr.
  TITLE   Folylpolyglutamate synthetase gene sequence variances having
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  JOURNAL   Patent: US 6537759-A 1 25-MAR-2003;
               Variagenics, Inc.; Cambridge, MA
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Qy   62 ACATGTCACCCGGCCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   393 ACATGTCACCCGGCCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG 452

Qy   122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGTGCTGTCGATGGGATGGGGACCA 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   453 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGTGCTGTCGATGGGATGGGGACCA 512

Qy   182 TGATCCAGCGGGAGAAGCTAAACGAACACTTCCCAGGTTCAGGAATTTAAAGATCATG 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   513 TGATCCAGCGGGAGAAGCTAAACGAACACTTCCCAGGTTCAGGAATTTAAAGATCATG 572

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Qy   422 GCTCTGCGAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAGA 481
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Db   753 GCTCTGCGAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAGA 812

Qy   482 GGTTGTTGGCAGGGGCTCTGGGTCGGGAAGATTCCAAGGATCAGGTTGAGG 541
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Db   813 GGTTGTTGGCAGGGGCTCTGGGTCGGGAAGATTCCAAGGATCAGGTTGAGG 872

Qy   542 AAAGGCCGATTATAGGAACATCACATTGATGAGCTTGTGAAGCATACCAAGAGACAGG 601
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Qy   782 CAGGAGAGGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGATTAATT 841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   842 GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG 901
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1173 GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG 1232

Qy   902 CCTATGTCCTCTGTTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAA 961
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1233 CCTATGTCCTCTGTTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAA 1292

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Db   1293 CGCCTTCTATGATGGCCAAGCACCTAAAGATTTTGCATGNATGGCTTGGTCAATATAG 1352

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Db   1353 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1412

Qy   1082 ATTGTAAGCCTAGAAGTTCCACCTGCCCACTGCTTTGAAGGACATATGTTACTGTCTGGTC 1141
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Db   1473 TAGAGCCCTTCAGGATTGGACCGTACCACCAACTTGTTAACATTGTTAACATTGGAGAGCGGCTGTAATG 1532

Qy   1202 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAAACTATGAAGAAGCCTGT 1261
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Db   1533 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAAACTATGAAGAAGCCTTGT 1592

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Db   1713 ACATCGCAAAGGTACCTTTGTGCATCGAACTCCTCCAATTTGCTGTGATTGAAGCTGGGT 1772

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Db 1773 TAAAGTGCTGCCAAGGGAGGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACG 1832

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Qy 1862 ACCATGCAATCAAGTCTGGCATGCATGGAGTGAATGCTGAAGTGCTGGAAACCTCCCTGTGT 1921
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Db 2193 ACCATGCAATCAAGTCTGGCATGCATGGAGTGAATGCTGAAGTGCTGGAAACCTCCCTGTGT 2252

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Qy 2102 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA 2161
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Db 2433 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA 2492

Qy 2162 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATTGAAATTGTTG 2221
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Db 2493 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATTGAAATTGTTG 2552

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Qy 2582 TGATTTTTTGTTGCCAAGGAAATGGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG 2641
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Db   4113  ATTATGCATTGAGGAGAACAATATCTGTCGGCTGAGGTTGAGGAATGGCTTGGACCCATTT  4172

Qy   3842  TGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTGCCTTTTTTATTCTTGATGATCCT  3901
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Qy   3902  CAAGGAAATACAACCTAG  3919
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Db   4231  CAAGGAAATACAACCTAG  4248
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RESULT 12

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AR438495

LOCUS       AR438495                 7224 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 1 from patent US 6664062.
ACCESSION   AR438495
VERSION     AR438495.1  GI:42663366
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7224)
  AUTHORS   Stanton,V.P. Jr.
  TITLE     Thymidylate synthase gene sequence variances having utility in
            determining the treatment of disease
  JOURNAL   Patent: US 6664062-A1 16-DEC-2003;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match             98.9%;  Score 3876.2;  DB 6;  Length 7224;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 3896;  Conservative  0;  Mismatches   20;  Indels    2;  Gaps   1;
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Qy      2  GTCACCCTGTGGGAGCACGTCTTCTCTGCCGCCCTCCGCGCAAGGAGGAGACTCGACA    61
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Db    333  GTCACCCTGTGGGAGCACGTCTTCTCTGCCGCCCTCCGCGCAAGGAGGAGACTCGACA   392

Qy     62  ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG   121
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Db    393  ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG   452

Qy    122  ATGAGATCAATGCCATTCGCAGAGAAGGAGGATTATGGTGCTGAGGAGTGGGGACCA   181
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Db    453  ATGAGATCAATGCCATTCGCAGAGAAGGAGGATTATGGTGCTGAGGAGTGGGGACCA   512

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Db    513  TGATCCAGCGGAGAAGCTAAACGAAGAGACACTTCCGAGGTCAGGAATTTAAAGATCATG   572

Qy    242  CCAGGCCGCTGAAAGGAGAAGCTAAAGGCAACAATGACACTTTAAGTATAACTCAGCCTGA   301
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Db    573  CCAGGCCGCTGAAAGGAGAAGCTAAAGGCAACAATGACACTTTAAGTATAACTCAGCCTGA   632

Qy    302  AAATCCATAAGGAATACTTGCTTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA   361
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Db    633  AAATCCATAAGGAATACTTGCTTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA   692

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Db    693  GCACTAGTATTGCCCAAGCTGACTATGCCTTGAACACTTGGCCTACCGGATGAACATGT   752

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Db    873  AAAGGCCGGATTATAGGAACATCATGATGAGCTTGTTGAAGCATCAAGAGCAGAGCAGG   932

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Qy    662  CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATCCGACAGA   721
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Db   1053  GGCCTATCTTATTCAGGGACGATCGTTGATAAAAGTGGGCGGAGGACTCTTTCCGACAGA  1112

Qy    722  GGCCTATCTTATTCAGGGACGATCGTTGATAAAAGTGGGCGGAGGACTCTTTCCGACAGA   781
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Db   1113  CAGGAGAGGGATTTGTCATCAGCGTGTCATCAGCNTGTCCGCAGNTGTCCGCAGNTGTCC  1172

Qy    782  CAGGAGAGGGATTTGTCATCAGCGTGTCATCATCAGCNTGTCCGCAGNTGTCCGCAGNTGTCC   841

Qy    842  GTGCTTTGGGTGCAGTCGAGATGAGACCTTTTATTGAAAATAATGGAAAATGTACAACAG   901
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1173  GTGCTTTGGGTGCAGTCGAAATGAGACCTTTTATTGAAAATAATGGAAAATGTACAACAG  1232

Qy    902  CCTATGTCCTCTGTATCCCAATGCAGTCTTCCCACACCTTTGGTGACTATGATGAAA   961
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1233  CCTATGTCCTCTGTATCCNAATGCAGTCTTCCCACACCTTTGGTGACTATGATGAAA  1292

Qy    962  CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAG  1021
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1293  CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGNATGGCTTGGTCAATATAG  1352

Qy   1022  TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGGAAATTGCTGAAGCTGTGAAAA  1081
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1353  TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGGAAATTGCTGAAGCTGTGAAAA  1412

Qy   1082  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCTGGTC  1141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1413  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCTGGTC  1472

Qy   1142  TAGAGCCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCGTGTAATG  1201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1473  TAGAGCCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCGTGTAATG  1532

Qy   1202  TTGCAGGATCAAGGAAGTTTGCTAAAACTCATCATGGCAGGAAACTATCGAAGAAGCCTTGT  1261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1533  TTGCAGGATCAAGGAAGTTTGCTAAAACTCATCATGGCAGGAAACTATCGAAGAAGCCTTGT  1592

Qy   1262  GTGTTGCCAAAGTGCAGGTGAAATGGCAGTTGGATGTCAACATGGATGATG  1321
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Db   1593  GTGTTGCCAAAGTGCAGGTGAAATGGCAGTTGGATGTCAACATGGATGATG  1652

Qy   1322  GCATGCTAGATGTGCAAGTGCAATGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAG  1381
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   1653  GCATGCTAGATGTGCAAGTGCAATGCAATGACCAGATTTGCAACTTAATNGCTTCCGAGCCAG  1712

Qy   1382  ACATCGCAAAGTACTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGT  1441
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Db   1713  ACATCGCAAAGTACTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGT  1772

Qy   1442  TAAAGTGCTGCCAAGGAAGTGCCAAGGTACCATTGTCAATAGCATTAGTGCATTAGTGCAACAATGT  1501
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1773  TAAAGTGCTGCCAAGGAAGTGCCAAGGTACCATTGTCAATAGCATTAGTGCATTAGTGCA  1832
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Qy  2582 TGATTTTTGTTGCCAAGAAATGGAGAGATTAGCTATAAGGATCCATTGTTGATTGGAG 2641
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Db  2913 TGATTTTTGTTGCCAAGAAATGGAGAGATTAGCTATAAGGATCCATTGTTGATTGGAG 2972

Qy  2642 GAGCAACCACTTCAAAAACCCACACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 2701
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Db  2973 GAGCAACCACTTCAAAAACCCACACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 3032

Qy  2702 TAATCCATGTCTCCGACGCGTCCAAGAGTGTGTGTGTTCCCAGCTGTTAGATGAAA 2761
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Db  3033 TAATCCATGTCTCCGACGCGTCCAAGAGTGTGTGTGTTCCCAGCTGTTAGATGAAA 3092

Qy  2762 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGATATTAGACAGGACC 2821
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Qy  2882 TCCAAATGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGACCCAGG 2941
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Qy  2942 TCTTTGAAGACTATGACCTGCGAGAAGCTGGTGACTACACATTGACTGGAAGCCTTTCTTTG 3001
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Qy  3182 TCCAAGACGACATTCACCTGTACGCAGAGGCTGCGTGCCCCAGGCTGCGAGAGCCCATAG 3241
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3513 TCCAAGACGACATTCACCTGTACGCAGAGGCTGCGTGCCCCAGGCTGCGAGAGCCCATAG 3572

Qy  3242 CCACTTTCTATGGGTAAGGCAACACAGGCTGAGAAGGAACTCTGCCAGCACGGAGCCATACT 3301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3573 CCACTTTCTATGGGTAAGGCAACACAGGCTGAGAAGGAACTCTGCCAGCACGGAGCCATACT 3632

Qy  3302 ACTGCCTCTCAGACTTCATCGCTTCGGGGTTATAAGTTCAGCCGGCTGT 3361
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Qy  3542 TCGCAGACCTGCCGAAGGTTGCGGTGGCGGTTACAAGGGCATCCGGCTCCTGCGTACCCCAGCC 3601
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Db  3873 TCGCAGACCTGCCGCGGTGGCGGTTACAAGGGCATCCGGCTACCCCGGCCTACCCCAGCC 3932

Qy  3602 AGCCCGACCACCACCGAGAAGTCGCAGACTCGCAGACATCGAGACATCTACAG 3661
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Db  3933 AGCCCGACCACCACCGAGAAGTCGCAGACATCGAGACATCTACAG 3992

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Qy  1502 ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1561
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Qy  1682 TCCTAACCATTGGGACTGGAATGGAGGAACAACAACTTGTATGCCATTAATTTATCCATG 1741
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Db  2013 TCCTAACCATTGGGACTGGAATGGAGGAACAACAACTTGTATGCCATTAATTTATCCATG 2072

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Qy  1862 ACCATGCAATCAAGTCTGCGACATGGACATGGACATGCTGACTGAGATAGTGAATCTCCCTGTGT 1921
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Db  2253 ATGATGATATCCATAGAAGAACTTCTGCAGCTCTGTGAAGATCTCATCTGAATAAAGACC 2312

Qy  1982 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGAGGAAGAAAG 2041
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Db  2313 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGAGGGAAGAAAG 2372

Qy  2042 TCATTCAGACTGATGAGTGGGAGAAATGGCCCCTGTTGAGTATGCCCTTG 2101
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Qy  2342 TGCTTAACGGCACAGTAGAAGAAGAGGCACCCTTACCAGGGCACCATCGTGCTGGCCACTG 2401
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Qy  2402 TTTAAAAGCAAGCAGATATAATGGCCTGTCAGGACTTCATCACTCCCTTGGCTGCAATA 2461
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Db   3993  GCATTRAGGTTAACAGAATCAATCATTAGCAATGGCACTGCACCTGCTTCAGCAGTCTCAGCCTCTACT  4052
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Qy   3722  TCTCCAATTGAAGTCAACATATTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG  3781
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Db   4053  TCTCCAATTGAAGTCAACATATTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG  4112
Qy   3782  ATTATGCATTGAGGAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCCATTT  3841
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Db   4113  ATTATGCATTGAGGAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCCATTT  4172
Qy   3842  TGGGATATGATACAGACTAACTTTTTTTTTTTTTTGCCTTTTTATCTTGATGATCCT  3901
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Db   4173  TGGGATATGATACAGACTAAC--TTTTTTTTTTTTTTGCCTTTTTATTCTTGATGATCCT  4230
Qy   3902  CAAGGAAATACAACCTAG  3919
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Db   4231  CAAGGAAATACAACCTAG  4248
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RESULT 13

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LOCUS       AR562003                7224 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 1 from patent US 6759200.
ACCESSION   AR562003
VERSION     AR562003.1  GI:53975655
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7224)
  AUTHORS   Stanton,V.P. Jr.
  TITLE     Thymidine phosphorylase gene sequence variances having utility in
            determining the treatment of disease
  JOURNAL   Patent: US 6759200-A 1 06-JUL-2004;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1..7224
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match             98.9%;  Score 3876.2;  DB 6;  Length 7224;
Best Local Similarity   99.4%;
Matches 3896;  Conservative  0;  Mismatches  20;  Indels  2;  Gaps  1;
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Qy      2  GTCACCTGTGGAGAGCACGTCCTTCTCTGCCCGCCCCTCTGCCCAAGGAGGAGGACTCGACA  61
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Db    333  GTCACCTGTGGAGAGCACGTCCTTCTCTGCCCGCCCCTCTGCCCAAGGAGGAGGACTCGACA  392
Qy     62  ACATGTCACCCGCCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAGAGAAAACCCTGCGGG  121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393  ACATGTCACCCGCCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAGAGAAAACCCTGCGGG  452
Qy    122  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGTGCTGCTGGATGAGGGATGGGGACCA  181
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Db    453  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGTGCTGCTGGATGAGGGATGGGGACCA  512
Qy    182  TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG  241
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Db    513  TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG  572
Qy    242  CCAGGGCCGCTGAAAGGCAACAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC  301
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Db    573  CCAGGGCCGCTGAAAGGCAACAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC  632
Qy    302  AAATCCATAAGGAATACTTGCTGGCTGGGCAGATAATCATTGAAACAAATACTTTTAGCA  361
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Db    633  AAATCCATAAGGAATACTTGCTGGCTGGGCAGATAATCATTGAAACAAATACTTTTAGCA  692
Qy    362  GCACTAGTATTGCCCAAGCTGACTATGCCTATGGCCTTGAACACTTGCCTACCGGATGAACATGT  421
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Db    693  GCACTAGTATTGCCCAAGCTGACTATGCCTATGGCCTTGAACACTTGCCTACCGGATGAACATGT  752
Qy    422  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGCAGGAATTRAGA  481
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Db    753  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGCAGGAATTRAGA  812
Qy    482  GGTTGTTGGCAGGGGCTCTGGGTCCGGGGTGGGGAAGATTCCCATCTGTGG  541
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Qy    542  AAAGGCCGGATATAGGAACATCACATTGATGAGCTTGTTGAAGCATACCAAGAGCAGAGG  601
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Qy    602  CCAAAGGACTTCTGGATGGCGGGGGTTGCACTCAAGATCTTACTCATTCATTGGAGGAGAAATCTT  661
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Qy    662  CCAATGCCAAGGCAGCCAGCCTTGTTGCACTCAAAATCTTTTGAGGAGAAATATGCTCCCC  721
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Db    993  CCAATGCCAAGGCAGCCAGCCTTGTTGCACTCAAAATCTTTTGAGGAGAAATATGCTCCCC  1052
Qy    722  GGCCTATCTTTATTCAGGGACGATCGTTGATAAAGTGGGCGGCGGACTCTTTCCGACACAGA  781
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Db   1053  GGCCTATCTTTATTCAGGGACGATCGTTGATAAAGTGGGCGGCGGACTCTTTCCGACACAGA  1112
Qy    782  CAGGAGAGGGGATTTGTCATCAGCGTGCTCATGGAGAACCACCTCGATTGGATTAAATT  841
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Qy    842  GTGCTTTGGTGCAGCTGAGATGAGACCTTTATTGGAAATAATTGGAAAAATGTACAACAG  901
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Db   1173  GTGCTTTGGTGCAGCTGAGATGAGACCTTTATTGGAAATAATTGGAAAAATGTACAACAG  1232
Qy    902  CCTATGTCCTGTTATCCCAATGCAGGTCTTCCCACACCTTGGTGACTATGATGAAA  961
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Db   1233  CCTATGTCCTGTTATCCAATCNAATGCAGGTCTTCCACACCTTTGGTGACTATGATGAAA  1292
Qy    962  CGCCCTTCTATGATGATGCCAAGCACCTAAAGGATTTGTCTATGGATGGCTTGGTCAATATAG  1021
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Db   1293  CGCCCTTCTATGATGATGCCAAGCACCTAAAGGATTTGTCTATGGATGATGGCTTGGTCAATATAG  1352
Qy   1022  TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAAATTGCTGAAGCTGTGAAAA  1081
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Qy   1082  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTCTGTC  1141
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Db   1473  TAGAGCCCTTCAGGATTGGACCGTACACCAACCTTGTTGTAACATTGGAGCGCTGTAATG  1532
Qy   1202  TTTGCAGGATCAAGGAAGTTGTCAAACTATCATCATGGCAGGAAACTATGAAGAGAGCCTTGT  1261
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1533  TTTGCAGGATCAAGGAAGTTGTCAAACTATCATCATGGCAGGAAACTATGAAGAGAACTATGAAGAACTGT  1592
Qy   1262  GTGTTGCCAAAGTGCAGGTGAAAATGGAGCCCCAGGTGTTGATGTCAACATGGATGATG  1321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1593  GTGTTGCCAAAGTGCAGGTGAAAATGGAGCCCCAGGTGTTGATGTCAACATGGATGATG  1652
Qy   1322  GCATGCTAGATGTCCAAGTGACCAGAGATTTGCAACTTAATTGCTTCCGAGCCAG  1381
           ||||||||||||||||||||   ||||||||||||||||||| |||||||||||
Db   1653  GCATGCTAGATGTCCAAGTGCAATGACCAGATTTGCAACTTAATNGCTTCCGAGCCAG  1712
Qy   1382  ACATCCGAAAGTGACCTTGTGCATCGATCAGACTCCTCCAATTTTGTCTGTGATTGAAGCTGGGT  1441
           ||||| ||||||||||||||| | ||||| |||||||||||||||||||||||||||||||||||
Db   1713  ACATCGGAAAGTGACCTTGTGTCGATCGATCGACTCCTCCAATTTTGTCTGTGATTGAAGCTGGGT  1772
Qy   1442  TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTTAGTCTGAAGGAAGAAGGAGACG  1501
           |||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||
Db   1773  TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGAGGAGGAGGAGGACG  1832
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Qy   1502 ACTTCTTGGAGAAGGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1833 ACTTCTTGGAGAAGGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1892

Qy   1562 TTGATGAAGAAGGACAGGCAACAGAAACAGAAACAGAGTGTGCACCCGGCCT 1621
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1893 TTGATGAAGAAGGACAGGCAACAGAAACAGAAACAGAGTGTGCACCCGGCCT 1952

Qy   1622 ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAATA 1681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1953 ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAATA 2012

Qy   1682 TCCTAACCATTGGGACTGGAATGGAGAACAACAACTTGTATGCCATTAATTTTATCCATG 1741
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2013 TCCTAACCATTGGGACTGGAATGGAGAACAACAACTTGTATGCCATTAATTTTATCCATG 2072

Qy   1742 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 1801
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2073 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 2132

Qy   1802 TGTCCTTCTTCCTTCCGAGGAATGGGAGAAGCCATTCGAGAAGCAATGCATGGGGTTTCTTT 1861
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2133 TGTCCTTCTTCCTTCCGAGGAATGGGAGAAGCCATTCGAGAAGCAATGCATGGGGTTTCTTT 2192

Qy   1862 ACCATGCAATCAAGTCTGGCATGGCATGAGTGTCGGAAACCTCCCTGT 1921
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2193 ACCATGCAATCAAGTCTGGCATGGCATGAGTGTCGGAAACCTCCCTGT 2252

Qy   1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 1981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2253 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 2312

Qy   1982 CTGAGGCCACTGAGAAGAGCTCTTACGTTCTTACGTGTTGAGATGCCCAGACTCAAGGCACGAGGAGGAAGAAAG 2041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2313 CTGAGGCCACTGAGAAGAGCTCTTACGTTCTTACGTGTTGAGATGCCCAGACTCAAGGCACGAGGAGGAAGAAAG 2372

Qy   2042 TCATTCAGACTGATGAGTGGAGAAATGCGCCCTGTGAAGAACGCCCTTGAGTATGCCCTTG 2101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2373 TCATTCAGACTGATGAGTGGAGAAATGCGCCCTGTGAAGAACGCCCTTGAGTATGCCCTTG 2432

Qy   2102 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGGCCAGGTTAAACCAAAAAA 2161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2433 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGGCCAGGTTAAACCAAAAAA 2492

Qy   2162 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAATGAAAATTGTTG 2221
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2493 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAATGAAAATTGTTG 2552

Qy   2222 GTGATCTTTTTGGAGCTGAAAAATGTTTCTACCCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2553 GTGATCTTTTTGGAGCTGAAAAATGTTTCTACCCTCAGGTTATAAAGTCAGCCCGGGTTA 2612

Qy   2282 TGAAGAAGGCTGTTGGCCACCTTCATCCCTTTCATGGAAAAAGAGAAAACCAGAG 2341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2613 TGAAGAAGGCTGTTGGCCACCTTCATCCCTTTCATGGAAAAAGAGAAAACCAGAG 2672

Qy   2342 TGCTTAACGGCACAGTAGAAGAAGAGAGACCCTTACCAGGGCACCATCCTGCTGCCACTG 2401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2673 TGCTTAACGGCACAGTAGAAGAAGAGAGACCCTTACCAGGGCACCATCCTGCTGCCACTG 2732

Qy   2402 TTAAAGGCGACGTGCACGACATAGGTCAAGAACATAGTTGGAGTCCTTGGCTGCAATA 2461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2733 TTAAAGGCGACGTGCACGACATAGGTCAAGAACATAGTTGGAGTCCTTGGCTGCAATA 2792

Qy   2462 ATTTCCGAGTTATTGATTTAGGAGTCATGAGTCCATGTGATAAGATACTGCTC 2521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2793 ATTTCCGAGTTATTGATTTAGGAGTCATGAGTCCATGTGATAAGATACTGCTC 2852

Qy   2522 TTGACCACCAAAGCAGAATATCCGGTTGTCTGTCAGGACTTCATCACTCCTTCCCTGGATGAAA 2581
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2853 TTGACCACCAAAGCAGAATATCCGGTTGTCTGTCAGGACTTCATCACTCCTTCCCTGGATGAAA 2912

Qy   2582 TGATTTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATATAAGGGATTCCATTGTTGATTGGAG 2641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2913 TGATTTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATATAAGGATTCCATTGTTGATTGGAG 2972
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2642 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 2701

Qy   2973 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 3032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2702 TAATCCATGTCCTGGACGCGTCAAGAGTGTGGTGTGTCCCAGCTGTGTTAGATGAAA 2761

Qy   2702 TAATCCATGTCCTGGACGCGTCAAGAGTGTGGTGTGTCCCAGCTGTGTTAGATGAAA 2761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3033 TAATCCATGTCCTGGACCGGTCCCAAGAGTGTGGTGTGTCCCAGCTGTGTTAGATGAAA 3092

Qy   2762 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAAATATGAGAATATTAGACAGGACC 2821
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3093 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAAATATGAGAATATTAGACAGGAGNCC 3152

Qy   2822 ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAAGTGGTT 2881
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3153 ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAANTNGTT 3212

Qy   2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCAGTACACTGACCCCAGG 2941
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3213 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCAGTACACTGGACCCCAGG 3272

Qy   2942 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG 3001
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3273 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG 3332

Qy   3002 ATGTCTGGCAGCTCCGGGGCAAGTACACCCGGAGTCGAGGGCTTCCCCAAGATATTTAACGACA 3061
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3333 ATGTCTGGCAGCTCCGGGGCAAGTACACCCGGAGTCGAGGGCTTCCCCAAGATATTTAACGACA 3392

Qy   3062 AAACAGTAGGTGGAGAGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACAC 3121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3393 AAACAGTAGGTGGAGAGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACAC 3452

Qy   3122 TGATTAGTCAAAAGAAACTCCGGGCCCCGGGGTGTGGTGGGTTCTGGCCAGCACAGAGTA 3181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3453 TGATTAGTCAAAAGAAACTCCGGGCCCCGGGGTGTGGTGGGTTCTGGCCAGCACAGAGTA 3512

Qy   3182 TCCAAGACGACATTCACCTGTACGCGGAGGCTGCTGCGTGTCCCCAGGCTGCCCATAG 3241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3513 TCCAAGACGACATTCACCTGTACGCGGAGGCTGCTGCGTGTCCCCAGGCTGCCCATAG 3572

Qy   3242 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGAGCACGAGGAGCCATACT 3301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3573 CCACCTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGAGCACGAGGAGCCATACT 3632

Qy   3302 ACTGCCTCTCAGACTTCATCGCTCCCCTTGCATTCTGGCCATCCTGGGACTACCTGGGCCCTGT 3361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3633 ACTGCCTCTCAGACTTCATCGCTCCCCTTGCATTCTGGCCATCCTGGGACTACCTGGGCCTGT 3692

Qy   3362 TTGCCGTTGCCTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCATGGAGGCCATATGAGGTGACG 3421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3693 TTGCCGTTGCCTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCATGGAGGCCATATGAGGTGACG 3752

Qy   3422 ACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCAGGAGGCCTTTGCAGAAG 3481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3753 ACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCAGGAGGCCTTTGCGAGAAG 3812

Qy   3482 AGCTCCATGAAAGAAGAGTTCGCCGGAGAACTGTGGCGCCTACTGTGGCAGCTGGACG 3541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3813 AGCTCCATGAAAGAAGAGTTCGCCGGAGAACTGTGGCGCCTACTGTGGCAGCTGGACG 3872

Qy   3542 TCGGAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGAGACTGGGAGCTCCTGCGCCAGCC 3601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3873 TCGGAGACCTGCGCAGGCTGCGGTACAAGGGCATCCGCGAGACTGGGAGCTCCTGCGCCAGCC 3932

Qy   3602 AGCCCGACCACCACCGAGAAGCTCACCATGTGGAGACTCGAGACAATCGAGCAGTCTACAG 3661
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3933 AGCCCGACCACCACCGAGAAGCTCACCATGTGGAGACTGGACAATCGAGCAGTCTACAG 3992

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGCAATGCAATTGCTTCAGCGCTCTCACTT 3721
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3993  GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCGACGCAGTCTCAGCCTCTACT  4052
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3722  TCTCCAATTTGAAGTCACATATTTGCTGTGGGAAGAATTTCAAGGATCAGGTTGAGG     3781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4053  TCTCCAATTTGAAGTCACATATTTGCTGTGGGAAGAATTTCAAGGATCAGGTTGAGG     4112

Qy    543  TTTGTGGCAGGGGCTCTGGGTCCGACTAATAACACTCTCTGTGTCCCATCTGTGAA      543
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484  TTTGTGGCAGGGGCTCTGGGTCCGACTAATAACACTCTCTGTGTCCCATCTGTGAA      484

Qy    480  AGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCC    540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  AGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCC    481

Qy    603  AAAGGACTTCTGATGGCGGGGTGATATCTTACTCATTGAAACTATTTTGATACTTGCC    663
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544  AAAGGACTTCTGATGGCGGGGTGATATCTTACTCATTGAAACTATTTTGATACTTGCC    604

Qy    600  TGGGATATGATACAGACTAACTTTTTTTTTTTGCCTTTTATCTTGATGATCCT        540
           |||||||||||||||||||||||  ||||||||||||||||||||||||||
Db    541  AAAGGACTTCTGATGGCGGGGTGATATCTTACTCATTGAAACTATTTTGATACTTGCC    601

Qy    723  CAAGGAAATACAACCTAG      723
           ||||||||||||||||||
Db    664  AATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCGG    724

Qy    660  CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTCCGACACACA   720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  AATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCGG    661

Qy    843  GGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGT   843
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGT   781

Qy    903  GCTTTGGGTGCAGCTGAGATGAGAACCTTTATTGAAATAATTGGAAAATGTACAACAGCC   903
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840  GCTTTGGGTGCAGCTGAGATGAGAACCTTTATTGAAATAATTGGAAAATGTACAACAGCC   841

Qy    963  TATGTCCTCTGTTATCCCAATGGAGGTCTTCCCAACACCTTGGTGACTGATGAGAAACG   963
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900  TATGTCCTCTGTTATCCCAATGGAGGTCTTCCCAACACCTTGGTGACTGATGAGAAACG   901

Qy   1023  CCTTCATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGTCAATATAGTT      1023
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960  CCTTCATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGTCAATATAGTT       961

Qy   1083  GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAGAAGCTGTGAAAAT   1083
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020  GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAGAAGCTGTGAAAAT   1021

Qy   1143  TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGACATATGTTACTGTCTGGTCTA    1143
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080  TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGACATATGTTACTGTCTGGTCTA    1021

Qy   1203  GAGCCCTTCAGGATTGGACCGTACCACCAACTTCGTTAACATTGGAGAGCGCTGTAATGTT   1203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140  GAGCCCTTCAGGATTGGACCGTACCACCAACTTCGTTAACATTGGAGAGCGCTGTAATGTT   1081

Qy   1263  GCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAAGAGAAGCCTTGTGT   1263
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200  GCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAAGAGAAGCCTTGTGT   1141

Qy   1323  GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTGGATGTCAACATGGATGATGCGC   1323
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260  GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTGGATGTCAACATGGATGATGCGC   1201

Qy   1383  ATGCTAGATGGTTCCAAGTGCAATGCCAGATTTCGAACTTCATTGTCATTACCAA      1383
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320  ATGCTAGATGGTTCCAAGTGCAATGCCAGATTTCGAACTTCATTGTCATTACCAA      1261

Qy   1443  ATCGCAAAGGTACCTTTGTGCATCGACTCGTGATTGATTGAAGCTGGGTTA       1443
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380  ATCGCAAAGGTACCTTTGTGCATCGACTCGTGATTGATTGAAGCTGGGTTA       1321

Qy   1503  AAGTGCTGCCAAGGAAGGACGTCGATTGTCAATACGAGCTGAGGAAGGAGGACGAC      1503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440  AAGTGCTGCCAAGGGAGGACGTCGATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACGAC      1381

Qy   1563  TTCTTGGAGAAGGCCAGGAAGGCCAGGAAGCTGAATTAAAAGTCATGGCTTTT       1563
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500  TTCTTGGAGAAGGCCAGGAAGGCCAGGAAGCTGAATTAAAAGTCATGGCTTTT       1441
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Query Match             98.3%;  Score 3851;  DB 6;  Length 3856;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 3851;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;

Qy     64  ATGTCCACCCGGCTCCAAGACCTGTCCAACCGAAGGTCTGAAGAAACCCTGCCGGGAT    123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATGTCCACCCGGCTCCAAGACCTGTCCAACCGAAGGTCTGAAGAAACCCTGCCGGGAT     60

Qy    124  GAGATCAATGCCATTCTGCTAGAGAGAGGATTATGTGTCTGGATGAGGAGGATGGGGACCATG    183
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GAGATCAATGCCATTCTGCTAGAGAGAGGATTATGTGTCTGGATGAGGAGGATGGGGACCATG    120

Qy    184  ATCCAGCGGAGAAGCTAAAACGAAGAACACTTCCGAGGTCAGGAATTAAAGATCATGCC    243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ATCCAGCGGAGAAGCTAAAACGAAGAACACTTCCGAGGTCAGGAATTAAAGATCATGCC    180

Qy    244  AGGCCGCTGAAAGGCAACAATGACATTTAAGTAGTATAACTCAGCCTGATGTCATTTACCAA    303
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  AGGCCGCTGAAAGGCAACAATGACATTTAAGTAGTATAACTCAGCCTGATGTCATTTACCAA    240

Qy    304  ATCCATAAGGAATACTTGCTGCTGGGCAGATATCATTGAAACAAATACTTTTAGCAGC    363
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ATCCATAAGGAATACTTGCTGCTGGGCAGATATCATTGAAACAAATACTTTTAGCAGC    300

Qy    364  ACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCTACCGGATGAACATGTGC    423
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  ACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGTGC    360

Qy    424  TCTGCAGGAGTGGCCAGAGAAAAGCTGCCCGAGGAGGTAACTCTCCAGACAGCAGGAATTAAGAGG   483
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  TCTGCAGGAGTGGCCAGAGAAAAGCTGCCCGAGGAGGTAACTCTCCCAGACAGCAGGAATTAAGAGG   420
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Qy   1564  GATGAAGAAGGACAGGCAACAACAGACACAAAAATCAGAGTGTGCACCCGGGCCTAC  1623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  GATGAAGAAGGACAGGCAACAACAGACACAAAAATCAGAGTGTGCACCCGGGCCTAC  1560

Qy   1624  CATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATATC  1683
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATATC  1620

Qy   1684  CTTAACCATTGGACTGGAATGAGGAGGAACAACAACTTGTATGCCATTTATCTTATCATGCA  1743
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CTTAACCATTGGACTGGAATGAGGAGGAACAACAACTTGTATGCCATTTATCTTATCATGCA  1680

Qy   1744  ACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTTCCAACTTG  1803
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  ACAAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTTCCAACTTG  1740

Qy   1804  TCCTTCTCCTTCCGAGAATGGAAGCAATGCATGGGCGTTTTCCTTTAC  1863
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  TCCTTCTCCTTCCGAGAATGGAAGCAATGCATGGGCGTTTTCCTTTAC  1800

Qy   1864  CATGCAATCAAGTCTGCAGCTCTGTGAGATCTCATCTGGAATAAAGACCCT  1923
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  CATGCAATCAAGTCTGCAGCTCTGTGAGATCTCATCTGGAATAAAGACCCT  1860

Qy   1924  GATGATATCCATAAGGAACTTCTGCAGTCTCGTCGTGAAGATCTCATCTGAATAAAGACCCT  1983
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  GATGATATCCATAAGGAACTTCTGCAGTCTCGTCGTGAAGATCTCATCTGAATAAAGACCCT  1920

Qy   1984  GAGGCCACTGAGAAGCTCTTACGTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAGTC  2043
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  GAGGCCACTGAGAAGCTCTTACGTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAGTC  1980

Qy   2044  ATTCAGACTGATGAGTGAGGATGGAAATGGCCCTGTGTCGAGAAGAACGCCTTGAGTGTATGCCCCTTGTG  2103
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  ATTCAGACTGATGAGTGAGGATGGAAATGGCCCTGTGTCGAGAAGAACGCCTTGAGTGTATGCCCCTTGTG  2040

Qy   2104  AAGGGCATTGAAAAAACATATTATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAAA  2163
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Qy   2224  GATCTTTTTGGAGCTGTGTGGCCACCTTATTCCCTTTCTACCTGGTTATATAAAGTCAGCCCCGGGGTATG  2283
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Db   2161  GATCTTTTTGGAGCTGTGTGGCCACCTTATTCCCTTTCATGGTTATAAAGTCAGCCCCGGGGTATG  2220

Qy   2284  AAGAAGGCTGTTGGCCACCTTATTCACTCATCAATCATCAGGGCCACCATCGGTGCTGCCCACTGTT  2343
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Qy   2344  CTTAACCGGCACACATAGGCAAGAACATAGTTGGAGTAGTTATAAAGATCCTTGGCCCACCCATCGGTGCTGCCCACTGTTTACAGAGTG  2403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CTTAACCGGCACACATAGGCAAGAACATAGTTGGAGTAGTTATAAAGATCCTTGGCCCACCCATCGGTGCTGCCCACTGTTTACAGAGTG  2340

Qy   2404  AAAGGGACGACGTGCACGACAGTAGTTGGCCAAGGACTGAGTAGTTGCTATAATAAT  2463
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Db   2341  AAAGGGACGACGTGCACGACAGTAGTTGGCCAAGGACTGAGTAGTTGCTGCAATAAT  2400

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Db   2401  TTCCGAGTTATTGATTTGATTGACGAATATTTTGTTGCCAAGGAAATGAGAAATGAGAAATGAGACGA  2460

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Qy   2584  ATTTTTGTTGCCAAGGAAATGAGAAATGGCCAAGGTTGCCAAGGATTCCATTGTTGATTGGACGA  2643
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Qy   2944  TTTGAAGACTATGACTTGCAGAAGCTGGTGACTACATTGACTGGAAGCCTTTCTTTGAT  3003
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Qy   3064  ACAGTAGGTGGAGAGGCCAGGAGGCCAGGAAGTCTACGATGATGCCACAATATGCTGAACACACTG  3123
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RESULT 15
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DEFINITION Sequence 43 from Patent WO03087386.
ACCESSION   AX930571
VERSION   AX930571.1 GI:40312319
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE   1
AUTHORS   Kroeger,B., Zelder,O., Klopprogge,C., Schroeder,H. and Haefner,S.
TITLE   Methods for producing sulphurous fine chemicals
JOURNAL   Patent: WO 03087386-A 43 23-OCT-2003;
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ORIGIN

Query Match   96.6%; Score 3785.2; DB 6; Length 3798;
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Matches 3790; Conservative 0; Mismatches 0; Indels 8; Gaps 0;
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Db   1861  GATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGAAATAAAGACCCT  1920

Qy   1984  GAGGCCACTGAGAGTCCTCTTACGTATGCCCAGACTCAAGGCACAGCAGGAGGAAGAAGTC  2043
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  GAGGCCACTGAGAGTCCTCTTACGTATGCCCAGACTCAAGGCACAGCAGGAGGAAGAAGTC  1980

Qy   2044  ATTCAGACTGATGAGTGGAGAAATGGCGCCTTGAGTATGCCCTTGTG  2103
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  ATTCAGACTGATGAGTGGAGAAATGGCGCCTTGAGTATGCCCTTGTG  2040

Qy   2104  AAGGGCATTGAAAAACATATTATTGAGGATAACTGAAGCCAAGGTTAAACCAAAAAAAA  2163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  AAGGGCATTGAAAAACATATTATTGAGGATAACTGAAGCCAAGGTTAAACCAAAAAAAA  2100

Qy   2164  TATCCCGACCTCTCAATATAATTGAAGAATCCCCTGATGAATGAAATTGTTGGT  2223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  TATCCCGACCTCTCAATATAATTGAAGAATCCCCTGATGAATGAAATTGTTGGT  2160

Qy   2224  GATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTATG  2283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTATG  2220
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Qy   2284  AAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAGAAAGAGAAGAAAACCAGAGTG  2343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  AAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAGAAAGAGAAGAAAACCAGAGTG  2280

Qy   2344  CTTAACGGCACAGTAGAGAAGAAGACCCTTACCAGGCGCACCATCGTGCTGGCCACTGTT  2403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CTTAACGGCACAGTAGAGAAGAAGACCCTTACCAGGCGCACCATCGTGCTGGCCACTGTT  2340

Qy   2404  AAAGGGCACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAAT  2463
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  AAAGGGCACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAAT  2400

Qy   2464  TTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAGACTCGATGATACTGCTCTT  2523
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  TTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAGACTCGATGATACTGCTCTT  2460

Qy   2524  GACCACAAAGCAGATATAATTGGCTGTCAGGACTCATCACTCCTTCCCTGATGATGAAATG  2583
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  GACCACAAAGCAGATATAATTGGCTGTCAGGACTCATCACTCCTTCCCTGATGATGAAATG  2520

Qy   2584  ATTTTTGTGCCAAGAAATGAAAATGCCCAACAGTTAGCTGTATAGGATTCCATTGTTGAGGA  2643
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  ATTTTTGTGCCAAGAAATGAAAATGCCCAACAGTTAGCTGTATAGGATTCCATTGTTGAGGA  2580

Qy   2644  GCAACCACTTCAAAAAACCCACACAGCAGTTAAAAATAGCTCCGAGATACAGTGCACCTGTA  2703
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  GCAACCACTTCAAAAAACCCACACAGCAGTTAAAAATAGCTCCGAGATACAGTGCACCTGTA  2640

Qy   2704  ATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTGTTCCAGCTGTTAGATGAAAAT  2763
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  ATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTGTTCCAGCTGTTAGATGAAAAT  2700

Qy   2764  CTAAAGGATGAATACTTGAGGAAGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGTTTC  2823
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CTAAAGGATGAATACTTGAGGAAGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGTTTC  2760

Qy   2824  TATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGTTTC  2883
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  TATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGTTTC  2820

Qy   2884  CAAATGATTGGCTGTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGACCCAGGTC  2943
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  CAAATGATTGGCTGTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTC  2880

Qy   2944  TTTGAAGACTATGACCTGCAGAAGCTCGGTGGACTACATTGACTGGGACTCCTTCTTTGAT  3003
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  TTTGAAGACTATGACCTGCAGAAGCTCGGTGGACTACATTGACTGGGACTCCTTCTTTGAT  2940

Qy   3004  GTCTGGCAGCTCCCGGGCAAGTACCCGGAATCGAATGGAGGGCTTTAACGACAAA  3063
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  GTCTGGCAGCTCCCGGGCAAGTACCCGGAATCGAATGGAGGGCTTTAACGACAAA  3000

Qy   3064  ACAGTAGGTGGAGAGGCCAGGAAGGTTACGACGATGATGTCGGCCACAATATGTCGAACACACTG  3123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  ACAGTAGGTGGAGAGGCCAGGAAGGTTACGACGATGATGTCGGCCACAATATGTCGAACACACTG  3060

Qy   3124  ATTAGTCAAAAGAACTCCGGGCCCGGGGTGTCGTTCGGTTCTCGGCCACGCAGAGTATC  3183
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  ATTAGTCAAAAGAACTCCGGGCCCGGGGTGTCGTTCGGTTCTCGGCCACGCAGAGTATC  3120

Qy   3184  CAAGCAGACATTCACCTGGTTAAGGCCAACAGGTCTGAGAAGGACTCTGCCAGCAGCCCATAGCC  3243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  CAAGCAGACATTCACCTGGTTAAGGCCAACAGGTCTGAGAAGGACTCTGCCAGCAGCCCATAGCC  3180

Qy   3244  ACTTTCTATGGGTTAAGGCACAGGCTGAGAAGGACTCTGCCAGCACCGGAGCCCATACTAC  3303
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  ACTTTCTATGGGTTAAGGCACAGGCTGAGAAGGACTCTGCCAGCACCGGAGCCCATACTAC  3240

Qy   3304  TGCCTCTCAGACTTCATCGCTCTCCTGCATTCTGGCATCCGTCGTGACTACCTGGGCTGTTT  3363
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  TGCCTCTCAGACTTCATCGCTCTCCTGCATTCTGGCATCCGTCGTGACTACCTGGGCTGTTT  3300

Qy   3364  GCCGTTGCCTGCTTGTGGGTAGAGAGCTGAGCAGGATGGTGACGAC  3423
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Db   3364
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Db   3301 GCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGAC 3360
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Qy   3424 TACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCCAGAGAGCCTTTGCAGAAGAG 3483
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCCAGAGAGCCTTTGCAGAAGAG 3420

Qy   3484 CTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTCGAGCAGCTGGACGTC 3543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 CTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTCGAGCAGCTGGACGTC 3480

Qy   3544 GCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGCCAG 3603
          |||||||||| | |||||||||||||||||||||||||||||| |||||||||||||||
Db   3481 GCAGACCTGCGCGAGGCTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGCCAG 3540

Qy   3604 CCCGACCACACCGAGAAGCTCACCATGTGGAGACTCGCAGACATCGAGCAGTCTACAGGC 3663
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CCCGACCACACCGAGAAGCTCACCATGTGGAGACTTGCAGACATCGAGCAGTCTACAGGC 3600

Qy   3664 ATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCCAGTCTTCAGGCCTCTACTTC 3723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 ATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCCAGTCTCAGGCCTCTACTTC 3660

Qy   3724 TCCAATTTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT 3783
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Db   3661 TCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT 3720

Qy   3784 TATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATTTTG 3843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATTTTG 3780

Qy   3844 GGATATGATACAGACTAA 3861
          ||||||||||||||||||
Db   3781 GGATATGATACAGACTAA 3798
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Search completed: March 6, 2006, 20:35:18
Job time : 19274 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 6, 2006, 14:47:47 ; Search time 1474 Seconds
(without alignments)
17719.763 Million cell updates/sec

Title: US-10-607-712-1
Perfect score: 3919
Sequence: 1 ggtcacctgtggagcacg.........ctcaaggaaatacaacctag 3919

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   N_Geneseq_21:*
1: geneseqm1980s:*
2: geneseqm1990s:*
3: geneseqm2000s:*
4: geneseqm2001as:*
5: geneseqm2001bs:*
6: geneseqm2002as:*
7: geneseqm2002bs:*
8: geneseqm2003as:*
9: geneseqm2003bs:*
10: geneseqm2003cs:*
11: geneseqm2003ds:*
12: geneseqm2004as:*
13: geneseqm2004bs:*
14: geneseqm2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3884.8	99.1	7122	4	AAF31100	Aaf31100 Methionin
2	3884.8	99.1	7122	5	AAC91207	Aac91207 Human met
3	3884.8	99.1	7122	14	AEA63658	Aea63658 Methionin
4	3883.2	99.1	7224	4	AAF31101	Aaf31101 Methionin
5	3793.8	96.6	3920	2	AAV34063	Aav34063 Human met
6	3785.0	96.6	3798	10	ADI39109	Adi39109 Homo sapi
7	926.8	23.6	3780	10	ADI39113	Adi39113 Agrobacte
8	914.6	23.3	3786	8	ACA37652	Aca37652 Prokaryot
9	911.8	23.3	3684	8	ACA20972	Aca20972 Prokaryot
c 10	903	23.0	3762	11	ABD14844	Abd14844 Pseudomon
11	903	23.0	3795	11	ABD15089	Abd15089 Pseudomon
12	902.6	23.0	3669	8	ACA44722	Aca44722 Prokaryot
13	902.2	23.0	3705	8	ACA42279	Aca42279 Prokaryot
14	901.4	23.0	3705	10	ADI39093	Adi39093 Pseudomon
15	901	23.0	3750	10	ADF02792	Adf02792 Bacterial
16	899	22.9	3681	8	ACA32117	Aca32117 Prokaryot
17	895.8	22.9	3702	9	ADA30291	Ada30291 DNA encod
18	894	22.8	3705	8	ACA44248	Aca44248 Prokaryot
19	892.2	22.8	3717	8	ACA45414	Aca45414 Prokaryot
20	883.8	22.6	3684	8	ACA32726	Aca32726 Prokaryot
21	883.8	22.6	3684	10	ADI39086	Adi39086 Escherich
22	883.2	22.5	3681	8	ACA52977	Aca52977 Prokaryot
23	883.2	22.5	3681	10	ADI39082	Adi39082 Vibrio ch
24	877.6	22.4	3645	10	ADI39117	Adi39117 Chlorobiu
25	877.6	22.4	3645	10	ADI39099	Adi39099 Chlorobiu
26	873.2	22.3	3711	10	ADI39091	Adi39091 Pseudomon
27	867.8	22.1	3714	10	ADI39095	Adi39095 Nitrosomo
28	867.2	22.1	3684	8	ACA51700	Aca51700 Prokaryot
29	867	22.1	3822	10	ADI39084	Adi39084 Sinorhizo
30	865.2	22.1	3681	10	ADI39111	Adi39111 Vibrio fi
31	859	21.9	3681	8	ACA36141	Aca36141 Prokaryot
32	857.6	21.9	3771	8	ACA51042	Aca51042 Prokaryot
33	857.6	21.9	3771	10	ADI39088	Adi39088 Salmonell
34	854.4	21.8	3696	8	ACA53745	Aca53745 Prokaryot
35	840.8	21.5	3759	10	ADI39107	Adi39107 Rhodobact
36	835	21.3	3642	10	ADI39103	Adi39103 Clostridi
37	763.8	19.5	3777	10	ADI39101	Adi39101 Deinococc
38	749.2	19.1	3774	10	ADI39097	Adi39097 Bordetell
39	745.6	19.0	2796	8	ACA24643	Aca24643 Prokaryot
40	708.6	18.1	3157	8	ACA48896	Aca48896 Prokaryot
41	701	17.9	3138	11	ACH95623	Ach95623 Klebsiell
42	650.4	16.6	3954	10	ADI39105	Adi39105 Caulobact
43	621.4	15.9	2718	10	ADI39115	Adi39115 Ralstonia
44	615.8	15.7	2349	11	ABD15289	Abd15289 Pseudomon
45	477.8	12.2	1779	8	ACA26885	Aca26885 Prokaryot

ALIGNMENTS

RESULT 1
AAF31100
ID   AAF31100 standard; cDNA; 7122 BP.
XX
AC   AAF31100;
XX
DT   27-APR-2001 (first entry)
XX
DE   Methionine synthase coding sequence #1.
XX
KW   Analyte-binding enzyme; analyte analysis; ss.
XX
OS   Homo sapiens.
XX
PN   WO20102600-A2.
XX
PD   11-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018057.
XX
PR   06-JUL-1999; 99US-00347878.
PR   06-DEC-1999; 99US-00457205.
XX
PA   (GEAT) GEN ATOMICS.
XX
PI   Yuan C;
XX
DR   WPI; 2001-071583/08.
XX
PT   Assaying method, useful for prognosis and diagnosis of disease, comprises
PT   contacting sample with a mutant analyte-binding enzyme and detecting
PT   binding.
XX
PS   Disclosure; Page; 187pp; English.
XX
CC   The present invention relates to a method for assaying an analyte in a
CC   sample comprising: contacting the sample with a mutant analyte-binding
CC   enzyme which has binding affinity for the analyte or an immediate analyte
CC   enzymatic conversion product but has attenuated catalytic activity; and
CC   detecting resulting binding. The method is useful in monitoring
CC   biological systems/processes, or prognosis/diagnosis of disease caused by
CC   imbalances of the analytes. The present sequence is a coding sequence

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CC   used in the specification. Note: the present sequence is not shown in
CC   the specification, but was from Genbank, using information given in the
CC   specification
XX
SQ   Sequence 7122 BP; 2112 A; 1450 C; 1728 G; 1832 T; 0 U; 0 Other;

Query Match            99.1%;  Score 3884.8;  DB 4;  Length 7122;
Best Local Similarity  99.6%;  Pred. No. 0;
Matches 3904;  Conservative  0;  Mismatches 12;  Indels  2;  Gaps  1;

Qy      2 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCCCTCGCGCAAGGAGAGACTCGACA 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCCCTCGCGCAAGGAGAGACTCGACA 284

Qy     62 ACATGTCACCCGCTCCAAGACCTGTCGCAACCCGGCTCTGAAGAAGTCTGAAGAAACCCTGCGGG 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 ACATGTCACCCGCTCCAAGACCTGTCGCAACCCGGCTCTGAAGAAGTCTGAAGAAACCCTGCGGG 344

Qy    122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGAGGGGATGGGGACCA 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGAGGGGATGGGGACCA 404

Qy    182 TGATCCAGCGGGAGAAGTCAAACGAAGCAAACACTTCCGAGGTCAGGAATTTAAAGATCATG 241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 TGATCCAGCGGGAGAAGTCAAACGAAGCAAACACTTCCGAGGTCAGGAATTTAAAGATCATG 464

Qy    242 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTTCAGCCTGATGTCATTTACC 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTTCAGCCTGATGTCATTTACC 524

Qy    302 AAATCCATAAGGAATACTTGCTCGGTCCGGGCAGATATCATTGAAACAAATACTTTTAGCA 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 AAATCCATAAGGAATACTTGCTCGGTCCGGGCAGATATCATTGAAACAAATACTTTTAGCA 584

Qy    362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTTGAACACATGT 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTTGAACACATGT 644

Qy    422 GCTCTGCGAGAGTGGCCCAGAAAAGCTGCCGGAGGAGTAACTTCCAGACAGGAATTAAGA 481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 GCTCTGCGAGAGTGGCCCAGAAAAGCTGCCGGAGGAGTAACTTCCAGACAGGAATTAAGA 704

Qy    482 GGTTTGTGTGGCAGGGGCTCTCGGGGTTCGGGGTGTCCCATCTGTGG 541
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    705 GGTTTGTGTGGCAGGGGCTCTCGGGGTTCGGGGTGTCCCATCTGTGG 764

Qy    542 AAAGGCCGGATATAGGAACATCACATTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 601
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 AAAGGCCGGATATAGGAACATCACATTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 824

Qy    602 CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG 661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG 884

Qy    662 CCAATGCCAAGGACAGCCTGTTTGCACTCAAATCTTTTGAGGAGAAATATGCTCCCC 721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 CCAATGCCAAGGACAGCCTGTTTGCACTCAAATCTTTTGAGGAGAAATATGCTCCCC 944

Qy    722 GGCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGCGACTCTTTCCCGGACAGA 781
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 GGCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGCGACTCTTTCCCGGACAGA 1004

Qy    782 CAGGAGAGGGATTTGTCATCAGCGTGTCATGGAGAACCACTCTGCATTGGATTAAATT 841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 CAGGAGAGGGATTTGTCATCAGCGTGTCATGGAGAACCACTCTGCATTGGATTAAATT 1064

Qy    842 GTGCTTTGGGTGCAGCTGAGATGAGAACCTTTTATTGAAATAATTGGAAAATGTACAACAG 901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 GTGCTTTGGGTGCAGCTGAAATGAGAACCTTTTATTGAAATAATTGGAAAATGTACAACAG 1124

Qy    902 CCTATGTCCCTGTTATCCCAATGCAGTCTTCCCAACACCTTGGTGACTATGATGAAA 961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 CCTATGTCCCTGTTATCCCAATGCAGTCTTCCCAACACCTTGGTGACTATGATGAAA 1184

Qy    962 CGCCTTCTATGATGGCCAAGCACCTAAAGGAGGATTTTGCTATGGATGGTGGTCAATATAG 1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185 CGCCTTCTATGATGGCCAAGCACCTAAAGGAGGATTTTGCTATGGATGGTGGTCAATATAG 1244

Qy   1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1245 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1304

Qy   1082 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCGGTC 1141
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1305 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCGGTC 1364

Qy   1142 TAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATG 1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365 TAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATG 1424

Qy   1202 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGCAGCGGAACTATGAAGAAGCCTTGT 1261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1425 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGCAGCGGAACTATGAAGAAGCCTTGT 1484

Qy   1262 GTGTTGCCAAAGTGCAGTGAAATGGGAGCCCAGGTGTTGGATGTCAACATGCGATGATG 1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1485 GTGTTGCCAAAGTGCAGTGAAATGGGAGCCCAGGTGTTGGATGTCAACATGCGATGATG 1544

Qy   1322 GCATGCTAGATGTCCAAGTGCAATGACCAGATTTGCAATGTCATTAATTGCTTCCGAGCCAG 1381
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Db   1545 GCATGCTAGATGTCCAAGTGCAATGACCAGATTTGCAATGTCATTAATTGCTTCCGAGCCAG 1604

Qy   1382 ACATGCGAAAGTACCTTGTGCATCGACTCCTCCAATTTGCTGTGATTGCTGAAGCTGGGT 1441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1605 ACATGCGAAAGTACCTTGTGCATCGACTCCTCCAATTTGCTGTGATTGCTGAAGCTGGGT 1664

Qy   1442 TAAAGTGCTGCCAAGGGAAGTGCATTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGACG 1501
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1665 TAAAGTGCTGCCAAGGGAAGTGCATTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGACG 1724

Qy   1502 ACTTCTTGGAGAAGGCCAGGAGGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1725 ACTTCTTGGAGAAGGCCAGGAGGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1784

Qy   1562 TTGATGAAGAAGAACAGCAGGCAACAGAAGAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTGG 1621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1785 TTGATGAAGAAGAACAGCAGGCAACAGAAGAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTGG 1844

Qy   1622 ACCATCTGCTTGTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA 1681
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1845 ACCATCTGCTTGTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA 1904

Qy   1682 TCCTAACCATTGGGACTGGAATGGAACAACACAACTTGTATGCCATTAATTTTTATCCATG 1741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1905 TCCTAACCATTGGGACTGGAATGGAACAACACAACTTGTATGCCATTAATTTTTATCCATG 1964

Qy   1742 CAACAAAGTCATTAAAGAAAACATTACCTGGAGCCAGAGTAGTGAGAATAGTGGAGGTCTTTCCAACT 1801
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1965 CAACAAAGTCATTAAAGAAAACATTACCTGGAGCCAGAGTAGTGAGAATAGTGGAGGTCTTTCCAACT 2024

Qy   1802 TGTCCTTCTCCTTCCGGAGCCATTCGAGAAGCAATGCAATGCATGGGGTTTTCCTTT 1861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 TGTCCTTCTCCTTCCGGAGCCATTCGAGAAGCAATGCAATGCATGGGGTTTTCCTTT 2084

Qy   1862 ACCATGCAATCAAGTCTCGGCACTACAGCTCGGAGATAGTGAATGCTGGAAACCTCCCTGTGT 1921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 ACCATGCAATCAAGTCTCGGCACTACAGCTCGGAGATAGTGAATGCTGGAAACCTCCCTGTGT 2144

Qy   1922 ATGATGATATCCATAAGAACTTCATCTCGGAAGATCTCATCTGGAATAAAGACC 1981
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Db   2145 ATGATGATATCCATAAGAACTTCATCTCGGAAGATCTCATCTGGAATAAAGACC 2204

Qy   1982 CTGAGGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAG 2041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2205 CTGAGGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAG 2264
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Qy  2042 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTTG 2101
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2265 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTTG 2324

Qy  2102 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA 2161
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2325 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA 2384

Qy  2162 AATATCCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAAATTGTTG 2221
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Db  2385 AATATCCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAAATTGTTG 2444

Qy  2222 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCCGGGTTA 2281
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Db  2445 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCCGGGTTA 2504

Qy  2282 TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAAGAGAGAAAACCAGAG 2341
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2505 TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAAGAGAGAAAACCAGAG 2564

Qy  2342 TGCTTAACGGCACAGTAGAAGAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTG 2401
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2565 TGCTTAACGGCACAGTAGAAGAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTG 2624

Qy  2402 TTAAAGGCGACGTGCACGACACATAGTGGAGTAGTTCCTTGGCTGCAATA 2461
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Db  2625 TTAAAGGCGACGTGCACGACACATAGTGGAGTAGTTCCTTGGCTGCAATA 2684

Qy  2462 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATTGTGATGATAAGATACTGAAAGCTGCTC 2521
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2685 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATTGTGATGATAAGATACTGAAAGCTGCTC 2744

Qy  2522 TTGACCACAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA 2581
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Db  2745 TTGACCACAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA 2804

Qy  2582 TGATTTTTGTTGTTGCCAAGGAAGATTAGCTATAAGGATTCCATTGTTGATTGGAG 2641
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2805 TGATTTTTGTTGTTGCCAAGGAAGATTAGCTATAAGGATTCCATTGTTGATTGGAG 2864

Qy  2642 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTCGCACCTG 2701
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Db  2865 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTCGCACCTG 2924

Qy  2702 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGTTCCCAGCTGTTAGATGAAA 2761
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Db  2925 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGTTCCCAGCTGTTAGATGAAA 2984

Qy  2762 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAAATATTGAAGACAGGACC 2821
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2985 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAAATATTGAAGACAGGACC 3044

Qy  2822 ATTATGAGTCTCTCAAGGAGGAGGAGGAGTACTTACCCTTAAGTCAAGCCAGAAAAGTGGTT 2881
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3045 ATTATGAGTCTCTCAAGGAGGAGGAGGAGTACTTACCCTTAAGTCAAGCCAGAAAAGTGGTT 3104

Qy  2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG 2941
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Db  3105 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG 3164

Qy  2942 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG 3001
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3165 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG 3224

Qy  3002 ATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGCTTCCCCAAGATATTTAACGACA 3061
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Db  3225 ATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGCTTTCCCAAGATATTTAACGACA 3284

Qy  3062 AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACAC 3121
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Db  3285 AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACAC 3344

Qy  3122 TGATTAGTCAAAAGAAACTCCGGGGCGGGGTGTGGTTCGTGCCAGCACAGAGTA 3181
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3345 TGATTAGTCAAAAGAAACTCCGGGGCGGGGTGTGGTTCGTGCCAGCACAGAGTA 3404

Qy  3182 TCCAAGACGCATTCACCTGTACGACGAGAGCTGCTGTGCCCAGGCTGCAGAGCCCATAG 3241
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3405 TCCAAGACGCATTCACCTGTACGACGAGAGCTGCTGTGCCCAGGCTGCAGAGCCCATAG 3464

Qy  3242 CCACTTTCTATGGGTTAAGGCAACAGCTGAGAAGACTCTGCCAGCACGAGCCATACT 3301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3465 CCACTTTCTATGGGTTAAGGCAACAGCTGAGAAGACTCTGCCAGCACGAGCCATACT 3524

Qy  3302 ACTGCCCTCCAGACTTCATCGTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT 3361
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Db  3525 ACTGCCCTCCAGACTTCATCGTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT 3584

Qy  3362 TTGCCGTTGCCTGCTTGTTGGGGTAGAAGAGCTGAGCAAGGCTGAGGATGAGGATGGTGACG 3421
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3585 TTGCCGTTGCCTGCTTGTTGGGGTAGAAGAGCTGAGCAAGGCTGAGGATGAGGATGGTGACG 3644

Qy  3422 ACTACAGCAGCATCATGGTCAAGGGCGTCTGCGGGACCGGCTGCAGCTGGACG 3481
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Db  3645 ACTACAGCAGCATCATGGTCAAGGGCGTCTGCGGGACCGGCTGCAGCTGGACG 3704

Qy  3482 AGCTTCCATGAAAAGAGTTCGCGCAAGAACTGTGGGCCTACTGTGCAGTGAGCAGCTGGACG 3541
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3705 AGCTTCCATGAAAAGAGTTCGCGCAAGAACTGTGGGCCTACTGTGCAGTGAGCAGCTGGACG 3764

Qy  3542 TCGCAGACCTGCGAGGTTGCGCGTACAAGGGCATCCGCCCCCGCTCCTGGCTACCCCAGCC 3601
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3765 TCGCAGACCTGCGAGGTTGCGCGTACAAGGGCATCCGCCCCGGCTCCTGGCTACCCCAGCC 3824

Qy  3602 AGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGACAGTCTACAG 3661
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Db  3825 AGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGACAGTCTACAG 3884

Qy  3662 GCATTAGGTTAACAGAATCATTAGCAATGAATGCCACCTGCTTCAGCAGTCTCAGGCCTCTACT 3721
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3885 GCATTAGGTTAACAGAATCATTAGCAATGAATGCCACCTGCTTCAGCAGTCTCAGGCCTCTACT 3944

Qy  3722 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 3781
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Db  3945 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 4004

Qy  3782 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT 3841
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Db  4005 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT 4064

Qy  3842 TGGGATATGATCAGACTAACTTTTTTTTTTTTTTGCCTTTTTATCTTGATGATCCT 3901
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Db  4065 TGGGATATGATCAGACTAAC--TTTTTTTTTTTTTGCCTTTTTATTCTTGATGATCCT 4122

Qy  3902 CAAGGAAATACAACCTAG 3919
         ||||||||||||||||||
Db  4123 CAAGGAAATACAACCTAG 4140
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PN   WO200071754-A1.
XX
PD   30-NOV-2000.
XX
PF   24-MAY-2000; 2000WO-US014354.
XX
PR   25-MAY-1999; 99US-00318448.
XX
PA   (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI   Johnson WG, Stenroos ES;
XX
DR   WPI; 2001-025174/03.
XX
PT   Diagnosing a developmental disorder, e.g. schizophrenia, by forming
PT   datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
PT   and environmental variables affecting an individual and then comparing
PT   these DS with reference DS.
XX
PS   Disclosure; Page 115-117; 156pp; English.
XX
CC   The present invention provides a novel method of estimating the
CC   susceptibility of an individual to a developmental disorder using genetic
CC   and environmental variables. The method can be used in the diagnosis,
CC   prevention and treatment of disorders such as schizophrenia, spina bifida
CC   cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
CC   attention deficit disorder, obsessive compulsive disorder, chronic
CC   multiple tic syndrome and learning disorders such as dyslexia
XX
SQ   Sequence 7122 BP; 2112 A; 1450 C; 1728 G; 1832 T; 0 U; 0 Other;

Query Match   99.1%; Score 3884.8; DB 5; Length 7122;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3904; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

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Qy      2 GTCACCTGTGGAGAGCACGTCTTCTGCCGCCCTCGCCGAGGAGGAGACTCGACA       61
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Db    225 GTCACCTGTGGAGAGCACGTCTTCTGCCGCCCTCGCCGAGGAGGAGACTCGACA      284

Qy     62 ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCGAGGTCTGAAGAAACCCTGCGGG    121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCGAGGTCTGAAGAAACCCTGCGGG   344

Qy    122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGAGGGATGGGGACCA   181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGAGGGATGGGGACCA   404

Qy    182 TGATCCAGCGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG   241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 TGATCCAGCGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG   464

Qy    242 CCAGGCCCGCTGAAAGCGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGCTCAGCGCTGCTCATTTACC   301
          |||||||||||||||||||||||||
Db    465 CCAGGCCCGCTGAAAGGCCCGAGGAGGTAACTCTTCCAGACAGCTCAGCGCTGCTCATTTACC  524

Qy    302 AAATCCATAAGGAATACTTGCTGCTGGGCCAGATAATCATTGAAACAAATACTTTTAGCA   361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 AAATCCATAAGGAATACTTGCTGCTGGGCCAGATAATCATTGAAACAAATACTTTTAGCA   584

Qy    362 GCACTAGTATTGCCCAAGCTGACTATGCCCTTGGCCATGCCTTGCGGATGGAACATGT    421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 GCACTAGTATTGCCCAAGCTGACTATGCCCTTGGCCATGCCTTGCGGATGGAACATGT   644

Qy    422 GCTCTGCGAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAAGA   481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 GCTCTGCGAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGCAGAATTAAGA  704

Qy    482 GGTTTGTGTGCAGGGGCTCGGGTCCGACTAAGAGACTCTCGTGTCCCCATCTGTGG    541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 GGTTTGTGTGCAGGGGCTCGGGTCCGACTAAGAGACTCTCGTGTCCCCATCTGTGG   764

Qy    542 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGTTGAAGCATACCAAGAGACAGG   601
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGTTGAAGCATACCAAGAGACAGG   824

Qy    602 CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG    661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG   884

Qy    662 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC    721
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC   944

Qy    722 GGCCTATCTTATTTCAGGAGGACGATCGTTGATAAAGTGGGGCGGACTCTTTCCGGACAGA   781
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Db    945 GGCCTATCTTATTTCAGGAGGACGATCGTTGATAAAGTGGGGCGGACTCTTTCCGGACAGA  1004

Qy    782 CAGGAGGAGGATTGTCATCAGCGTGTCTCATGGAGACCACCTCGCATTGGATTAAATT    841
          ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   1005 CAGGAGGAGGATTGTCATCAGCGTGTCTCATGGAGACCACCTCTACATTGGATTAAATT  1064

Qy    842 GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGAAAATGTACACACAG    901
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1065 GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGAAAATGTACAACACAG  1124

Qy    902 CCTATGTCCTCTGTTATCCCAATGCAGTCTTCCCACACCTTTGGTGACTATGATGAAA    961
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 CCTATGTCCTCTGTTATCCCAATGCAGTCTTCCCACACCTTTGGTGACTATGATGAAA  1184

Qy    962 CGCCTTCCATGATGGCCAAGCACCTAAAGGATTTGCTATGATGGCTTGGTCAATATAG   1021
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185 CGCCTTCCATGATGGCCAAGCACCTAAAGGATTTGCTATGATGGCTTGGTCAATATAG  1244

Qy   1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA  1081
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1245 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1304

Qy   1082 ATTGTAAGCCTAGAGTTCCACCTGCCTTGAAGGACATATGTTACTGTCTGGTC       1141
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1305 ATTGTAAGCCTAGAGTTCCACCTGCCTTGAAGGACATATGTTACTGTCTGGTC      1364

Qy   1142 TAGAGCCCCTTGCAGGATTGGACGTGTACCACCAACTTGTTGAACATTGGAGAGCGCTGTAATG  1201
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365 TAGAGCCCCTTGCAGGATTGGACGTGTACCACCAACTTGTTGAACATTGGAGAGCGCTGTAATG 1424

Qy   1202 TTGCAGGATCAAGGAAGTTGCTCAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGT   1261
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1425 TTGCAGGATCAAGGAAGTTGCTCAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGT  1484

Qy   1262 GTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATG   1321
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1485 GTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATG  1544

Qy   1322 GCATGCTAGAGTGTGTCCAAGTGCAATGACCCAGATTTGCAACTAACTTTGCTTCCGAGCCAG  1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1545 GCATGCTAGAGTGTGTCCAAGTGCAATGACCCAGATTTGCAACTAACTTTGCTTCCGAGCCAG 1604

Qy   1382 ACATCGCAAAGTCACTTTGTGCATCGGCAGATATCATTGAAACAAAATACTTTTAGCA    1441
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1605 ACATCGCAAAGTCACTTTGTGCATCGGCAGATATCATTGAAACAAAATACTTTTAGCA   1664

Qy   1442 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGGCATTGTCAATAGGAAGCATGAACATGT  1501
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1665 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGGCATTGTCAATAGGAAGGAGGAGGACG  1724

Qy   1502 ACTTCTTGGAGAAGGCCAGGAAGCCAGGAGATTAAAAAGTATGAGCTGCTATATGTGGTGGCTT  1561
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1725 ACTTCTTGGAGAAGGCCAGGAAGCCAGGAGATTAAAAAGTATGAGCTGCTATATGTGGTGGCTT 1784

Qy   1562 TTGATGAAGGAACAGGCAACAGCAACAAATCAGAGTGTGCACCCGGGCCT       1621
          |||||||||||||||||| |||||| ||||||||||||||||||||||||
Db   1785 TTGATGAAGGAACAGGACAGGACAGCAACAGAAATCAGAGTGTGCACCCGGGCCT    1844

Qy   1622 ACCATCTGCTTGTGAAAAAACTGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA  1681
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1845 ACCATCTGCTTGTGAAAAAACTGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1904
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Qy   1682 TCCTAACCATTGGACTGGAATGAGGAACACAACTTGTATGCCATTAATTTTATCCATG 1741
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1905 TCCTAACCATTGGACTGGAATGAGGAACACAACTTGTATGCCATTAATTTTATCCATG 1964

Qy   1742 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTCCAACT 1801
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1965 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTCCAACT 2024

Qy   1802 TGTCCTTCTCCTTCCGAGGAATGGAAGCAATGCAATGCAATCGAAGCCATTCGAGAAC 1861
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 TGTCCTTCTCCTTCCGAGGAATGGAAGCAATGCAATGCAATCGAAGCCATTCGAGAAC 2084

Qy   1862 ACCATGCAATCAAGTCTGCGACATGGAGCATGGAGTAGTGAATGCTGGAAACCTCCCT 1921
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 ACCATGCAATCAAGTCTGCGACATGGAGCATGGAGTAGTGAATGCTGGAAACCTCCCT 2144

Qy   1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 1981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 2204

Qy   1982 CTGAGGGCACTGAGAGAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAAG 2041
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2205 CTGAGGGCACTGAGAGAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAAG 2264

Qy   2042 TCATTCAGACTGATGAGTGAGTGAGAAAATGGCCCTGTGAAGAACACGCCTTGAGTATGCCCTTG 2101
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2265 TCATTCAGACTGATGAGTGAGTGAGAAAATGGCCCTGTGAAGAACACGCCTTGAGTATGCCCTTG 2324

Qy   2102 TGAAGGGCATTGAAAAACATATATTGAGGATACTGAGGAAGCCAGGTTAAACCAAGAAG 2161
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2325 TGAAGGGCATTGAAAAACATATATTGAGGATACTGAGGAAGCCAGGTTAAACCAAGAAG 2384

Qy   2162 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAATTGTTG 2221
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2385 CCACCTTCTATGGGTTAAGGACCCCTGATGAATGAAATTGTTG 2444

Qy   2222 GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCCGGTTA 2281
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2445 GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCCGGTTA 2504

Qy   2282 TGAAGAAGGCTGTGTGGCCACCTTATCCCTTCATGGAAAAGAAGAGAAACCAGAG 2341
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2505 TGAAGAAGGCTGTGTGGCCACCTTATCCCTTCATGGAAAAGAAGAGAAGAAACCAGAG 2564

Qy   2342 TGCTTAACGGCACAGTAGAAGAAGAGGACCCCTTACCAGGGCACCATCGTGCTGGCCACTG 2401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2565 TGCTTAACGGCACAGTAGAAGAAGAGGACCCCTTACCAGGGCACCATCGTGCTGGCCACTG 2624

Qy   2402 TTAAAGGCGACGTGCACGACATAGGCAAGACAAGAACATAGTTGGAGTAGTCCATTGCTGCAATA 2461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2625 TTAAAGGCGACGTGCACGACATAGGCAAGACAAGAACATAGTTGGAGTAGTCCATTGCTGCAATA 2684

Qy   2462 ATTTCCGAGTTATTGATTTAGGAGTCATGAGTCCATGTGATAAGATCGATGAAAGCTGCTC 2521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2685 ATTTCCGAGTTATTGATTTAGGAGTCATGAGTCCATGTGATAAGATCGATGAAAGCTGCTC 2744

Qy   2522 TTGACCACAAAGCAGATGAAATGGCTGGGAAATGGGAAATGGCCTGTCATCATCCCTGGATGAAA 2581
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2745 TTGACCACAAAGCAGATGAAATGGCTGGGAAATGGGAAATGGCCTGTCATCATCCCTGGATGAAA 2804

Qy   2582 TTGACTTTGTTGCCAAAGACATTGAGAGAGATTAGCTATARAGGATTCCATTGTTGATTGGAG 2641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2805 TTGACTTTGTTGCCAAAGACATTGAGAGAGATTAGCTATARAGGATTCCATTGTTGATTGGAG 2864

Qy   2642 GAGCAACCACTTCAAAAACCCACCACACAGCAGTTAAAATAGTCCGAGATACAGTGCACCTG 2701
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2865 GAGCAACCACTTCAAAAACCCACCACACAGCAGTTAAAATAGTCCGAGATACAGTGCACCTG 2924

Qy   2702 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGTTCCCGAGTTGTTAGATGAAA 2761
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2925 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGTGTGTTCCCGAGTTGTTAGATGAAA 2984
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Qy   2762 ATCTAAAGGATGAATACTTTGAGGAGAGAGAAATCATGGAAGATATTGAAGATATTAGACAGGACC 2821
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2985 ATCTAAAGGATGAATACTTTGAGGAGAGAGAAATCATGGAAGATATTGAAGATATTAGACAGGACC 3044

Qy   2822 ATTATGAGTCTCTCAAGGAGAGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGTGTT 2881
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3045 ATTATGAGTCTCTCAAGGAGAGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGTT 3104

Qy   2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCACCGTTATTGGGACCCAGG 2941
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3105 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCACCGTTATTGGGACCCAGG 3164

Qy   2942 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGACTACATTGACTGGCTACTGGAAGCCTTTCTTTG 3001
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3165 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGACTACATTGACTGGCTACTGGAAGCCTTTCTTTG 3224

Qy   3002 ATGTCTGGCAGCTCCGGGGCCAAGTACCCGGAATCGAGGCTTCCCAAGATATTAACGACA 3061
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3225 ATGTCTGGCAGCTCCGGGGCCAAGTACCCGGAATCGAGGCTTCCCAAGATATTAACGACA 3284

Qy   3062 AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGGATGCCCACACATGCTGAACACAC 3121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3285 AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGGATGCCCACAAATGCTGAACACAC 3344

Qy   3122 TGATTAGTCAAAAGAAACTCCCGGGCCCGGGGGTGTGGTTGGGTCTGGCCAGCACAGAGTA 3181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3345 TGATTAGTCAAAAGAAACTCCCGGGCCCGGGGGTGTGGTTGGGTCTGGCCAGCACAGAGTA 3404

Qy   3182 TCCAAGACGACATTCACCTGTACGCAGAGGCTCGTGCGCCGGCTCTGCCAGCACGGAGCAGCCATAG 3241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3405 TCCAAGACGACATTCACCTGTACGCAGAGGCTCGTGCGCCGGCTCTGCCAGCACGGAGCAGCCATAG 3464

Qy   3242 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGACTCTGCCAGCACGGAGCAGCCATACT 3301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3465 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGACTCTGCCAGCACGGAGCAGCCATACT 3524

Qy   3302 ACTGCCTCTCAGACTTCATCGCTCCCCTGCATTCTCGGCATCGGCATTCTGGGATCCTGGGCCTGT 3361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3525 ACTGCCTCTCAGACTTCATCGCTCCCCTGCATTCTCGGCATCGGCATTCTGGGATCCTGGGCCTGT 3584

Qy   3362 TTGCCGGTTGCCTGCTTTGGGTAGAAGAGCTGAGAAGCTGCAAGGGCTATGAGGATGATGGTGACG 3421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3585 TTGCCGGTTGCCTGCTTTGGGTAGAAGAGCTGAGAAGCTGCAAGGGCTATGAGGATGATGGTGACG 3644

Qy   3422 ACTACAGACAGCATCATCGTCAAGGCGCGTCAAGGCGTCGGGGACCGGCCTGGGGACCAGCCATACT 3481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3645 ACTACAGACAGCATCATCGTCAAGGCGCGTCAAGGCGTCGGGGACCGGCCTGGGGACCAGCCATACT 3704

Qy   3482 AGCTCCATGAAAGAGTTCGCCGAGAACTGTCGGGCAGTGAACTGTGTGGCCAGTGAGCTGACGACG 3541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3705 AGCTCCATGAAAGAGTTCGCCGAGAACTGTCGGGCAGTGAACTGTGTGGCCAGTGAGCTGACGACG 3764

Qy   3542 TCGCAGACCTGCCGAAGGTTGCGGTGCGCTGCGCCAGGGGCATCCCGGCGCTCCTGGCTCACCCCAGCC 3601
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3765 TCGCAGACCTGCCGAAGGTTGCGGTGCGCTGCGCCAGGGGCATCCCGGCGCTCCTGGCTCACCCCAGCC 3824

Qy   3602 AGCCCGACCACCACACCCGAGAGCTCGAGACTCGACACATCTCAGCGACCAGTTCAGAGCCTCACAG 3661
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3825 AGCCCGACCACCACACCCGAGAGCTCGAGACTCGACACATCTCAGCGACCAGTTCAGAGCCTCTACAG 3884

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGGCAATCATTAGCAATGGCAACCTGCTTCAGGATCCAAGGATTCCAAGGATCTCACTTGTCTGTGTTGGAG 3721
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3885 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGGATCCAAGGATCTCACTTGTCTGTGTTGGAG 3944

Qy   3722 TCTTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATTCAGGTTGAGG 3781
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3945 TCTTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATTCAGGTTGAGG 4004

Qy   3782 ATTATGCATTGAGGAAGAACATATCTGGCGTGAGGTTGAGAAATGGCTTGGACCCATTT 3841
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4005 ATTATGCATTGAGGAAGAACATATCTGGCGTGAGGTTGAGAAATGGCTTGGACCCATTT 4064

Qy   3842 TGGGATATGATACAGACTAACTTTTTTTTTTTTTTGCCTTTTTATCTTGATGATCCT 3901
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Qy  122  ATGAGATCAATGCCATTCTGCGAAGAGAGGATTATGGTGTCTGGATGAGGGATGGGGACCA  181
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  345  ATGAGATCAATGCCATTCTGCGAAGAGAGGATTATGGTGTCTGGATGAGGGATGGGGACCA  404

Qy  182  TGATCCAGCGGAGAAGCTAAACGAACAACACTTCCGAGGTCAGGAATTTAAAGATCATG    241
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  405  TGATCCAGCGGAGAAGCTAAACGAACAACACTTCCGAGGTCAGGAATTTAAAGATCATG    464

Qy  242  CCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC   301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  465  CCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC   524

Qy  302  AAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA   361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  525  AAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA   584

Qy  362  GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAAACACTTGGCCTACCGGATGAACATGT  421
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  585  GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAAACACTTGGCCTACCGGATGAACATGT  644

Qy  422  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA   481
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  645  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA   704

Qy  482  GGTTTGTGCGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG   541
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  705  GGTTTGTGCGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG   764

Qy  542  AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGAGCAGG  601
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  765  AAAGGCCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGAGCAGG  824

Qy  602  CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTCACTCACTCATTTTGATACTG       661
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  825  CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTCACTCACTCATTTTGATACTG       884

Qy  662  CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC   721
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  885  CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC   944

Qy  722  GGCCTATCTTATTTCAGGGACGATCGTTGATAAAAGTGGGGGGACTCCTTCCGGACAGA   781
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  945  GGCCTATCTTATTTCAGGGACGATCGTTGATAAAAGTGGGGGGACTCCTTCCGGACAGA  1004

Qy  782  CAGGAGAGGGAGTTTGTCATCAGCGTGTCATCAGCGTGTCATGGAGGACCACTCTGCATTGGATTAAATT  841
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1005  CAGGAGAGGGAGTTTGTCATCAGCGTGTCATCAGCGTGTCATGGAGGACCACTCTGCATTGGATTAAATT 1064

Qy  842  GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG   901
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1065  GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG  1124

Qy  902  CCTATGTCCTCTGTTATCCCAATGCAGTCTTCCCACACCTTTGGTGACTATGATGAAA    961
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1125  CCTATGTCCTCTGTTATCCCAATGCAGTCTTCCCACACCTTTGGTGACTATGATGAAA   1184

Qy  962  CGCCTTCTCATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAG 1021
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1185  CGCCTTCTCATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAG 1244

Qy 1022  TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1081
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1245  TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1304

Qy 1082  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCTGGTC  1141
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1305  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCTGGTC  1364

Db 1142  TAGAGCCCTTCAGGATTGGACCGTACCACCAACTTTGTTAACATTGGAGAGCGCTGTAATG 1201
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1365  TAGAGCCCTTCAGGATTGGACCGTACCACCAACTTTGTTAACATTGGAGAGCGCTGTAATG 1424

Qy 1202  TTGCAGGATGCAAGAAGTTGCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGT  1261
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Db 4065  TGGGATATGATACAGACTAAC--TTTTTTTTTTTTTGCCTTTTTTATTCTTGATGATCCT 4122
         ||||||||||||||||||||||  ||||||||      ||||||   |||||||||||||
Qy 3902  CAAGGAAATACAACCTAG 3919
         ||||||||||||||||||
Db 4123  CAAGGAAATACAACCTAG 4140
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RESULT 3
AEA63658

ID   AEA63658   standard; DNA; 7122 BP.
XX
AC   AEA63658;
XX
DT   08-SEP-2005 (first entry)
XX
DE   Methionine synthase, MTR, DNA sequence, SEQ ID 2.
XX
KW   Neuroleptic; Nootropic; Tranquilizer; folate metabolism;
KW   psychiatric disorder; schizophrenia; autism;
KW   attention deficit hyperactivity disorder; obsessive-compulsive disorder;
KW   gene; ds; Methionine synthase; chromosome 1.
XX
OS   Homo sapiens.
XX
PN   US6912492-B1.
XX
PD   28-JUN-2005.
XX
PF   23-MAY-2000; 2000US-00577266.
XX
PR   25-MAY-1999; 99US-0136198P.
XX
PA   (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI   Johnson WG, Stenroos ES;
XX
DR   WPI; 2005-442724/45.
XX
PT   Estimating the susceptibility of an individual to have offspring that
PT   develop a developmental disorder comprises analyzing the nucleic acids
PT   and/or proteins for genes involved in folate, pyridoxine, and/or
PT   cobalamin metabolism.
XX
PS   Disclosure; SEQ ID NO 2; 84pp; English.
XX
CC   The present invention relates to a method (M1) for estimating the
CC   susceptibility of an individual to have offspring that develop a
CC   developmental disorder. The method comprises analyzing the nucleic acids
CC   and/or proteins from the biological sample, where analyzing results in a
CC   partial or full genotype for the alleles of two or more genes involved in
CC   folate, pyridoxine, and/or cobalamin metabolism. The present sequence is
CC   one such gene involved in folate metabolism. The method is also useful
CC   for diagnosing, preventing, and treating developmental disorders, e.g.
CC   schizophrenia, autism, attention deficit hyperactivity disorder, or
CC   obsessive-compulsive disorder. The protein encoded by the present
CC   sequence is also known as 5-methyltetrahydrofolate-homocysteine S-
CC   methyltransferase. The present sequence is located on chromosome 1q43.
XX
SQ   Sequence 7122 BP; 2112 A; 1450 C; 1728 G; 1832 T; 0 U; 0 Other;

Query Match   99.1%; Score 3884.8; DB 14; Length 7122;
Best Local Similarity   99.6%; Pred. No. 0;
Matches 3904; Conservative   0; Mismatches   12; Indels   2; Gaps   1;

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Qy    2  GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCCTGCCGCAAGGAGGAGGACTCGACA  61
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  225  GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCCTGCCGCAAGGAGGAGGACTCGACA 284

Qy   62  ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCGAAGGTCTGAAGAAACCCTGCGGG 121
         |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  285  ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAACCCTGCGGG 344
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Db 2505 TGAAGAAGGCTGTGTTGGCCACCTTATCCCTTTCATGGAAAAGAGAGAAGAGAGAAACCAGAG 2564
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2342 TGCTTAACGGCACAGTAGAAGAGAGAAGAGAGAAGAGA 2401

Db 2565 TGCTTAACGGCACAGTAGAAGAGAGAAGAGAGAAGAGA 2624

Qy 2402 TTAAAGGCGAGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA 2461

Db 2625 TTAAAGGCGAGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA 2684

Qy 2462 ATTTCCAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTC 2521

Db 2685 ATTTCCAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTC 2744

Qy 2522 TTGACCACAAAGCAGATAAATTGGCCGTGTCAGGACTCATCACTCCTTCCCTGGATGAAA 2581

Db 2745 TTGACCACAAAGCAGATAAATTGGCCGTGTCAGGACTCATCACTCCTTCCCTGGATGAAA 2804

Qy 2582 TGATTTTTGTTGCCAAGGAAATGGACGAGAGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG 2641

Db 2805 TGATTTTTGTTGCCAAGGAAATGGACGAGAGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG 2864

Qy 2642 GAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGTCCGAGATACAGTGCCACCTG 2701

Db 2865 GAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGTCCGAGATACAGTGCCACCTG 2924

Qy 2702 TAATCCATGTCCTGGACGCGTCCAAGTGTCCCAGCTGTGTTCCCAGCTGTGTAGATGAAA 2761

Db 2925 TAATCCATGTCCTGGACGCGTCCAAGTGTCCCAGCTGTGTTCCCAGCTGTGTAGATGAAA 2984

Qy 2762 ATCTAAAGGATGAAATACTTTGAGGAAATCATGGAAGAATATTAGACAGGACC 2821

Db 2985 ATCTAAAGGATGAAATCATTTGAGGAAATCATGGAAGAATATTAGACAGGACC 3044

Qy 2822 ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTCGTT 2881

Db 3045 ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTCGTT 3104

Qy 2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGGACTACACATTGACTGGAAGCCTTCTTG 2941

Db 3105 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGGACTACACATTGACTGGAAGCCTTCTTG 3164

Qy 2942 TCTTTGAAGACTATGACCTCCGGGGCCAAGTGCCAGGAAGTGCTCTACGATGATGCGAGAGTGGAGAGGC 3001

Db 3165 TCTTTGAAGACTATGACCTCCGGGGCCAAGTGCCAGGAAGTGCTCTACGATGATGCGAGAGTGGAGAGGC 3224

Qy 3002 ATGTCTGGCAGCTCCGGGGCCAAGTGCCAGGAAGTGCTCTACGATGATGCGAGAGTGGAGAGGC 3061

Db 3225 ATGTCTGGCAGCTCCGGGGCCAAGTGCCAGGAAGTGCTCTACGATGATGCGAGAGTGGAGAGGC 3284

Qy 3062 AAACAGTAGGTGGAGAGGCCAGGAAGTGCAGGAGGGCACCAGGAGGGGAAGAAAG 3121

Db 3285 AAACAGTAGGTGGAGAGGCCAGGAAGTGCAGGAGGGCACCAGGAGGGGAAGAAAG 3344

Qy 3122 TGATTAGTCAAAAGAAACTCCGGGGTGTGGTTGGGTTGGTGGTGTCTGCGCTGCGAGAGCCCATAG 3181

Db 3345 TGATTAGTCAAAAGAAACTCCGGGGTGTGGTTGGGTTGGTGGTGTCTGCGCTGCGAGAGCCCATAG 3404

Qy 3182 TCCAAGACGACATTCACCTGTTAAGGCAACAGCTCTGCCAGAGGACTCTGCGCTGCGAGAAGCCCATACT 3241

Db 3405 CCACTTCTCTATGGGTTAAGGCAACAGCTCTGCCAGAGGACTCTGCGCTGCGAGAAGCCCATACT 3464

Qy 3242 ACTGCCCTCTCAGACTTCATCGCTCCCTTGCATTCGGCATCCGTGACTACCTGGGCCTGT 3301

Db 3465 ACTGCCCTCTCAGACTTCATCGCTCCCTTGCATTCGGCATCCGTGACTACCTGGGCCTGT 3524

Qy 3302 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCCGGTTA 3361

Db 3525 ACTGCCCTCTCAGACTTCATCGCTCCCTTGCATTCTGCGCATCCGTGACTACCTGGGCCTGT 3584

Qy 3362 TTGCCGTTGCCTGCTTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGTGACG 3421

Db 3585 TTGCCGTTGCCTGCTTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGTGACG 3644

Db 1425 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1484
          TTGCACGGATCAAGGAGGAAGTTTGCTAAACTACTCATCATGGCCAGGAAAACTATGAGAAGAAGCCTTGT
Qy 1262 GTGTTGCCAAAGTGCAGGTGGAAATGGGAAGGTGTTGGATGTCAACATGGATGATG 1321

Db 1485 GTGTTGCCAAAGTGCAGGTGGAAATGGGAAGGTGTTGGATGTCAACATGGATGATG 1544

Qy 1322 GCAATGCTAGATGGTCAAGTGCCAATGACCCAGATTTTGCTCAACTTAATTGCTTCCGAGCCAG 1381

Db 1545 GCAATGCTAGATGGTCAAGTGCCAATGACCCAGATTTTGCTCAACTTAATTGCTTCCGAGCCAG 1604

Qy 1382 ACATCCGCAAAGTACCTTTGTGCATGCAATGGAGTCGTGTGATTGAAGCTGGGT 1441

Db 1605 ACATCCGCAAAGTACCTTTGTGCATGCAATGGAGTCGTGTGATTGAAGCTGGGT 1664

Qy 1442 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAAGGAGGACG 1501

Db 1665 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAAGGAGGACG 1724

Qy 1502 ACTTCTTGGAAGAGGCCAGGAAGATAAAAAGTAAAAAGTGTGCACCCGGCCT 1561

Db 1725 ACTTCTTGGAAGAGGCCAGGAAGATAAAAAGTAAAAAGTGTGCACCCGGCCT 1784

Qy 1562 TTGATGAAGAAGGGCAACAGGCAACAGAACAGAACAGAAAACAGAAAAATCAGAGTGGGCTT 1621

Db 1785 TTGATGAAGAAGGGCAACAGGCAACAGAACAGAACAGAAAACAGAAAAATCAGAGTGGGCTT 1844

Qy 1622 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1681

Db 1845 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1904

Qy 1682 TCCTAACCATTGGGACTCGGAATGAGGAGCAACAACTTGTATGTGCCATTAATTTATCCATG 1741

Db 1905 TCCTAACCATTGGGACTGAGGAATGAGGAGCAACAACTTGTATGTGCCATTAATTTATCCATG 1964

Qy 1742 CAACAAAAGTCATTGAAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTTCCAACT 1801

Db 1965 CAACAAAAGTCATTGAAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTTCCAACT 2024

Qy 1802 TGTCCTTCTCCTCCGGAATGGAGTGAGAAGCAATGCATTCGAGAAGCAATGCATGGGGTTTCCTTT 1861

Db 2025 TGTCCTTCTCCTCCGGAATGGAGTGAGAAGCAATGCATTCGAGAAGCAATGCATGGGGTTTCCTTT 2084

Qy 1862 ACCATGCAATCAAGTCTGGCATGGACATGGAAGTAGTGATGAGATCTCATCTGAAGAATAAAGACC 1921

Db 2085 ACCATGCAATCAAGTCTGGCATGGACATGGAAGTAGTGATGAGATCTCATCTGAAGAATAAAGACC 2144

Qy 1922 ATGATGATATCCATAAGGAAGCTCTTACGTTACGTTATGCCCAGACTCAAGGCACAGGAGGGACAGAAAGAAG 1981

Db 2145 ATGATGATATCCATAAGGAAGCTCTTACGTTACGTTATGCCCAGACTCAAGGCACAGGAGGGACAGAAAGAAG 2204

Qy 1982 CTGAGGCCACTGAGAACGTCTGATGAGTGGAGAAATGGCCCTTG 2041

Db 2205 CTGAGGCCACTGAGAACGTCTGATGAGTGGAGAAATGGCCCTTG 2264

Qy 2042 TCATTCAGACTACTGAGTGATGAGTGGAGAAATGGCGAAGACGCCCTTGAGTATGAGTATGCCCTTG 2101

Db 2265 TCATTCAGACTACTGAGTGATGAGTGGAGAAATGGCGAAGACGCCCTTGAGTATGAGTATGCCCTTG 2324

Qy 2102 TGAAGGGCATTGAAAAACCCGACCTTCTCAAATAATATTATTGAGGAGACCCCTGAAATGGAATGAAAATTGTTG 2161

Db 2325 TGAAGGGCATTGAAAAACCCGACCTCTCAATAATATTATTGAGGAGACCCCTGAAATGGAATGAAAATTGTTG 2384

Qy 2162 AATATCCCCGACTTCTCAAATATTATTGAGGATACTGAGGAGACCCCTGAGGTTAAACCAAAAAA 2221

Db 2385 AATATCCCCGACTTCTCAATAATATTATTGAGGATACTGAGGAGACCCCTGAGGTTAAACCAAAAAA 2444

Qy 2222 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCCGGTTA 2281

Db 2445 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCCGGTTA 2504

Qy 2282 TGAAGAAGGCTGTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAGAAGAGAGAAACCAGAG 2341

CC   The present invention relates to a method for assaying an analyte in a
CC   sample comprising: contacting the sample with a mutant analyte-binding
CC   enzyme which has binding affinity for the analyte or an immediate analyte
CC   enzymatic conversion product but has attenuated catalytic activity; and
CC   detecting resulting binding. The method is useful in monitoring
CC   biological systems/processes, or prognosis/diagnosis of disease caused by
CC   imbalances of the analytes. The present sequence is a coding sequence
CC   used in the present invention. Note: the present sequence is not shown in
CC   the specification, but was from Genbank, using information given in the
CC   specification
XX
SQ   Sequence 7224 BP; 2108 A; 1491 C; 1761 G; 1864 T; 0 U; 0 Other;

Query Match   99.1%; Score 3883.2; DB 4; Length 7224;
Best Local Similarity   99.6%; Pred. No. 0;
Matches 3903; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

Qy   2 GTCACCTGTGGAGCACGTCTTCTGCCCGCCCCTGCCAAGGAGGAGGACTCGACA 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   333 GTCACCTGTGGAGCACGTCTTCTGCCCGCCCCTGCCAAGGAGGAGGACTCGACA 392

Qy   62 ACATGTCACCCGCGTCCAAGACCTGTCGCAACCGAGAGGTCTGAAGAAACCCTGCGGG 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   393 ACATGTCACCCGCGTCCAAGACCTGTCGCAACCGAGAGGTCTGAAGAAACCCTGCGGG 452

Qy   122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGGATGGGACCA 181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   453 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGGATGGGACCA 512

Qy   182 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAGAGATCATG 241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   513 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAGAGATCATG 572

Qy   242 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTGACATATCATTGAAACAAATACTTTTAGCA 301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   573 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTGACATATCATTGAAACAAATACTTTTAGCA 632

Qy   302 AAATCCATAAGGAATACTTGCTGGCTGGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA 361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   633 AAATCCATAAGGAATACTTGCTGGCTGGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA 692

Qy   362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   693 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 752

Qy   422 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAAGA 481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   753 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAAGA 812

Qy   482 GGTTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTCCCATCTGTGG 541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   813 GGTTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTCCCATCTGTGG 872

Qy   542 AAAGGCCGATTATAGGAACATCATTGATGAGCTTGTTGAAGCATACCAAGAGCAGCAGG 601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   873 AAAGGCCGATTATAGGAACATCATTGATGAGCTTGTTGAAGCATACCAAGAGCAGCAGG 932

Qy   602 CCAAAGGACTTCTTGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG 661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   933 CCAAAGGACTTCTTGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG 992

Qy   662 CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC 721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   993 CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC 1052

Qy   722 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA 781
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1053 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA 1112

Qy   782 CAGGAGAGGAGTTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT 841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1113 CAGGAGAGGAGTTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT 1172

Qy   3422 ACTACAGCAGCAGCATCATGTCAAGGGACGTGGGGGACCGGCCTTTGCAGAAG 3481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3645 ACTACAGCAGCAGCATCATGTCAAGGGACGTGGGGGACCGGCCTTTGCAGAAG 3704

Qy   3482 AGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGCCAGTGAGCAGCTGACG 3541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3705 AGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGCCAGTGAGCAGCTGACG 3764

Qy   3542 TCGCAGACCTGCGAAGGTGCGGTACAAGGGCATCCGCCCGGCTCCTCGGCTACCCCAGCC 3601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3765 TCGCAGACCTGCGAAGGTGCGGTACAAGGGCATCCGCCCGGCTCCTCGGCTACCCCAGCC 3824

Qy   3602 AGCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACAG 3661
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3825 AGCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACAG 3884

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGGCAATGCATGCTCGCACCTGCTTCAGGCCTCTCACT 3721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3885 GCATTAGGTTAACAGAATCATTAGCAATGGCAATGCATGCTCGCACCTGCTTCAGGCCTCTCACT 3944

Qy   3722 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGAAGATTTCCAAGGATCAGGTTGAGG 3781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3945 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGAAGATTTCCAAGGATCAGGTTGAGG 4004

Qy   3782 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATTT 3841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4005 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATTT 4064

Qy   3842 TGGGATATGATGATACAGACTAACTTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCCT 3901
          |||||||||||||||||||||||||| ||||| |||||||||||||||||||||||||
Db   4065 TGGGATATGATGATACAGACTAAC--TTTTTTTTTTTTTTGCCTTTTTTATTCTTGATGATCCT 4122

Qy   3902 CAAGGAAATACAACCTAG 3919
          ||||||||||||||||||
Db   4123 CAAGGAAATACAACCTAG 4140

RESULT 4
AAF31101
ID   AAF31101 standard; cDNA; 7224 BP.
XX
AC   AAF31101;
XX
DT   27-APR-2001 (first entry)
XX
DE   Methionine synthase coding sequence #2.
XX
KW   Analyte-binding enzyme; analyte analysis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200102600-A2.
XX
PD   11-JAN-2001.
XX
XX   30-JUN-2000; 2000WO-US018057.
PF
XX
PR   06-JUL-1999;   99US-00347878.
PR   06-DEC-1999;   99US-00457205.
XX
PA   (GEAT) GEN ATOMICS.
XX
PI   Yuan C;
XX
DR   WPI; 2001-071583/08.
XX
PT   Assaying method, useful for prognosis and diagnosis of disease, comprises
PT   contacting sample with a mutant analyte-binding enzyme and detecting
PT   binding.
XX
PS   Disclosure; Page; 187pp; English.
XX

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Qy   842  GTGCTTTGGGTGTGGTGCAGCTGAGATGAGAGACCTTTATTGAAATAATTGAAAAATGTACAACAG  901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1173  GTGCTTTGGGTGTGGTGCAGCTGAAATGAGAGACCTTTATTGAAATAATTGAAAAATGTACAACAG  1232

Qy   902  CCTATGTCCTCTGTTATCCCAATGGCCAAGCACCTAAAGATTTGCTATGGATGGCTTGGTCAATATAG  961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1233  CCTATGTCCTCTGTTATCCCAATGGCCAAGCACCTAAAGATTTGCTATGGATGGCTTGGTCAATATAG  1292

Qy   962  CGCCTTCTATGATGGCCAAGCACCTAAAGACACCTAAAGATTTTGCTATGGATGGCTTGGTCAATATAG  1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1293  CGCCTTCTATGATGGCCAAGCACCTAAAGACACCTAAAGATTTTGCTATGGATGGCTTGGTCAATATAG  1352

Qy  1022  TTGGAGGATGCTGTGGGTCAACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA  1081
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1353  TTGGAGGATGCTGTGGGTCAACCAGATCATATCAGCGGAAATTGCTGAAGCTGTGAAAA  1412

Qy  1082  ATTGTAAGCCTAGAGTTCCACCTGCCCACTGCTTTGAAGGACATATGTTACTGTCTGGTC  1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1413  ATTGTAAGCCTAGAGTTCCACCTGCCCACTGCTTTGAAGGACATATGTTACTGTCTGGTC  1472

Qy  1142  TAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGGCGCTGTAATG  1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1473  TAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGGCGCTGTAATG  1532

Qy  1202  TTTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGAAACTATGAAGAGCCTTGT  1261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1533  TTTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGAAACTATGAAGAGCCTTGT  1592

Qy  1262  GTGTTGCCAAAGTGCAGGTGGAAATGGAGCCCAGTTGTGGATGTCAACATGGATGATG  1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1593  GTGTTGCCAAAGTGCAGGTGGAAATGGAGCCCAGTTGTGGATGTCAACATGGATGATG  1652

Qy  1322  GCATGCTAGAATGGTCCAAGTGCAATGACCCAGATTTTGCAACTTAATTGCTTCCGAGCCAG  1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1653  GCATGCTAGAATGGTCCAAGTGCAATGACCCAGATTTTGCAACTTAATTGCTTCCGAGCCAG  1712

Qy  1382  ACATCGCAAAGTACCTTTTGTGCATGGAAGTGGGT  1441
          ||||||||||||||||||||||||||||||||||
Db  1713  ACATCGCAAAGTACCTTTGTGCATGGAAGTGGGT  1772

Qy  1442  TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTGTATAGTCTCAATAGTGTCTGAAGGAGAGGACG  1501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1773  TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTGTATAGTCTCAATAGTGTCTGAAGGAGAGGACG  1832

Qy  1502  ACTTCTTGGAGAAGGGCCAGGAAGATTAAAAACTATGGAAGTCTGTCTATGGTGTCATGGCTT  1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1833  ACTTCTTGGAGAAGGGCCAGGAAGATTAAAAACTATGGAAGTCTGTCTATGGTGTCATGGCTT  1892

Qy  1562  TTGATGAAGAAGGAGCAACAGGGCAACAGAGAAATCAGAGTGTGCCACCCGGGCCT  1621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1893  TTGATGAAGAAGGAGCAACAGGGCAACAGAGAAATCAGAGTGTGCCACCCGGGCCT  1952

Qy  1622  ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA  1681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1953  ACCATCTGCTTGTGAAAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA  2012

Qy  1682  TCCTAACCATTGGACTGGATGCGAATGGAGGAGCAACAACTTGTATGCCATTAATTTATCCATG  1741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2013  TCCTAACCATTGGACTGGATGCGAATGGAGGAGCAACAACTTGTATGCCATTAATTTATCCATG  2072

Qy  1742  CAACAAAAGTCATTAAAGAAACATTACCTGGAGCAGAATAAGTCGGAGGTCTTTCCCAACT  1801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2073  CAACAAAAGTCATTAAAGAAACATTACCTGGAGCAGAATAAGTCGGAGGTCTTTCCAACT  2132

Qy  1802  TGTCCTTCCTTCCGAGGAATGGAGAAGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTT  1861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2133  TGTCCTTCCTTCCCGAGGAATGGAGAAGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTT  2192

Qy  1862  ACCAGTCGAATCAAGTCTCGGCATGGAATGCTCGGACTACGTGAAACCTCCCTGTGT  1921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2193  ACCAGTCAATCAAGTCTCGGCATGGAATGCTCGGACTACGTGAAACCTCCCTGTGT  2252

Qy  1922  ATGATGATATCCATAAGGAACTTCTGCAGACTTCTGTGAAGATCTCATCTGGAATAAAGACC  1981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2253  ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC  2312

Qy  1982  CTGAGGGCCACTGAGAAGCTCTTACGTTATGCCAAA  2041
          ||||||||||||||||||||||||||||||||||||
Db  2313  CTGAGGGCCACTGAGAAGCTCTTACGTTATGCCAAA  2372

Qy  2042  TCATTCAGACTGATGACTGACTGGAAAAATGGCCCTTG  2101
          ||||||||||||||||||||||||||||||||||||||
Db  2373  TCATTCAGACTGATGACTGACTGGAAAAATGGCCCTTG  2432

Qy  2102  TGAAGGGCATTGAAAACATATTATTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAA  2161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2433  TGAAGGGCATTGAAAACATATTATTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAA  2492

Qy  2162  AATATCCCGACCTCTCAATATAATTGAAGAACCCTGATGAATGAATGAAATTGTTG  2221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2493  AATATCCCGACCTCTCAATATAATTGAAGAACCCCCTGATGAATGAAATGAAATTGTTG  2552

Qy  2222  GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAGTCAGCCCGGGTTA  2281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2553  GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA  2612

Qy  2282  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAAGAGAAACCAGAG  2341
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2613  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAAGAGAAACCAGAG  2672

Qy  2342  TGCTTAACGGCACAGTGAGAAGGAGACCCTTACCAGGGCGACCATGCTGCTGGCCACTG  2401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2673  TGCTTAACGGCACAGTGAGAAGGAGACCCTTACCAGGGCGACCATGCTGCTGGCCACTG  2732

Qy  2402  TTAAAGGCGACGTGCACGACAATAGTTGGAGTAGTCCTTGGCTGTCAATA  2461
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2733  TTAAAGGCGACGTGCACGACAATAGTTGGAGTAGTCCTTGGCTGTCAATA  2792

Qy  2462  ATTTCCCAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATCTGCTC  2521
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2793  ATTTCCCAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATCTGCTC  2852

Qy  2522  TTGACCACAAAGCAGATAATAATTGGCTGTGACTCATCTCCTCCTCCTGGATGAAA  2581
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2853  TTGACCACAAAGCAGATAATAATTGGCTGTGACTCATCTCCTCCTCCTGGATGAAA  2912

Qy  2582  TGATTTTTGTTGCCAAGGAAATGGAGAATTAGCTATAAATCTCCGAGATTGTTGAG  2641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2913  TGATTTTTGTTGCCAAGGAAATGGAGAATTAGCTATAAATCTCCGAGATTGTTGAG  2972

Qy  2642  GAGCAACCACTTCAAAAACCCAAAAACCCACACAGCAGTTAAAAATAGCTCCGAGATACAGGACC  2701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2973  GAGCAACCACTTCAAAAAACCCAAAAACCCACACAGCAGTTAAAAATAGCTCCGAGATACAGGACC  3032

Qy  2702  TAATCCATGTCCTGGACGCGTCCCAGAGTGGTGTCCAGCTGTTAGATGAAA  2761
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3033  TAATCCATGTCCTGGACGCGTCCCAGAGTGGTGTCCAGCTGTTAGATGAAA  3092

Qy  2762  ATCTAAAGGAATGAATACTTTGGAGGAGGAGAGAAATCATGGAAGATATTAGACAGGACC  2821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3093  ATCTAAAGGAATGAATACTTTGGAGGAGGAGAGAAATCATGGAAGATATTAGACAGGACC  3152

Qy  2822  ATTATGAGTCTCTCAAGGAGGAGGAGAACCCTTAAGTCAAGCCAGAAAAAGTGTT  2881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3153  ATTATGAGTCTCTCAAGGAGGAGGAGAACCCTTAAGTCAAGCCAGAAAAAGTGTT  3212

Qy  2882  TCCAAATGGATTGGCTGTCTGAAACCTCACCCAGTGAAGCCACCGTTTATTGGGACCCAGG  2941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3213  TCCAAATGGATTGGCTGTCTGAAACCTCACCCAGTGAAGCCACCGTTTATTGGGACCCAGG  3272

Qy  2942  TCTTTGAAGACTATGACCTCGAAGAGTCTGGACTACATTGACTGAGGCCTTTCTTTG  3001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3273  TCTTTGAAGACTATGACCTCGAAGAGTCTGGACTACATTGACTGAGGCCTTTCTTTG  3332

Qy  3002  ATGTCTGCAGCTCCGGGCAAGTACCCGGAATCGAGGCTTCCCAAGTATCTGAAGATCTCATCTGAAGATCTGAAGAGATAAAGACCA  3061
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Db  3333  ATGTCTGGCAGCCAAGTACCCGATCCGAATCGAGCTTTCCAAGATATTTAACGACA  3392
Qy  3062  AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCACAATATGCTGAACACAC  3121
            ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  3393  AAACAGTAGGTGGAGACGGCCAGGAAGGTCTACGATGATGCCACAATATGCTGAACACAC  3452
Qy  3122  TGATTAGTCAAAAGAAACTCCGGGGCCCGGGGTGTGGTTGGGTTCTGGCCAGCACAGAGTA  3181
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  3453  TGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGGTTGGGTTCTGGCCAGCACAGAGTA  3512
Qy  3182  TCCAAGACGACATTCACCTGTACGGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAG  3241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3513  TCCAAGACGACATTCACCTGTACGGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAG  3572
Qy  3242  CCACTTCTATGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGAGCCATACT  3301
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3573  CCACCTTCTATGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGAGCCATACT  3632
Qy  3302  ACTGCCTCTCAGACTTCATCGGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3633  ACTGCCTCTCAGACTTCATCGGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3692
Qy  3362  TTGCCGGTTGCCTGCTTTGGGGTAGAACAGCTGAGCCAAGGCTATGAGGATGGTGACG  3421
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db  3693  TTGCCGGTTGCCTGCTTTGGGGTAGAACAGCTGAGCCAAGGCCTATGAGGATGGTGACG  3752
Qy  3422  ACTACAGCAGCATCATGTCAAGGGCGCTGGGGACCCGCTGGGCAGAGGCCTTTGCGAAAG  3481
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  3753  ACTACAGCAGCATCATGTCAAGGGCTCAGGGGACCCGCTGGGCAGAGGCCTTTGCGAAAG  3812
Qy  3482  AGTCCATGAAAGAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGCTGAGCTGACG  3541
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3813  AGTCCATGAAAGAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGCTGAGCTGACG  3872
Qy  3542  TCGCAGACCTGCGAAGGTTGCGTACAAGGGTACAAGGGACATCGGCTCCTGGCTACCCCAGCC  3601
            ||||||||||||| ||| |||||||||| ||||||||||||||| ||||||||||||||||
Db  3873  TCGCAGACCTGCGCAGGCTGCGTACAAGGGTACAAGGGACATCCGCGGCTCCTGGCTACCCCAGCC  3932
Qy  3602  AGGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACAG  3661
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3933  AGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACAG  3992
Qy  3662  GCATTAGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACT  3721
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3993  GCATTAGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACT  4052
Qy  3722  TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGAAGATTTCCAAGGATCAGGTTGAGG  3781
            |||||||||||||| ||  ||||||||||||| ||||||||||||||||||||||||||||
Db  4053  TCTCCAATTTGAAGTCCAGGCTCCAAATATTTTGCTGTGTGGGAAGATTTCCAAGGATCAGGTTGAGG  4112
Qy  3782  ATTATGCATTGAGGAAGAACATATCTGTGGCTTGAGGTTGAGGAAAATGGCTTGGACCCATTT  3841
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4113  ATTATGCATTGAGGAAGAACATATCTGTGGCTTGAGGTTGAGGAAAATGGCTTGGACCCATTT  4172
Qy  3842  TGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTGCCTTTTTATCTTGATGATCCT  3901
            |||||||||||||||||||||||  |||||||||||||||||||||||| |||||||| ||
Db  4173  TGGGATATGATACAGACTAAC--TTTTTTTTTTTTTTTTGCCTTTTTATTCTTGATGATCAT  4230
Qy  3902  CAAGGAAATACAACCTAG  3919
            ||||||||||||||||||
Db  4231  CAAGGAAATACAACCTAG  4248
```

RESULT 5
AAV34063
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ID   AAV34063 standard; cDNA; 3920 BP.
XX
AC   AAV34063;
XX
DT   01-MAR-1999  (first entry)
XX
DE   Human methionine synthase cDNA (wild-type).
XX
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KW   Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW   cardiovascular disease; colon cancer; diagnosis; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             64..3861
FT                   /tag= a
FT                   /EC_number= "2.1.1.13"
XX
PN   CA2217153-A.
XX
PD   27-MAY-1998.
XX
PF   97CA-02217153.
XX
PR   27-NOV-1997;
PR   96US-0031964P.
PR   20-JUN-1997;  97US-0050310P.
XX
PA   (MART-) MARTINEX R & D INC.
XX
PI   Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR   WPI; 1998-569373/49.
DR   P-PSDB; AAW68594.
XX
PT   DNA encoding methionine synthase polypeptide - and corresponding
PT   polypeptide, cells, antibody and therapeutic methods.
XX
PS   Claim 6; Fig 3; 64pp; English.
XX
CC   This cDNA clone encodes human wild-type methionine synthase (see
CC   AAW68594). A survey of the NCBI databases yielded several sequences
CC   corresponding to methionine synthases from different organisms.
CC   Comparison of these sequences generated 4 very conserved regions.
CC   Degenerate oligonucleotides (see AAV34064-104) based on these conserved
CC   sequences were used as primers for RT-PCR with human and mouse mRNA. PCR
CC   products were subcloned, sequenced and aligned. Additional sequences were
CC   subsequently obtained by further PCR and inverse PCR. The full-length
CC   sequence encodes a 1265-amino acid protein of predicted mol.wt. 141 kDa.
CC   Using FISH, the gene was mapped to human chromosome band 1q43. Mutations
CC   in this gene are associated with hyperhomocysteinaemia. One missense
CC   mutation (2758 C to G) and a 3 bp deletion (2640-42) have been identified
CC   in patients of the cblG complementation group. A polymorphism (2756 A to
CC   G) has also been detected. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease,
CC   and colon cancer. Methods for detecting sequence variants for methionine
CC   synthase, involving SSCP analysis or RFLP polymorphism analysis, are
CC   claimed, as are methods for screening for therapeutic compounds that
CC   modulate methionine synthase activity
XX
SQ   Sequence 3920 BP; 1114 A; 866 C; 975 G; 965 T; 0 U; 0 Other;
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Query Match             96.8%;  Score 3793.8;  DB 2;  Length 3920;
Best Local Similarity   98.5%;  Pred. No. 0;
Matches  3861;  Conservative    0;  Mismatches   57;  Indels    3;  Gaps  3;

Qy      1  GGTCACCTGTGGAGAGCACGTCTTCTCTGCGCGCCCTCTGCGCCAAGGAGGAGGACTCGAC   60
           ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db      1  GGTCACCTGTGGAGAGCACGTCTTCTCTGCGCGCCCCTCTGCGCCAAGGAGGAGGACTCGAC   60

Qy     61  AACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAGAGAAAACCCTGCGG  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  AACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAGAGAAAACCCTGCGG  120

Qy    121  GATGAGATCAATGCCATTCTGCTGAAGAGGATTATGTGTCTGGATGAGGATGGGGACC  180
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GATGAAATCAATGCCATTCTGCTGAAGAGGATTATGTGTCTGGATGAGGATGGGGACC  180

Qy    181  ATGATCCAGCGGGAGAAGTAAACGAAGAACACTTCCGAGGTCAGGAGTTAAAGATCAT  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ATGATCCAGCGGGAGAAGTAAACGAAGAACACTTCCGAGGTCAGGAGTTAAAGATCAT  240
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Qy  1321  GGCATGCTGAGATGGTCCAAGTGCAATGACCAGAATTTTGCAACTTAATTGCTTCCGAGCCA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  GGCATGCTGAGATGGTCCAAGTGCAATGACCAGAATTTTGCAACTTAATTGCTTCCGAGCCA  1380

Qy  1381  GACATCGCAAAGTACTTGTGCATCGGAGTGCATTGCAATAGCATTAGTCTGAAGGAAGAGGAC  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  GACATCGCAAAGTACTTGTGCATCGGAGTGCATTGCAATAGCATTAGTCTGAAGGAAGAGGAC  1440

Qy  1441  TTAAAGTGCTGCCAAGGAAAGTGCATTGCATTGTCAATAGCATTAGTCTGAAGGAAGAGGAC  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  TTAAAGTGCTGCCAAGGAAAGTGCATTGCATTGTCAATAGCATTAGTCTGAAGGAAGAGGAC  1500

Qy  1501  GACTTCTTGGAGAGGGCCAGGAAGATTAAAAGTATGGAGCTGCTGCTATGTGGTCATGGCT  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  GACTTCTTGGAGAGGGCCAGGAAGATTAAAAGTATGGAGCTGCTGCTATGTGGTCATGGCT  1560

Qy  1561  TTTGATGAAGAGGACAGGCAACAGAGAAACAGACAAAATCAGAGTGTGCACCCGGGCC  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TTTGATCAAGAGCACAGGCAACACAGAGAAACAGACAAAATCAGAGTGTGCACCCGGGGC  1620

Qy  1621  TACCATCTGCTTGTGAAAAAACTGGCTTAATCCAAATGACATTATTTTGACCCTAAT  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  TACCATCTTGTGAAAAAACTCGGCTTAATCCAAATGACATTATTTTCACCCTAAT  1680

Qy  1681  ATCCTAACCATTGGACTGGAATGGAGGAACAACAACTTGTATGCCCATTAATTTTATCCAT  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  ATCCTAACCATTGGACTGGAATGGAGGAACAACAACTTGTATGCCCATTAATTTTATCCAT  1740

Qy  1741  GCAACAAAAGTCATTAAAGAGAAACATTACCTGGAGGCCAGAATAAGTGGAGGTCTTTCCAAC  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  GCAACAAAAGTCATTAAAGAGAAACATTACCTGGAGGCCAGAATAAGTGGAGGTCTTTCCAAC  1800

Qy  1801  TTGTCCTTCCTTCCGAGGAGAGCTTCTTACGTTATGCCCAGACTCAAGGCACCAGGAGGAAGAAA  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TTGTCCTTCCTTCCGAGGAGAGCTTCTTACGTTATGCCCAGACTCAAGGCACCAGGAGGAAGAA  1860

Qy  1861  TACCATGCAATCAAGTCTCGGCCATGGACATGTGAATGCTGACATGAGTAGTGAAACCTCCCTGTG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  TACCATCAATCAAGTCTCGGCCATGGACATGTGAATGCTGACATGAGTAGTGAAACCTCCCTGTG  1920

Qy  1921  TATGATGATATCCATAAGGACAACTTCTGAGATCTCATCTGAAGATCTCATCTGGAATAAAGAC  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  TATGATGATATCCATAAGGACAACTTCTGAGATCTCATCTGAAGATCTCATCTGGAATAAAGAC  1980

Qy  1981  CCTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACGAGGAGGAAGAAA  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CCTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACGAGGAGGAAAGAA  2040

Qy  2041  GTCATTCAGACTGATGAGTGAGGAAATGGCCCGTGTCGAAGAACGCCTTGAGTATGCCCTT  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  GTCATTCAGACTGATGAGTGAGGAAATGGCCCGTGTCGAAGAACGCCTTGAGTATGCCCTT  2100

Qy  2101  GTGAAGGGCATTGAAAAACATATTATTGAGGAAGTTAAACCAAAA  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  GTCAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGTTAAACCAAAA  2160

Qy  2161  AAATATCCCGGACCTCTCAATATAATTGAAGGACCCCTGATGAATGGAATGAAAATTGTT  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  AAATATCCCGGACCTCTCAATATAATTGAAGGACCCCTGATGAATGGAATGAAAATTGTT  2220

Qy  2221  GGTGATCTTTTTGGAGCTGGAAAACATATGTTTCTACCTCAGGTTAAACCAAGCCAGGAAGCCAGGAACCAGA  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGTGATCTTTTTGGAGCTGGAAAACATATGTTTCTACCTCAGGTTAAACCAAGCCAGGAAGCCAGGAACCAGA  2280

Qy  2281  ATGAAGAAGGCTGTTGGCCACTGAGAGACCCTTACCCAGGGCACCCTTG  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  ATGAAGAAGGCTGTTGGCCACTGAGAGACCCTTACCCAGGGCACCCTTG  2340

Qy  2341  GTGCTTAACGACAGTAGAAGAAGAGACCCTTACCAGGGCACCCTTGGCGCCACT  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  GTCCTTAACGGCACAGTAGAAGAAGAGACCCTTACCAGGGCACCCTTGGCGCCACT  2400

Qy  2401  GTTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTGCAAT  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GTTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTCCTTGGCTGCAAT  2460
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Qy  241   GCCAGGCCGCTGAAAGGCCAACAATGACATTTTAAGTATAACTTCAGCCTGATGTCATTTAC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241   GCCAGGCCGCTGAAAGGCCAACAATGACATTTTAAGTATAACTTCAGCCTGATGTCATTTAC  300

Qy  301   CAAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGC  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301   CAAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGC  360

Qy  361   AGCACTAGTATTGCCCAAGCTACTATGGCCTTGAACACTTGGCCTACCGATGACATG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361   AGCACTAGTATTGCCCAAGCTACTATGGCCTTGAACACTTGGCCTACCGGATGAACATG  420

Qy  421   TGCTCTCGCAGGAGTGGCCAGAAAAGCTGCCGGAGGTAACTCTCCAGACAGGGAATTAAG  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421   TGCTCTCGCAGCAGTGGCCAGAAAAGCTGCCGGAGGTAACTCTCCAGACACGGAATTAAG  480

Qy  481   AGGTTGTGGCAGGGGCTCGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481   AGGTTCTGGCAGGGGCTCGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTG  540

Qy  541   GAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTGAAGCATACCAAGAGCAG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541   GAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTGAAGCATACCAAGAGCAG  600

Qy  601   GCCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601   GCCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACT  660

Qy  661   GCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661   GCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCC  720

Qy  721   CGGCCTATCTTTATTCAGGGACGATCGTGATAAAGTGGGCCGGCCCGCACTCTTTTCCGGACAG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721   CGGCCTATCTTTATTCAGGGACGATCGTGATAAAGTGGGCCGGCCCGCACTCTTTTCCGGACAG  780

Qy  781   ACAGGAGGGGATTTGTCATCAGCGTGTCTGCATTGGATTAAAT  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781   ACAGGAGGGGATTTGTCATCAGCGTGTCTGCATTGGATTAAAT  840

Qy  841   TGTGCTTTGGGTCAGCTGAGATGAGACCTTTTATTGAAATAATTGAAAATTGTACAACA  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841   TGTGCTTTGGGTCAGCTGAGATGAGACCTTTTATTGAAATAATTGAAAATTGTACAACA  900

Qy  901   GCCTATGTCCCTGTTATCCCAATGCCAGGTCTTCCCAACACCTTGGTGACTATGATGAA  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901   GCCTATGTCCCTGTTATCCCAATGCCAGGTCTTCCCAACACCTTGGTGACTATGATGAA  960

Qy  961   ACGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTGTGATGGCTTGGTGATGCCTGGT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961   ACCCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTGTGATGGCTTGGTGATCAATATA  1020

Qy  1021  GTTGGGAGGATGTGTGGGTCAACACCAGTCACACCACGTAAACTTGTGAAGGCGCTGTGAAA  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GTTGGGAGGATGCTGTGTGGGTCAACACCAGTCACACCACGTAAACTTGTGAAGCGCTGTGAAA  1080

Qy  1081  AATTGTAAGCCTAGAGTTCCACCTGCCACTGCACCCACCCACGATTTTGCTGCTGCTGGT  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  AATTGTAAGCCTAGAGTTCCACCTGCCACCGCACCCACCCACGATTTTGCTGCTGCTGGT  1140

Qy  1141  CTAGAGCCCTTCAACGATTGGATACCACCAGACACTGTAAACTTGTTAACATTGGAAGAGCCTTG  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  CTAGAGCCCTTCAACGATTGGATACCACCAGACACTGTAAACTTGTTAACATTGGAAGAGCCTTG  1200

Qy  1201  GTTGCAGGATCAAGGAAGTTTGCTAACATGTCATCATGCCAGGAAACTATGAAGAGCCTG  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GTTGCAGGATCAAGGAAGTTTGCTAACATGTCATCATGCCAGGAAACTATGAAGAGCCTG  1260

Qy  1261  TGTGTTGCCAAGTGCAGGTGGAAATGGGAAATGTCAACATGGATGAT  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  TGTGTTGCCAAGTGCAGGTGGAAATGGGAAATGTCAACATGGATGAT  1320
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Qy    2401 GTTAAAGGCGACGTGCACGACAGAAGCAAGAACATAGTTGGAGTAGTTCCTTGGCTGCAAT 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 GTTAAAGGCGACGTGCACGACAGAAGCAAGAACATAGTTGGAGTAGTTCCTTGGCTGCAAT 2460

Qy    2461 AATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCT 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 AATTTCCGAGTTATTGATTTAGGAGTGATGACTCCATGTGATAAGATACTGAAAGCTGCT 2520

Qy    2521 CTTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGGATGAA 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 CTTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGGATGAA 2580

Qy    2581 ATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGA 2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 ATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGA 2640

Qy    2641 GGAGCAACCACTTCAAAAACCCACACAGCAGTAAAATAGTTCCGAGATACAGTGCACCT 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 GGAGCAACCACTTCAAAAACCCACACAGCAGTAAAATAGTTCCGAGATACAGTGCACCT 2700

Qy    2701 GTAATCCATGTCCTGACGCGTCCAAGAGTGGTGTGTGTTCCCAGCTGTTAGATGAA 2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 GTAATCCATGTCCTGACGCGTCCAAGAGTGGTGTGTGTTCCCAGCTGTTAGATGAA 2760

Qy    2761 AATCTAAAGGATGAATACTTTGAGGAGGAGAGCAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGT 2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 AATCTAAAGGATGAATACTTTGAGGAGGAGAGCAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGAT 2820

Qy    2821 CATTATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGT 2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 CATTATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGAT 2880

Qy    2881 TTCCAAATGGATTGGCTGTCTGACAACCTCACCCCAGTGAAGCCCACAGTTTATTGGGACCCAG 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TTCCAAATGGATTGGCTGTCTGACAACCTCACCCCAGTGAAGCCCACAGTTTATTGGGACCCAG 2940

Qy    2941 GTCTTTGAAGACTATGACCTGCGAGAGCTGGTGGACTACATTCATTGACTGGAAGCCTTCTTT 3000
           ||||||||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db    2941 GTCTTTCAAGACTATGACCTGCGAGAGCTGGTGGACTACATTGACTGGAACCCCTTCTTT 3000

Qy    3001 GATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGCTTCCCCAAGATATTAACGAC 3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 GATGTCTGCAGCTCCGGGGCAAGTCAAGTACCCGAATCGAGCTTCCCCACATATTAACCAC 3060

Qy    3061 AAAACAGTAGGTGGAGAGGCCAGGAAGTCTACGACGTCTACGATGATGCCCACAACACA 3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 AAAACAGTAGGTGGAGAGGCCAGGAAGTCTACGACGTCTACGATGATGCCCACAATGCTGAACACA 3120

Qy    3121 CTGATTAGTAGTCAAAAGAAACTCCGGGGCGTGGTTCGGTGGTTCGGCCAGCACAGAGT 3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121 CTGATTAGTAGTCAAAAGAAACTCCGGGGCGTGGTTCGGTGGTTCGGCCAGCACAGAGT 3180

Qy    3181 ATCCAAGACGACATTCACCTGTCCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTG 3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181 ATCCAAGACGACATTCACCTGTCCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTG 3240

Qy    3241 GCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGACTCTGCCACCACGGAGCCATAC 3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241 GCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGACTCTGCCACCACGGAGCCATAC 3300

Qy    3301 TACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGGGATCCGGTGACTTCTGGGCCTG 3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 TACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGGGATCCGGTGACTTCTGAGCCTG 3360

Qy    3361 TTTGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGGTGAC 3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 TTTGCCGTTGCCTGCTTTGGGGTAGAAGACCTCAAGGCGCCTATGAGGATGATGGTGAC 3420

Qy    3421 GACTACAGCAGCAGCATCATGTCAAGGTCAAGGCGCTGGGGGACCGGCTTTGCAGAA 3480
           |||||||||||||||||||||||| ||||||||||||||||||||||||| ||||||||
Db    3421 GACTACAGCAGCAGCATCATGTCAAGGTCAAGGCGCTGGGGGACCGGCTTTGCAGAA 3480

Qy    3481 GAGCTCCATGAAAGAGTTCGCCCGAGAACTGTGGGCCTACTGTGGCAGTGACCAGCTGGAC 3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    3481 GAGCTCCATGAAAGAGTTCGCCCGAGAACTGTGGGCCATCATGTGGGCCTGCCGGCTGGAC 3540

Qy    3541 GTCGCAGACCTGCGAAGGTTGCGGGTACAAGGGCATCCGGCTCCTGGCTACCCCAGC 3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 GTCGCAGACCTGCGAAGGTTGCGGGTACAAGGGCATCCGGCTCCTGGCTACCCCAGC 3600

Qy    3601 CAGCCGACCACACCGAGAAGTCACCATGTGAGACTCGAGACATCGAGCAGTCTACA 3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 CAGCCCCACCACACCGAGAAGTCACCATGTGACACTCGGACACTCGAGCAGTCTACA 3660

Qy    3661 GGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCA-GGCCTCTA 3719
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    3661 GCCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGGGCCTCTCAGGGGCCTCTA 3720

Qy    3720 CTTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGGAAGAATTCCAAGGATCAGGTTGA 3779
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 CTTCTCCAATTTCAGGTCC-AATATTTGCTGTAGGCAAGAATTTCCAAGGATCAGGTTGA 3779

Qy    3780 GGATTATGCATTGAGGAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGAGACCCAT 3839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3780 GGATTATGCATTGAGGAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGAGACCCAT 3839

Qy    3840 TTTGGGATATGATACAGACTAACTTTTTTTTTTTTT-GCCTTTTTATCTTGATGAT 3898
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    3840 TTTGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTGGCCCTTTTTATCTTGATGAT 3899

Qy    3899 CCTCAAGGAAATACAACCTAG 3919
           |||||||||||||||||||||
Db    3900 CCTCAAGGAAATACAACCTAG 3920
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RESULT 6
ADI39109
ID   ADI39109 standard; DNA; 3798 BP.
XX
AC   ADI39109;
XX
DT   22-APR-2004 (first entry)
XX
DE   Homo sapiens metH DNA.
XX
KW   fermentation; methionine; Coryneform bacterium; methionine synthase;
KW   MetH; animal feed additive; sulphur; human nutrition; animal nutrition;
KW   cosmetic; pharmaceutical; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..3798
FT   /*tag= a
FT   /product= "metH"
XX
PN   WO2003087386-A2.
XX
PD   23-OCT-2003.
XX
PF   16-APR-2003; 2003WO-EP004010.
XX
PR   17-APR-2002; 2002DE-01017058.
XX
PA   (BADI) BASF AG.
XX
PI   Kroeger B, Zelder O, Klopprogge C, Schroeder H, Haefner S;
XX
DR   WPI; 2003-877106/81.
DR   P-PSDB; ADI39110.
XX
PT   Fermentative production of sulfur-containing compounds, particularly L-
PT   methionine, useful as feed additives, by using Coryneform bacteria that
PT   overexpress methionine synthase.
XX
PS   Claim 5; SEQ ID NO 43; 304pp; German.
XX

CC   This invention describes a novel method for the fermentative production
CC   of methionine by growing a sulphur-producing Coryneform bacteria that
CC   expresses at least one heterologous nucleic acid encoding a protein with
CC   methionine synthase (MetH) activity. Methionine accumulates in the medium
CC   or the cells. The method can be used to produce an L-methionine-
CC   containing animal feed additive by culturing an L-Met-producing
CC   microorganism, removing water from the resulting broth, removing 0-100%
CC   of the biomass formed and drying the product to produce the feed additive
CC   in powdered or granular form. The nucleic acid encoding MetH has sequence
CC   homology less than 100% with respect to the metH coding sequence of
CC   Corynebacterium glutamicum ATCC 13032. Optionally at least one other gene
CC   in the methionine biosynthesis pathway (e.g. aspartate kinase,
CC   glyceraldehyde-3-phosphate dehydrogenase or 3-phosphoglycerate kinase) is
CC   also amplified or mutated so that it is not affected by metabolites. Also
CC   at least one metabolic pathway that reduces production of methionine is
CC   at least partly switched off (e.g. homoserine kinase, threonine
CC   dehydratase or threonine synthase). The method is especially used to
CC   produce L-methionine, useful as an additive for animal feeds. More
CC   generally sulphur-containing fine chemicals are useful in human and
CC   animal nutrition, cosmetics and pharmaceuticals. This sequence encodes a
CC   metH protein described in the disclosure of the invention.
XX
SQ   Sequence 3798 BP; 1082 A; 809 C; 982 G; 925 T; 0 U; 0 Other;

Query Match   96.6%; Score 3785.2; DB 10; Length 3798;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 3790; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

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Qy    64 ATGTCACCCGGCTCCAAGACCTGTCCCAACCCGAAGGTCTGAAGAAACCCTGCCGGAT 123
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGTCACCCGGCTCCAAGACCTGTCCCAACCCGAAGGTCTGAAGAAACCCTGCCGGAT 60

Qy   124 GAGATCAATGCCATTCTGCAGAAGAGATTATGTGTCTGGATGGGAGGGATGGGGACCATG 183
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GAGATCAATGCCATTCTGCAGAAGAGATTATGTGTCTGGATGGGAGGGATGGGGACCATG 120

Qy   184 ATCCAGCGGGAGAAGCTAAACGAAGAGACACTTCCGAGGTCAGGAATTTAAAGATCATGCC 243
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ATCCAGCGGGAGAAGCTAAACGAAGAGACACTTCCGAGGTCAGGAATTTAAAGATCATGCC 180

Qy   244 AGGCCGCTGAAAGGCAACAATGACATTTAAGTAGTATAACTCAGCCTGATGTCATTTACCAA 303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGGCCGCTGAAAGGCAACAATGACATTTAAGTAGTATAACTCAGCCTGATGTCATTTACCAA 240

Qy   304 ATCCATAAGGAATACTTGCTGCTGGGCAGATACTTTAGTAGC 363
         ||||||||||||||||||||||||||||||||||||||||||
Db   241 ATCCATAAGGAATACTTGCTGCTGGGCAGATACTTTAGTAGC 300

Qy   364 ACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGAACATGTGC 423
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGAACATGTGC 360

Qy   424 TCTGCGAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAAGAGG 483
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCTGCGAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAAGAGG 420

Qy   484 TTTGTGTGGCAGGGGCTCGGGGTTCGGCTGGGCCGACTAATAAGAACACTCTCGTGTCCCCATCTGTGGAA 543
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTGTGTGGCAGGGGCTCGGGGTTCGGCTGGGCCGACTAATAAGAACACTCTCGTGTCCCCATCTGTGGAA 480

Qy   544 AGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCC 603
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCC 540

Qy   604 AAAGGACTTCTGGATGCGCGGGGTTGATATCTTCTTACTCATTGAAACTATTTTTGATACTGCC 663
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGGACTTCTGGATGCGCGGGGTTGATATCTTCTTACTCATTGAAACTATTTTTGATACTGCC 600

Qy   664 AATGCCAAGGCAGCGCCTTGTTGCACTCCAAAATCTTTTGGAGGAAAATGCTCCCCGG 723
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AATGCCAAGGCAGCAGCCTTGTTGCACTCCAAAATCTTTTGGAGGAAAATGCTCCCCG 660

Qy   724 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGCACTCTTTCCGGACAGACA 783
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGCACTCTTTCCGGACAGACA 720

Qy   784 GGAGAGGGATTTGTCATCAGCGTGTCTCATGGGAGAACCACTCTGCATTGGATTAAATTGT 843
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GGAGAGGGATTTGTCATCAGCGTGTCTCATGGGAGAACCACTCTGCATTGGATTAAATTGT 780

Qy   844 GCTTTGGGTGCAGCTGAGATGAGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCC 903
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GCTTTGGGTGCAGCTGAGATGAGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCC 840

Qy   904 TATGTCCTGTTATCCCAATGCAGGTCTTCCCAACACCTTGGTGACTATGATGAAACG 963
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TATGTCCTGTTATCCCAATGCAGGTCTTCCCAACACCTTGGTGACTATGATGAAACG 900

Qy   964 CCTTCATGATGGCCAAGCACCTAAAGCATTTGCTATGGATGGCTTGGTCAATATAGTT 1023
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CCTTCATGATGGCCAAGCACCTAAAGCATTTGCTATGGATGGCTTGGTCAATATAGTT 960

Qy  1024 GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1083
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1020

Qy  1084 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTCTA 1143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTCTA 1080

Qy  1144 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCGCTGTAATGTT 1203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCGCTGTAATGTT 1140

Qy  1204 GCAGGATCAAGGAAGTTGCTAAACTCATCATCATGGCAGGAAACTATGAAGAAGCCTTGTGT 1263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GCAGGATCAAGGAAGTTGCTAAACTCATCATCATGGCAGGAAACTATGAAGAAGCCTTGTGT 1200

Qy  1264 GTTGCCAAAGTGCAGGTGGAAATGGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATGGC 1323
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GTTGCCAAAGTGCAGGTGGAAATGGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATGGC 1260

Qy  1324 ATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCGGAC 1383
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGAC 1320

Qy  1384 ATCGCAAAGGTACCTTTGTCATGCATGCTGTGATTGAGAAGCTGGGTTA 1443
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ATCGCAAAGGTACCTTTGTCATGCATGCTGTGATTGAGAAGCTGGGTTA 1380

Qy  1444 AAGTGCTGCCAAGGAAGGACAGTGCATTGTCAATAGCATTTTTGAAGGAAGGAGGAGCAGAC 1503
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 AAGTGCTGCCAAGGAAGGACAGTGCATTGTCAATAGCATTTTTGAAGGAAGGAGGAACGAC 1440

Qy  1504 TTCTTGGAGAAGGCCAGGAAGCTGCCAGGAGGATTAAAAAGTATGGAGCGTCATGGCTTTT 1563
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 TTCTTGGAGAAGGCCAGGAAGCTGCCAGGAGGATTAAAAAGTATGGAGCGTCATGGCTTTT 1500

Qy  1564 GATGAAGAAGACAGGACAACAGAAAACAGACACAAAAATCAGAGTGTGCACCCGGCCTAC 1623
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 GATGAAGAAGACAGGACAACAGAAAACAGACACAAAAATCAGAGTGTGCACCCGGCCTAC 1560

Qy  1624 CATCTGCTTGTGAAAAAACTGGCTTTAATCCAAATGACATTATTTTGACCCTAATATC 1683
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 CATCTGCTTGTGAAAAAACTGGCTTTAATCCAAATGACATTATTTTGACCCTAATATC 1620

Qy  1684 CTAACCATTGGAACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATGCA 1743
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 CTAACCATTGGAACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATGCA 1680

Qy  1744 ACAAAGTCATTAAGAAACATTACCTGGACGCCAGAATAAGTGCACCGAATAAGTGCTCCCCTG 1803
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 ACAAAGTCATTAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTG 1740

Qy  1804 TCCTTCTTCCCTTCCGGAGGAATGCAATCGGAAGCCATTCGAGAGCAATCGAATGCATGGGGTTTCCTTTTAC 1863
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1741 TCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTCCTTTAC 1800

Qy   1864 CATGCAATCAAGTCTGGCATGACGAGATAGTGAAGAGCTGTCGGAAACCTCCCTGTGTAT 1923
          ||||||| |||||||||||||||| |||||||||||||||| | ||||||||||||||||
Db   1801 CATGCAATCAAGTCTGGCATGACACATGGGGATAGTGAAGAGCTGTCGGAAACCTCCCTGTGTAT 1860

Qy   1924 GATGATATCCAATAAGGAACTTCTGCAGCTTCGTGAAGACTCATCTGAAGATCTCATCTGGAATAAAGACCCT 1983
          |||||||||||||||||||||||||||| | |||||||||||||||||||||||||||||
Db   1861 GATGATATCCAATAAGGAACTTCTGCAGCTTCATCTGAAGATCTCATCTGGAATAAAGACCCT 1920

Qy   1984 GAGGCCACTGAGAAGTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAGTC 2043
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GAGGCCACTGAGAAGTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAGTC 1980

Qy   2044 ATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTGATGCCCTTGTG 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTGATGCCCTTGTG 2040

Qy   2104 AAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGCCAGGTTAAACCAAAAAAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGCCAGGTTAAACCAAAAAAA 2100

Qy   2164 TATCCCCGACCTTCAATATAATTGAAGGACCCCTGATGAATGAATTGTTGGT 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TATCCCCGACCTTCAATATAATTGAAGGACCCCTGATGAATGAATTGTTGGT 2160

Qy   2224 GATCTTTTGGAGCTGAAAAATGTTCTACCTCAGTTATAAAGTCAGCCCCGGGGTTATG 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GATCTTTTGGAGCTGAAAAATGTTCTACCTCAGTTATAAAGTCAGCCCCGGGGTTATG 2220

Qy   2284 AAGAAGGCGTGTTGGCCACCTTATCCCTTTCATGCGAAAAAGAAAGAAACCAGAGTG 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AAGAAGGCGTGTTGGCCACCTTATCCCTTTCATGCGAAAAAGAAAGAAACCAGAGTG 2280

Qy   2344 CTTAACGGCACAGTAGAAGAGGAGACCCTTACCAGGGCACCATCGTGTGCCACTGTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CTTAACGGCACAGTAGAAGAGGAGACCCTTACCAGGGCACCATCGTGTGCCACTGTT 2340

Qy   2404 AAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTTGGCTGCAATAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTTGGCTGCAATAAT 2400

Qy   2464 TTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTT 2523
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTT 2460

Qy   2524 GACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGATGAAATG 2583
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGATGAAATG 2520

Qy   2584 ATTTTTGTTGCCAAGGAAATGGAAGATTAGCTATAGGATTCCATTGTTGATTGGAGGA 2643
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ATTTTTGTTGCCAAGGAAATGGAAGATTAGCTATAGGATTCCATTGTTGATTGGAGGA 2580

Qy   2644 GCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTA 2703
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTA 2640

Qy   2704 ATCCATGTCCTGACGCGTCCAAGAGTGTGGTGTTCCCAGCTGTTGTAGATGAAAAT 2763
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ATCCATGTCCTGACGCGTCCAAGAGTGTGGTGTTCCCAGCTGTTGTAGATGAAAAT 2700

Qy   2764 CTAAAGATGATGAACTTTGAGGAAATCATGAAGAATATTAGACAGAGACCAT 2823
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTAAAGATGATGAACTTTGAGGAAATCATGAAGAATATTAGACAGAGACCAT 2760

Qy   2824 TATGAGTCTCTCAAGGAGGAGACTACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTC 2883
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TATGAGTCTCTCAAGGAGGAGACTACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTC 2820

Qy   2884 CAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGTC 2943
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGTC 2880
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Qy   2944 TTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACACTACGTTCTTTGAT 3003
          ||||||||||||||||||||||||||||||||||||||||||   |||||||
Db   2881 TTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACACTACGTTCTTTGAT 2940

Qy   3004 GTCTGGCAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACAAA 3063
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   2941 GTCTGGCAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTAACGACAAA 3000

Qy   3064 ACAGTAGGTGGAGGAGGCCAGGAAAGTCTACGATGATGCCACCAATATGCTGAACACACTG 3123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 ACAGTAGGTGGAGGAGGCCAGGAAAGTCTACGATGATGCCACCAATATGCTGAACACACTG 3060

Qy   3124 ATTAGTCAAAAGAAACTTCCGGACCTGCGAGAACGCCTGAGTGGGTTGGTTGGGTTCGGCCAGCACAGAGTATC 3183
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 ATTAGTCAAAAGAAACTTCCGGACCTGCGAGAACGCCTGAGTGGGTTGGTTGGGTTCGGCCAGCACAGAGTATC 3120

Qy   3184 CAAGACGACATTCACCTTGTACGGCAGAGGCGAGAACGACTCTGCCAGCACCGAGCCATACTAC 3243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 CAAGACGACATTCACCTTGTACGGCAGAGGCGAGAACGACTCTGCCAGCACCGAGCCATACTAC 3180

Qy   3244 ACTTTCTATGGGTTAAGGCAACAGGCTCAGAAGGACTCTGCCAGCACCGAGCACCTGGGCCTGTTT 3303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 ACTTTCTATGGGTTAAGGCAACAGGCTCAGAAGGACTCTGCCAGCACCGAGCACCTGGGCCTGTTT 3240

Qy   3304 TGCCTCTCAGACTTCATCGCTCCTTGCATCTCGTGACTACCTGGGCCTGTTT 3363
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGCCTCTCAGACTTCATCGCTCCTTGCATCTCGTGACTACCTGGGCCTGTTT 3300

Qy   3364 GCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGAC 3423
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGAC 3360

Qy   3424 TACAGCAGCATCATGGTTCGGGTACAAGGCGCATCCGCCGTCCTGGCCTTGCAGAGAGAG 3483
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TACAGCAGCATCATGGTTCGGGTACAAGGCGCATCCGCCGTCCTGGCCTTGCAGAGAGAG 3420

Qy   3484 CTCCATGAAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGTCAGCTGGACGTC 3543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 CTCCATGAAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGTCAGCTGGACGTC 3480

Qy   3544 GCAGACCGCGGAGAGGTTGCGGCTGCGATCCGCCGCCCCAGCCAG 3603
          |||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCAGACCGCGGAGAGGTTGCGGCTGCGATCCGCCGCCCCAGCCAG 3540

Qy   3604 CCCGACCACCACCGAGAGCTCACCATGTGGAGACTCGCGAGACTCGCACGAGCAGTCTACAGGC 3663
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CCCGACCACCACCGAGAGCTCACCATGTGGAGACTTGCGAGACTTGCACGAGCAGTCTACAGGC 3600

Qy   3664 ATTAGGTTAACAGAATCATTAGCACATGCAATGCTGCTTCAGCGCCTCTCACTTC 3723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 ATTAGGTTAACAGAATCATTAGCACATGCAATGCTGCTTCAGCGCCTCTCACTTC 3660

Qy   3724 TCCAATTTGAAGTCCAAAATATTTGCTGTGGGAGGATCAGGTTGAGGAT 3783
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TCCAATTTGAAGTCCAAAATATTTGCTGTGGGAGGATCAGGTTGAGGAT 3720

Qy   3784 TATGCATTGAGGAAGAACATATCGTGGCTTGTGAGGTTGAGAAATGGCTTGGACCCATTTTG 3843
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATGCATTGAGGAAGAACATATCGTGGCTTGTGAGGTTGAGAAATGGCTTGGACCCATTTTG 3780

Qy   3844 GGATATGATACAGACTAA 3861

Db   3781 GGATATGATACAGACTAA 3798
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RESULT 7
ADI39113
ID   ADI39113 standard; DNA; 3780 BP.
XX
AC   ADI39113;
XX
DT   22-APR-2004 (first entry)

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XX
DE   Agrobacterium tumefaciens metH DNA.
XX
KW   fermentation; methionine; Coryneform bacterium; methionine synthase;
KW   MetH; animal feed additive; sulphur; human nutrition; animal nutrition;
KW   cosmetic; pharmaceutical; gene; ds.
XX
OS   Agrobacterium tumefaciens.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..3780
FT                  /*tag= a
FT                  /product= "metH"
FT                  /partial
FT                  /note= "no ATG start codon"
XX
PN   WO200308786-A2.
XX
PD   23-OCT-2003.
XX
PF   16-APR-2003; 2003WO-EP004010.
XX
PR   17-APR-2002; 2002DE-01017058.
XX
PA   (BADI ) BASF AG.
XX
PI   Kroeger B, Zelder O, Klopprogge C, Schroeder H, Haefner S;
XX
DR   WPI; 2003-877106/81.
DR   P-PSDB; ADI39114.
XX
PT   Fermentative production of sulfur-containing compounds, particularly L-
PT   methionine, useful as feed additives, by using Coryneform bacteria that
PT   overexpress methionine synthase.
XX
PS   Claim 5; SEQ ID NO 47; 304pp; German.
XX
CC   This invention describes a novel method for the fermentative production
CC   of methionine by growing a sulphur-producing Coryneform bacteria that
CC   expresses at least one heterologous nucleic acid encoding a protein with
CC   methionine synthase (MetH) activity. Methionine accumulates in the medium
CC   or the cells. The method can be used to produce an L-methionine-
CC   containing animal feed additive by culturing an L-Met-producing
CC   microorganism, removing water from the resulting broth, removing 0-100%
CC   of the biomass formed and drying the product to produce the feed additive
CC   in powdered or granular form. The nucleic acid encoding MetH has sequence
CC   homology less than 100% with respect to the metH coding sequence of
CC   Corynebacterium glutamicum ATCC 13032. Optionally at least one other gene
CC   in the methionine biosynthesis pathway (e.g. aspartate kinase,
CC   glyceraldehyde-3-phosphate dehydrogenase or 3-phosphoglycerate kinase) is
CC   also amplified or mutated so that it is not affected by metabolites. Also
CC   at least one metabolic pathway that reduces production of methionine is
CC   at least partly switched off (e.g. homoserine kinase, threonine
CC   dehydratase or threonine synthase). The method is especially used to
CC   produce L-methionine, useful as an additive for animal feeds. More
CC   generally sulphur-containing fine chemicals are useful in human and
CC   animal nutrition, cosmetics and pharmaceuticals. This sequence encodes a
CC   metH protein described in the disclosure of the invention.
XX
SQ   Sequence 3780 BP; 745 A; 1102 C; 1181 G; 752 T; 0 U; 0 Other;

Query Match      23.6%;  Score 926.8; DB 10; Length 3780;
Best Local Similarity   55.5%;  Pred. No. 8.7e-253;
Matches 2055;  Conservative   0;  Mismatches 1567;  Indels  78;  Gaps  11;

Qy  149 GGATTATGTGTCTGGATGGAGGGATGGGACCCATGATCCAGCGGAGAAGCTAAACGAAG 208
            | ||||| |||| || ||||| |||||| | ||||||| |||||| ||||
Db   92 GCATCCTCATTCTCGATGGTGCCATGGCACGCAGATCCAGAGGTCTCGGTTTTGACGAGG 151

Qy  209 AACACTTCCGAGGTCAGGAATTTAAAGATCATGCCAGCCGCTGAAAGGCAACAATGACA 268
            || |||||||| || ||||  | ||||||  || ||||| |||||| ||
Db  152 ATCATTTTCGTGCGCGACCGTTTATCGCTGCGCCTGCGCCTGTCACCAGAGAACGACC 211
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Db       1286 TCGAGTTCCTGAACCTCATCGCCGCCGAGCCTGACATTGCCCGTGTGCCCGTCATGATCG 1345

Qy       1409 ACTCCTCCAATTTTGCTGTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCATTG 1468

Db       1346 ACTCATCCAAGTTCGAGATCATCGAGGCCGGCCTGAAATGCGTGCAGGGCAAATCGATCG 1405

Qy       1469 TCAATAGCATTAGTCTGAAGGAAGGAGAGGACGACTTCTTGGAGAAGGCCAGGAAGATTA 1528

Db       1406 TCAATTCCATTTCGCTGAAGGAAGGCGAGGAGAAGTTTCTCCAGCAGGCTCGGCTCGTCC 1465

Qy       1529 AAAAGTATGGAGCTGCTATGGTGGTCATGGCTTTTGATGAAGAAGGACAGGCAACAGAAA 1588

Db       1466 ACAATTACGGTGCGGCGGTTGTCGTCATGGCCTTTGATGAGGTCGGGCAGGCGGATACCT 1525

Qy       1589 CAGACACAAAAATCAGAGTGTGCACCCGGGCCTACCATCTGCTTGTGAAAAAACTGGGCT 1648

Db       1526 ATCAGCGCAAGGTGGAAATCTGCGCGCGCGCCTACAAGCTTCTGACCGAAAAGGCCGGTC 1585

Qy       1649 TTAATCCAAATGACATTATTTTTGACCCTAATATCCTAACCATTGGGACTGGAATGGAGG 1708

Db       1586 TGTCTCCGGAAGACATCATCTTCGACCCGAATGTGTTTGCGGTAGCTACGGGCATCGAGG 1645

Qy       1709 AACACAACTTGTATGCCATTAATTTTATCCATGCAACAAAAGTCATTAAAGAAACATTAC 1768

Db       1646 AGCACAATAATTACGGCGTGGACTTCATCGAGGCCACCAAGACCATCCGCGAAACCATGC 1705

Qy       1769 CTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTGTCCTTCTCCTTCCGAGGAATGGAAG 1828

Db       1706 CGCTCACGCATATTTCCGGGGGCGTTTCCAACCTGTCCTTCTCCTTCCGCGGCAATGAGC 1765

Qy       1829 CCATTCGAGAAGCAATGCATGGGGTTTTCCTTTACCATGCAATCAAGTCTGGCATGGACA 1888

Db       1766 CGGTGCGTGAGGCGATGCATGCCGTGTTCCTCTATCACGCCATTCAGGTCGGCATGGATA 1825

Qy       1889 TGGAGATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGC 1948

Db       1826 TGGGCATCGTCAACGCCGGGCAGCTTGCGGTTTACGACAATATCGATGCGGAACTGCGCG 1885

Qy       1949 AGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTT 2008

Db       1886 AGGCCTGCGAAGACGTGGTGCTGAACCGCCGCGACGATGCCACGGAGCGTCTGCTCGAGG 1945

Qy       2009 ATGCCCAGACT---CAAGGCACAGGAGGGAAGAAAGTCA---TTCAGACTGATGAGTGGA 2062

Db       1946 TGGCGGAGCGTTTCCGTGGTACGGGTGAAAAACAGGCCAAGGTGCAGGATCTTTCCTGGC 2005

Qy       2063 GAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTTGTGAAGGGCATTGAAAAACATA 2122

Db       2006 GCGAGTATCCCGTTGAAAAGCGGCTGGAACATGCTCTGGTCAACGGCATTACCGACTATA 2065

Qy       2123 TTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAAATATCCCCGACCTCTCAATA 2182

Db       2066 TCGAGGCCGATACGGAAGAGGC---------ACGCCAGCAGGCCGCCCGCCCGCTGCATG 2116

Qy       2183 TAATTGAAGGACCCCTGATGAATGGAATGAAAATTGTTGGTGATCTTTTTGGAGCTGGAA 2242

Db       2117 TCATCGAAGGGCCGCTGATGGCCGGTATGAATGTGGTGGGTGACCTGTTCGGTTCCGGCA 2176

Qy       2243 AAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTATGAAGAAGGCTGTTGGCCACC 2302

Db       2177 AGATGTTCCTGCCACAGGTGGTGAAATCCGCCCGTGTGATGAAGCAGGCGGTTGCCGTTC 2236

Qy       2303 TTATCCCTTTCATGGAAAAAGAAAGAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAG 2362

Db       2237 TGCTGCCTTACATGGAAGAGGAAA------------------AGCGCCTGAATGGCGGTT 2278

Qy       2363 AAGAGGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTTAAAGGCGACGTGCACGACA 2422

Db       2279 CCGAGCGCAGTGCCGCCGGCAAGGTGCTAATGGCGACCGTGAAGGGCGACGTGCACGATA 2338

Qy       2423 TAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCCGAGTTATTGATTTAG 2482

Db       2339 TCGGCAAGAACATCGTCGGCGTTGTGCTAGCCTGCAACAATTACGAGATCATTGATCTCG 2398

Qy       2483 GAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGACCACAAAGCAGATATAA 2542

Db       2399 GCGTGATGGTGCCGACGACGAAAATCCTCGAAACGGCGATCGCCGAAAAGGTGGATGTGA 2458

Qy       2543 TTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAATGATTTTTGTTGCCAAGGAAA 2602

Db       2459 TCGGCCTCTCCGGCCTCATCACCCCGTCGCTGGATGAGATGGTGCATGTGGCGGCCGAAA 2518

Qy       2603 TGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAACCC 2662

Db       2519 TGGAGCGACAGGGTTTCGACATTCCGCTGCTGATCGGCGGTGCGACGACCAGCCGTGTGC 2578

Qy       2663 ACACAGCAGTTAAAATAGCTCCGAGATAC---AGTGCACCTGTAATCCATGTCCTGGACG 2719

Db       2579 ATACGGCGGTAAAAATCCATCCGCGTTACGAGCAGGGGCAGGCGATCTATGTCACCGACG 2638

Qy       2720 CGTCCAAGAGTGTGGTGGTGTGTTCCCAGCTGTTAGATGAAAATCTAAAGGATGAATACT 2779

Db       2639 CCTCGCGCGCGGTGGGCGTCGTTTCAGCGCTCCTCTCCGAAGAGCAGAAGCCCGCTTATA 2698

Qy       2780 TTGAGGAAATCATGGAAGAATATGAAGATATTAGACAGGACCATTATGAGTCTCTCAAGG 2839

Db       2699 TCGACGGCATCCGAGCCGAATATGCCAAGGTGGCGGAAGCCCATGCCCGCAATGAGCGCG 2758

Qy       2840 AGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGATTGGCTGT 2899

Db       2759 AAAAGCAGCGCCTGCCGCTTTCCCGCGCCCGGGAGAATGCGCACAAGATCGACTG---GT 2815

Qy       2900 CTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATGACC 2959

Db       2816 CGAGCTACAGCGTTGTCAAGCCGCAGTTCTTCGGCACCAAGGTTTTTGAGACCTATGATC 2875

Qy       2960 TGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTGATGTCTGGCAGCTCCGGG 3019

Db       2876 TGGAAGAGCTTTCCCGTTACATCGACTGGACGCCGTTCTTCCAGACCTGGGAATTGAAGG 2935

Qy       3020 GCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAACGACAAAACAGTAGGTGGAGAGG 3079

Db       2936 GCC---------------GTTTCCCGGCGATCCTTGAAGACGAAAAGCAGGGCGAGGCGG 2980

Qy       3080 CCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACACTGATTAGTCAAAAGAAAC 3139

Db       2981 CGCGGCAGCTTTATGCCGATGCGCAGGCCATGCTTGCGAAGATCATCGAGGAAAAGTGGT 3040

Qy       3140 TCCGGGCCCGGGGTGTGGTTGGGTTCTGGCCAGCACAGAGTATCCAAGACGACATTCACC 3199

Db       3041 TCCGACCACGCGCGGTGATCGGCTTCTGGCCGGCCAATGCCGTGGGTGACGATATCAGGC 3100

Qy       3200 TGTACGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAGCCACTTTCTATGGGTTAA 3259

Db       3101 TCTTTACGGATGAAGGTCGG---------AAGGAAGAGTTGGCGACGTTCTTCACGCTGC 3151

Qy       3260 GGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACTACTGCCTCTCAGACTTCA 3319

Db       3152 GCCAGCAGCTTTCCAAGCGCGATGGCCG------TCCGAACGTGGCGCTGTCCGATTTCG 3205

Qy       3320 TCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTTGCCGT---TGCCTGCT 3376

Db       3206 TCGCGCCCGTCGATAGCGGCGTTGCCGATTATGTCGGCGGTTTCGTGGTAACGGCGGGTA 3265

Qy       3377 TTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGACTACAGCAGCATCA 3436

Db       3266 TCGAGGAAGTGGCGATTGCCGAGCGCTTCGAGCGGGCCAATGACGATTATTCGTCCATCC 3325

Qy       3437 TGGTCAAGGCGCTGGGGGACCGGCTGGCAGAGGCCTTTGCAGAAGAGCTCCATGAAAGAG 3496

Db       3326 TCGTCAAGGCGTTGGCTGACCGTTTTGCCGAAGCCTTTGCCGAGCGTATGCATGAGCGCG 3385

Qy       3497 TTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGACGTCGCAGACCTGCGAA 3556

Db       3386 TGCGCAAGGAGTTCTGGGGTTATGCGCCGGACGAGGCTCTTGCCGGTGACGATCTGATAG 3445
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CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 3786 BP; 695 A; 1293 C; 1265 G; 533 T; 0 U; 0 Other;

Query Match   23.3%; Score 914.6; DB 8;   Length 3786;
Best Local Similarity   54.8%; Pred. No. 2.7e-249;
Matches 2055; Conservative   0; Mismatches 1634; Indels   60; Gaps   10;

Qy   121 GATGAGATCAATGCCATTCTGCAGAAGAGGATTATGTGCTGCTGGATGGAGGATGGGGACC 180
            || |||| ||||||| |||||| ||| | | |||| | || |||||||| |||||||
Db   82 GACGAACTGACGGCGGCGCTCGCCCAGCCGGATCATGTGATCGACGGCGCCATGGGCACC 141

Qy   181 ATGATCCAGCGGGAGAAGCTAAACGAAGAAGAACACTTCCGAGTCGATGAGTTAAAGATCAT 240
            |||||||||| |||| ||| |||| | ||||| |||||| |||||||| |||| ||
Db   142 GCGATCCAGCGGACCGCCCCCGACGAGCCCGGCTACCGCGGCGGCGGTTCAAGGACTGG 201

Qy   241 GCCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTAC 300
            | ||||||| || ||||||||| | ||| || |||| |||| | |||| ||||
Db   202 CCGAGGCGATCTGTCGGCAACAACGACCTGCTCAACCTGACGCAGCCCAGATCATCGAG 261

Qy   301 CAAATCCATAAGGAATACTTGCTCGGTGGGGCAGATATCATTGAAACAAATACTTTTAGC 360
            | | || || ||||| |||||||| |||| || ||||| || || |||||||
Db   262 GGCATTCACCGCGAGTACCTCGAGGCGGCGCGCCACATCCTCGAGACCAACACCTTCAAC 321

Qy   361 AGCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACGGATGAACATG 420
            ||||| | ||||| | |||||||| || ||| |||| ||| |||| || |||
Db   322 GCGAACGCGATCTCGCTGTCCGACTACGGCCATGCGGAGGAGGTACGAGCTGAACTAC 381

Qy   421 TGCTCTGCAGAGTGGCCAGAAAAGTGCCGAGGAGGTAACTCTCCAGACACAGAATTAAG 480
            | | || | |||| ||| |||||| | | ||||| ||||| | |
Db   382 GCCGGCGCCGCCCTGGCCCGTAAGGCCCGTAAGGCCGGACGAGTTCAGCACCC---CGGACAAGCCC 438

Qy   481 AGGTTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTTCGTGTCCCCATCGTG 540
            |||| | || ||||||| ||||| ||||||| || |||| || |||||| |||
Db   439 CGCTACGTCGCCGGGGCGCTGGGGCTGGGGCGCCGGACCGGTCGCGGCCGGACTCGCCGGACGTC 498

Qy   541 GAAAGGCCGATTATACGAACATCACATTTGATGAGCTGTTGAAGCATACCAAGAGACAG 600
            || || | | |||||| | ||||||| | | |||||||| |||||||||
Db   499 AACGATCCGGGGCCCGGGCGAAGGTCACCTACGACGAGCTGGTCCCGCCGCTCACCTCGAGGCG 558

Qy   601 GCCAAAGGACTTCTGATGCCGGGGTGATATCTTCACTTCCTGATCTCGAGACGATCTTCGACACG 618
            |||| || ||| || | ||||| | ||| |||||||||| ||| |||| |||||||
Db   559 GCCAACGGCCTGCTGTCGACGGGCGTCGACCTTCGAGCTCGAGAGCGATCTGTCGTCACACG 618

Qy   661 GCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCC 720
            |||| |||||||| | ||| |||| | ||||| | || |||||| || ||||
Db   619 TTGAACGCCAAGGCTGCGGTTTCGCCCTCGAGACGCGGCGCTCGAACAGCGCGGCGCGCGC 678

Qy   721 CGCCTATCTTATTTCAGGACGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAG 780
            | | | | || |||| |||| |||| || | || || || | |||| ||||||
Db   679 TGGCCGGTCATCATCCGGGCCGCCACCATCACCGATGCCTCCGGGGCGAACCGTGTCCGGGCAG 738

Qy   781 ACAGGAGGAGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAAT 840

Db 1813 TTCCACGCCATCAAGGCCGGCTTGGACATGGGCATCGTCCAACCGCGGCGCGTGGTGCCC 1872
Qy 1921 TATGATGATATCCATAAGGAACTTCTGCAGCTTCTGTGAGATCTCATCTGGAATAAAGAC 1980

Db 1873 TACGACTCGATCGACCCCGAGCTGCGGGACCGCGATCGAGGACGTCGTGCTGACCGCCGC 1932
Qy 1981 CCTGAGGCCACTGAGAGAGCTCTTACGTTATGCCAG------ACTCAAGGCACAGGAGGG 2034

Db 1933 GAGGACGGGGCCGAGAGAGCTGCTGTGAGATCGCGGAGATCGGCGGTTCAACAAGTCCGC 1992
Qy 2035 AAGAAAGTCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGACCTTGAGTAT 2094

Db 1993 TCGGAGGATTCGGCGGCGGCCGAGTGGCGCGGCGGCCTGCCGGTCCGGGATCACGCGCAC 2052
Qy 2095 GCCCTTGTGAAGGGCATTGAAAAACATATTATTGAGGATACTACTGAGGAAGCCAGG---TTA 2151

Db 2053 GCCCTGGTCAAGGGCATCGACGCCCAGTCGACGAGGACACCGAGGAGTTGCGGGCCGAG 2112
Qy 2152 AACCAAAAAAAAATATCCCGACTTCTCAATATAATTGAAGGACACCCTGATGAATGGAATG 2211

Db 2113 ATTGCGGCCGGGTGGCCGGGCACCCTGATCGAGGTGATCGATCGGCAGTCGACGGCATG 2172
Qy 2212 AAAATTGTTGGTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGTTATAAGTCA 2271

Db 2173 AACGTCGTCGGCGACCTGTTCGCGTTCCCCCAGGTTGGTGGTGAAGTCG 2232
Qy 2272 GCCCGGGTTATGAAGAGGCGTCTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAGAAA 2331

Db 2233 GCCCGGGTGGATGAAGAAGAGGCCCGGTCCGCCTACCTTGTGATGTCGTTCATCGAGGCGGAGAAGAA 2292
Qy 2332 GAAACCAGAGTGCTTAACGGCACAGTAGAAGAGGACCCCTTACCAGGGCACCATCGTG 2391

Db 2293 GAGTCCGGGTGTCCGGTTCCA-------AGGACACCAACGCGGCCACCATCGTG 2337

Db 2392 CTGGCCACTGTTAAAGGCGACGTGCACGACATAGTTGGAGTAGTCCTT 2451
Qy 2392 CTGGATGAAATGATTTTTGTTGCCAAGAAATGGAGAGATTAGCTATAAGGATTCCATTG 2451

Db 2338 ATGGCGACCGTCAAGGGCGACGTGCACGTTCCACGGCAAGAACATCGTCGAGTGTCTG 2397
Qy 2338 CTGACGCAGATGTCCAACTTGCGCCCGAGATGGAACGGCAGGGCCTGCGAGATCCGCGCTG 2457

Db 2452 GGCTGCAATAATTCCGAGTGTATTGATTGAGTCATGACTCATCCATGTGATAAGATACTG 2511
Qy 2452 TTGATTGGAGGAGCAACCACTTCAAAAACCCACCACAGCAGCAGTGAAAATAGCTCGAGATAC 2691

Db 2398 CAGTGCAACAACTTCGAGGTGATCGACCTCGGTGTGATGTGCCGGGCCCAGAGATCCTC 2457
Qy 2578 CTGATCGCGGCGGGCGGCGACCACCTCGCGGGCGGTCCAAGAGTGTGGTGTTCCCAGCTG 2637

Db 2512 AAAGCTGCTCTTGACCACAAAGACAGATATAATTGGCCTGTCGAGACTCATCACTCCTTCC 2571
Qy 2692 AGTGCACCTGTAATCCATGTCCTTGACGCGGTCCAAGAGTGTGGTCGGTCGGCTCCGGCTG 2751

Db 2458 GATGCTGCGAAAGACGACCATCGGGCTGTCCGGCCTGTCGCGCGGGGCTCCGATCACCCCGTCC 2517
Qy 2638 TCCGGCCCCGGTGTGGTCGGGTCAAGGACGCTCCCGGCTCCGGCTG 2697

Db 2572 CTGGATGAAATGATTTTTGTTGCCAAGAAATGGAGAGATTAGCTATAAGGATTCCATTG 2631
Qy 2752 TTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGAGGAAATATGAAGATATT 2811

Db 2518 CTGACGCAGATGTCCAACTTGCGCCCGAGATGGAACGGCAGGGCCTGCGAGATCCGCGCTG 2577
Qy 2698 CTGGACGACAAGCAGCAGCGGCCGCCCTCCCTGCTGGAGGAGAGAGACTACGCGTCGCT- 2756

Db 2632 TTGATTGGAGGAGCAACCACTTCAAAAACCCACCACAGCAGCAGTGAAAATAGCTCGAGATAC 2691
Qy 2812 AGACAGGACCATTATGAGTCTCTCAGAAGAACAGCGCGGCCGATGGTGACCTTAAGCCAGA 2871

Db 2578 CTGATCGCGGCGGGCGGCGACCACCTCGCGGGCGGTCCAAGAGTGTGGTGTTCCCAGCTG 2637
Qy 2757 --GCGGGAACGGCACGCGCCGATGGTGACGCTGAAAAAGGCCCGC 2814

Db 2692 AGTGCACCTGTAATCCATGTCCTTGACGCGGTCCAAGAGTGTGGTCGGTCGGCTCCGGCTG 2751
Qy 2872 AAAAGTGGTTTCCAAATGATTGGCGTGTGAACCTCACCAGTGTCGTGTCCCACGTTTATT 2931

Db 2638 TCCGGCCCCGGTGTGGTCGGGTCAAGGACGCTCCCGGCTCCGGCTG 2697
Qy 2815 GCCAACCGGACGACTGGACGGCTACACGCGCCGGATCGGCGGTGGCG 2874

Db 2752 TTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGAGGAAATATGAAGATATT 2811
Qy 2932 GGGACCCAGGTCTTTGAAGACTTCAGGACTACGCGCCGCGAGTCGGTGCTGCGCGAGAAG 2991

Db 2698 CTGGACGACAAGCAGCAGCGGCCGCCCTCCCTGCTGGAGGAGAGAGACTACGCGTCGCT- 2756
Db 2875 GGAATACGGGAATTTCAGGACTACGCGCCGCGAGTCGGTGCTGCGCGAGAAG 2934

Db 2812 AGACAGGACCATTATGAGTCTCTCAGAAGAACAGCGCGGCCGATGGTGACGCTGAAAAAGGCCCGC 2871

Db 2757 --GCGGGAACGGCACGCGCCGATGGTGACGCTGAAAAAGGCCCGC 2814

Db 2872 AAAAGTGGTTTCCAAATGATTGGCGTGTGAACCTCACCAGTGTCGTGTCCCACGTTTATT 2931

Db 2815 GCCAACCGGACGACTGGACGGCTACACGCGCCGGATCGGCGGTGGCG 2874

Db 2932 GGGACCCAGGTCTTTGAAGACTTCAGGACTACGCGCCGCGAGTCGGTGCTGCGCGAGAAG 2991

Db 2875 GGAATACGGGAATTTCAGGACTACGCGCCGCGAGTCGGTGCTGCGCGAGAAG 2934

Db 739 GTCACCGGAGGGGTTCTGGAACTCGATCCGGCACGCGCGATGCGGGTCGGGCTCAAC 798
Qy 841 TGTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGAAAAATGTACAACA 900

Db 799 TGCGCCCTGGGCGCACCGGAGATCGGCGCCCTACATCGCCGAGGTGTCGCCATCGCGGAC 858
Qy 901 GCCTATGTCCTGTTATCCCAATGCAGGTCTTCCCAACACCTTGGTGACTATGATGAA 960

Db 859 ACCTTCGTTCCTGCTACCCGAACGCGGCCGGCCTTCGGCAGGTACGACGACGAG 918
Qy 961 ACGGCCTTCTATGATGAGCCAAGCACCTAAAGGATTTTGCTATGATGATGGCTTGGTGTCAATATA 1020

Db 919 TCCCCGGAGCGGTCAGCCTCCTACATCGCCGACTTCGGCGAGGCCGGCCTGGTCAACAATC 978
Qy 1021 GTTGGAGGATGCTGTGGGTCAACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAA 1080

Db 979 GTCGGGCCGTTGCTGCGGAACCGGCTGAGTCGTCGAG 1038
Qy 1081 AATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGT 1140

Db 1039 GGCAAGCCGCGCCGG----CGAGGTGCCGCAGATTCCGGTGGCCACCCG--GCTCTCCGGC 1092
Qy 1141 CTAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCTGTAAT 1200

Db 1093 CTCGAGCGGCTCAACATCACCGACGACTCGGCTGTTCGTGAACATCGGCGAGCGCACCAAC 1152
Qy 1201 GTTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAAACTATGAAGAGCCTTG 1260

Db 1153 ATCACCGGCTCGGCCCGGTTCCGCCAACCTGATCAAGGCTGAGGTCATCGGAGCCGGCGCTG 1212
Qy 1261 TGTGTTGCCAAAGTGCAGGTGAAGGTGGATGTCAAGATGGATGAT 1320

Db 1213 TCGGTCGCCTCGCAGCAGGTGGAGGTCGGTGCCGTGGAGGTGCATCGACATCAACATGGACGAG 1272
Qy 1321 GGCATGCTAGATGGTCCAAGTGCAATGACTCTGTGTGCTCTATGGTGTCATGGCT 1380

Db 1273 GGCATGAATCGACGGCGTCGCCGCGGACCGGTTCACCCAGGCGTGATGGCC 1332
Qy 1381 GACATCGCAAAGTACCTTTGTCGATCGATCCTCCCAATTTTGTGTTGAAGCTGGG 1440

Db 1333 GACATCAGCAGCGGGTCAGGCGATCGACTCCTTCCAAGTGGGAAGGTCCAGCGGCCGGC 1392
Qy 1441 TTAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTTCGAAGGGAGGAGGAGAC 1500

Db 1393 CTGAAGAACGTGCGAGGGCAAGGCCATCGTCAACTCGATCTCTTTGAAGGAGGGGGCGAGGAG 1452
Qy 1501 GACTTCTTGGAGAAGAGGCCAGGAAGAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCT 1560

Db 1453 AAGTTCGTCGGCGAGGCGCGGCTGTGCCGCAAGTGACCGGCCGGCCGCGTCGTGATGGCC 1512
Qy 1561 TTTGATGAAGAAGCAACATCATTGAGCAAAATCATAAGTAGTGAAGCTGACCCGGGCC 1620

Db 1513 TTCGACGAACAGGGTCAGGCGCAGAGGTCGGGTTCGCCGGTCCACCTTCGGGGGGCATCTGCCGCGCGGCC 1572
Qy 1621 TACCATCGTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTTTTGACCCTAAT 1680

Db 1573 TACCGGCGTGACCGAAGAGGTCGGGTTCCCGGCAGCATCATCTTCGACATCATCATCGACCCCCAAAC 1632
Qy 1681 ATCCTAACCATTGGACTGGAATGGAAGTGAGGAACACATTGTATGCCATTAATTTATCCAT 1740

Db 1633 TGCTTCGCGGCTGGCGCTGGACGACGCCGCATCGGCAGGAGCACGCAACCTCACCACGCGATCGAG 1692
Qy 1741 GCAACAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAAGTCTTTCCAAC 1800

Db 1693 GCCTGCGCCTGGGATCAAGGAACCTGCACCTCTTCCGGGGGGCATCTCGAAC 1752
Qy 1801 TTGTCCTTCTCTCCTTCCGGAGGAATTGGCAGGCCATTCGAAGCCAATGCAATGGGGTTTTCCTT 1860

Db 1753 GTGTTCGTTCTCGTTCCGGGGGGAAACACCCCGTCCGAGGGCGATCCACTCGGTTTCCTG 1812
Qy 1861 TACCATGCAATCAAGTCTGGCATGGCATGGACATGGACATGGAGAGATAGTGAATGCTGAAAACTCCCCTGTG 1920

Db 1813 ...

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KW    drug design; gene.
XX
OS    Acinetobacter baumannii.
XX
PN    WO200277183-A2.
XX
PD    03-OCT-2002.
XX
PF    21-MAR-2002; 2002WO-US009107.
XX
PR    21-MAR-2001; 2001US-0081524 2.
PR    06-SEP-2001; 2001US-0094899 3.
PR    25-OCT-2001; 2001US-0342923P.
PR    08-FEB-2002; 2002US-0072851.
PR    06-MAR-2002; 2002US-0362699P.
XX
PA    (ELIT-) ELITRA PHARM INC.
XX
PI    Wang L,   Zamudio C,   Malone C,   Haselbeck R,   Ohlsen KL,   Zyekind JW;
PI    Wall D,   Trawick JD,   Carr GJ,   Yamamoto R,   Forsyth RA,   Xu HH;
XX
DR    WPI; 2003-029926/02.
DR    P-PSDB; ABU17102.
XX
PT    New antisense nucleic acids, useful for identifying proteins or screening
PT    for homologous nucleic acids required for cellular proliferation to
PT    isolate candidate molecules for rational drug discovery programs.
XX
PS    Claim 14; SEQ ID NO 8842; 1766pp; English.
XX
CC    The invention relates to an isolated nucleic acid comprising any one of
CC    the 6213 antisense sequences given in the specification where expression
CC    of the nucleic acid inhibits proliferation of a cell. Also included are:
CC    (1) a vector comprising a promoter operably linked to the nucleic acid
CC    encoding a polypeptide whose expression is inhibited by the antisense
CC    nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC    polypeptide or its fragment whose expression is inhibited by the
CC    antisense nucleic acid; (4) an antibody capable of specifically binding
CC    the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC    proliferation or the activity of a gene in an operon required for
CC    proliferation; (7) identifying a compound that influences the activity of
CC    the gene product or that has an activity against a biological pathway
CC    required for proliferation, or that inhibits cellular proliferation; (8)
CC    identifying a gene required for cellular proliferation or the biological
CC    pathway in which a proliferation-required gene or its gene product lies
CC    or a gene on which the test compound that inhibits proliferation of an
CC    organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC    compound's activity; (11) a culture comprising strains in which the gene
CC    product is overexpressed or underexpressed; (12) determining the extent
CC    to which each of the strains is present in a culture or collection of
CC    strains; or (13) identifying the target of a compound that inhibits the
CC    proliferation of an organism. The antisense nucleic acids are useful for
CC    identifying proteins or screening for homologous nucleic acids required
CC    for cellular proliferation to isolate candidate molecules for rational
CC    drug discovery programs, or for screening homologous nucleic acids
CC    required for proliferation in cells other than S. aureus, S. typhimurium,
CC    K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC    prokaryotic essential genes. Note: The sequence data for this patent did
CC    not form part of the printed specification, but was obtained in
CC    electronic format directly from WIPO at
CC    ftp.wipo.int/pub/published_pct_sequences
XX
SQ    Sequence 3684 BP; 1088 A; 747 C; 833 G; 1016 T; 0 U; 0 Other;
```

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Qy   2992  CCTTTCTTGATGTCTGGCAGCTCCGGGGCAAGTACCGATCGAATGGAGGCTTCCCCAAGATA  3051
                  |||||||                                 ||||||||||||||||
Db   2935  CCGTTCTTCAACGCGCCTGGGAGAT------------------GAAGGGTCGCTTCCCCGACATC  2979

Qy   3052  TTTAACGACAAAACAGTAGGTGGAGAGGCCGAAGGTTCACGATGATGCCCACAATATG  3111
            ||||      |||   ||||||||||  ||  ||||| |||||||| ||||| |||||
Db   2980  CTCAACAACACCCGGCCACCGGGCAGGCGGCCGCCCAAGCTCTACGACGACGCCAGGAGATG  3039

Qy   3112  CTGAACACACTGATTAGTCAAAAGAACAAACTCCCGGCCCCGGGGTGTGGTTCTGGCCA  3171
            ||||| |||||   |||| ||  ||  ||      |||||||||||  |||  |||||||
Db   3040  CTCGACACCCTGATCAAGGAGGAAGTGGCTGCCCAACGCGGTGATCGGGTTCTTCCCG  3099

Qy   3172  GCACAGAGTATCCAAGACGACATTCACCTGTACGACGAGGCTGCTGCCCCAGGCTGCA  3231
            ||| |||     |   ||||   |||| ||||||||     ||    |   |||| |||
Db   3100  GCGAACGGCGATCGGCCCGGGTTTCGAAGACATGACTGAGCTGTACACCCGACACCCCGACACC  3159

Qy   3232  GAGCCCATAGCCACTTTCTATGGGTTAAGGCAACACGGCTGAGAAGGACTCTGCCAGCACG  3291
            |||     ||  ||||       ||    |||   |   |||||     ||||| |||||
Db   3160  GAGGTGCTGACCACGCTGCACCAGCGCTGCACCAACCTGCGCCCAGCAGGCGCACCGGACGGAATC---  3216

Qy   3292  GAGCCCATACTACTGCCTCTCAGACTTCATCGTCCTTGCATTCTGGCATCCGTGACTAC  3351
            ||||      |  ||  ||    |||  |||||| |||||  |  ||||||  |||| ||
Db   3217  ---CCGAACCGGTCGCTGGGCGACTACAGTCGCGCCCCCAAAGAAACGGGCACCGGGACTAC  3273

Qy   3352  CTGGGGCCTGTTGTTTGCCGT---TGCCTGCTTTGGGTAGAAGAGCTGAGCAACGGCCTATGAG  3408
            ||||| ||||| | |||||      ||  ||||||  ||  |     ||||| |||  |||||
Db   3274  ATCGGCGGCCCTTCGCGGTGACCGCGGGGCTGGACCGCAGCCAGGAGAAGATCGCGGAGTTCAAG  3333

Qy   3409  GATGATGGTGACGACTACAGCAGCATCATGTGTCAAGGCGCTGGGGACCGGCTGGCAGAG  3468
            ||||||||||    ||       ||      |||| |||||||||||||| |||| |||
Db   3334  GCGGCCCTGGACGACTACAGCCCGGATCCGTCTGGAGTCGATCCGCGACCGGCTGGCCGGAG  3393

Qy   3469  GCCTTTGCAGAGAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGTGGCAGT  3528
            |||  ||| |||||||   || | ||||| |||| ||||  ||| |   |||   ||||||
Db   3394  GCGTTCGCCGAACGGATGCACCGGGGTCCCGAAGGAGTTCTGGGCCTACCAGCCCGAC  3453

Qy   3529  GAGCAGCTGGACGTCGCAGACCTGCGAAGGTTGCCGTACAAGGGCATCCGCCCGGCTCCT  3588
            |||||||||||   ||||     |||   ||||  ||  |   ||||  |   ||||| |
Db   3454  GAGCAACTGGACAACGACGCACTCATCGACGAGAAGTACCGGGGGAATCCGGCCCGGACCCG  3513

Qy   3589  GGCTACCCCAGCCAGCCGAGCCGACCACCAGAGAAGCTCACCATGTGAGACTCGCAGACATC  3648
            |||||      |  |||||| ||  ||||  ||   ||   | |||   ||| |||||||||
Db   3514  GGCTACCCGGGCTCCCCGAGCACACCCGAGAAGGTGACGCTGTGGAAGTTGATGGACGTC  3573

Qy   3649  GAGCAGTCTACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTC  3708
            ||||||     |||       ||  |||  ||     |  ||||  |||||| | ||||
Db   3574  AAGGAGGCACCGGGTACCAGCGAGTCGATGGCCATGGTCGCCCGGCCCGTC  3633

Qy   3709  TCAGGGCCTCTACTTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGAAGATTTCCAAG  3768
            ||| |||  |||| ||  ||      ||   |||||||   ||  || ||||| | |||
Db   3634  AGCGGTTGGTATTTCTCGCACCCGAGTCGCAGTACTTCGTCGTGTCGGCGGTTGGCCCAG  3693

Qy   3769  GATCAGGTTGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGG  3828
            ||||||||   | ||     |||||| ||||  ||  |  ||||||||||  |||||
Db   3694  GACCAGGTCGCGCACTACGGCGAAGCCGAAGGCGCTGGACGCGCTGGCCGAGGCCGCTGG  3753

Qy   3829  CTTGGACCCATTTTGGGATATGATGATACAGA  3857
            |||||| ||||   |||| |||     ||||
Db   3754  CTGGGCCCCCAACCTCGGCTACAACCCCGA  3782
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RESULT 9
ACA20972
ID    ACA20972 standard; DNA; 3684 BP.
XX
AC    ACA20972;
XX
DT    19-JUN-2003  (first entry)
XX
DE    Prokaryotic essential gene #2629.
XX
KW    Antisense; ds; prokaryotic essential gene; cell proliferation;
```

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Query Match             23.3%;  Score 911.8;  DB 8;  Length 3684;
Best Local Similarity   55.3%;  Pred. No. 1.6e-248;
Matches 2070;  Conservative    0;  Mismatches 1557;  Indels 114;  Gaps    11;

Qy    128  TCAATGCCATTCTGCAGAAGACGGATTATGGTGCTGGATGGACGAGGGATGGGACCATGATCC  187
            ||||||||||||||||||||||||||||||||||||||||||||
Db     20  TAAAAGCGCTTCTTGCTAAACCCATTCGATTATTGATTGTGCAATGGAACCATGGAACCATGATCC  79

Qy    188  AGCGGGAGAAGCTAAACGAAGAACACTTCCGAGTCGCAGGTCAGGAATTTAAAGATCATGCCAGC  247
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The page contains a two-column nucleotide sequence alignment labeled with "Db" (database) and "Qy" (query) rows, with vertical bars (||||) indicating matched bases between sequences.

Left column:

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Db      |||| ||| |||||||| ||| ||| |||||  |||
     80 AGCGCCATAAATTGAAGAAGCTGACTATCGTGGTGAGCGGTTTGCTGATTGGGCACATG    139

Qy      CGCTGAAAGGCAACAATGACATTTTAAGTATAACTGACCTGATGTCATTTACCAAATCC    307
Db   248 ACTTAAAAGGTAACAATGACCTTTGTTCGTCGTTGGTTCTAACACAGCCTCAAATCATTCAAGGTATTC  199
     140

Qy   308 ATAAGGAATACTTGCTGGCTGGGCAGATATCATTTAGCAGCACTA                           367
Db   200 ATGAAGCTACCTCGATGCTGGTGCAGACATTATTGAAACCAACAGCTTTAACGGTACAC             259

Qy   368 GTATTGCCCAAGCTGACTATGGCCTTGAACAGTTGGCCTGCGATGAACAATGTGTTCTG             427
Db   260 GTGTTTTCAATGTCTGACTATCACATGGAAGATCTTGTTCCAGAGATTACCGTGAAGCAG            319

Qy   428 CAGGAGTGGCCAGAAAGCTGCCGAGAAAGCTGAACTCCAGACAGCAGGAATTAAGAGGTTTG          487
Db   320 CACGTTTAGCTAAAGCAGCTTGCGAAAAG---TATTCAACGCCAGAACGAAGCCTCGTTTTG         376

Qy   488 TGGCAGGGGCTCTGGTTCCGACTAAATAAGACACTCTCTGTGTCCCATCTGTGGAAAGGC            547
Db   377 TGGCAGTGTACTTGGGCCAACATCTCGTACATGTTCAATCTCTCCAGAATGTGAACAACC           436

Qy   548 CGGATTATAGGAACATCACATTGATGAGCTTGTTGAAGCATAACCAAGAGCAGGCCAAAG            607
Db   437 CTGCTTTTCGTGTAACATTAGCTTTGATGAACTAACAAAATTATATTGAAGCGACTCATG           496

Qy   608 GACTTCTGGATGCGGGGTTGATATCTTACTCATTGAAACTATTTTGTATACTGCCAATG             667
Db   497 CACTCAATTGAAGGTGGCAGACATTTATCCTGATCGGCATTGCTTTGTATTTGATACTTTAAACT      556

Qy   668 CCAAGGCAGCCTTGTTGTTGCACTCCAAATCTTTTGAGGAGAAAATATGCTCCCCGGCCTA          727
Db   557 GTAAAGCAGCGATTTTGCAGTCAAGAAGTCTTTAAACAAAATTGGTCGCGAATTACCAA            616

Qy   728 TCTTTATTTCAGGGACGATCGTTGATGATAAAGTGATGAAAGTGGGCGGCCGGACTCTTTCCGGACAGAGGAG  787
Db   617 TCTCATTCCGTGCAATGAACCAGTTCGTGAGCCATTCACTCGTATTCTTGTACCATG               676

Qy   788 AGGGATTTGTCATCAGCGGTGTCTCATGGAGAACCACTCTGCTCATTGGATTAAATTGTGCTT        847
Db   677 AAGCTTTCTGGAACTTCGTCCGGTTGCTTTGCTTTCAATCGGTTTTAACTGTGCCC               736

Qy   848 TGGGTGCAGCTGAGATGAGGACCTTTATTGAAATAATTGGAAAATGTACACACAGCCTATG          907
Db   737 TTGGTGCAGATGCCATGCGCCCTCACGTAAAAACTATTCGCATGGTCGCAGATACCTTTG           796

Qy   908 TCCTCTGTTGTATCCCAACTCAGTCTTCCCCAACACCTTGGTGACTATGATGAAACGCCTT          967
Db   797 TTTCAGCGCACCCAAATGCAGGCTTACCGAAACTCAGCATTTGGTGAAATGACGAAACTTCCAG       856

Qy   968 CTATGATGGCCAAGCACTACCAAGCTTTCTATGGATGGCTTGGCTCAATATAGTTGGAG            1027
Db   857 AGCAAACTGCAGCTTTTCTTAAAAGAGTTTGCTGAAAAGCGGTTTGATTGATTAACATTACTGGTG     916

Qy  1028 GATGCGTGTGGGTCAACACCAGCATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATTGTA         1087
Db   917 GTTGCTGTGGTTACGACACACCAGACCATATTGCCATGCGGTAAAATGCGGTAAAAAGACATTG      976

Qy  1088 AGCCTAGAGTTCCACTTGTTTTGGAAGGACATATGTTACTGTCTCGTCTGTAGAGC              1147
Db   977 CGCCTCGCCAAGTGCCCAAATGCCTTAAAATCCGTGAAAACGTTGCTCGGAA-----GCTTAACGTGTTTACCG  1030

Qy  1148 CCCTTCAGGATTGGCCAGCTGACACGGTGTACACCAACTTGTTAACATTGGAGGAGGCGCTGTAATGTTGCAG  1207
Db  1031 CATTTAATATTTATGATGATTCATTGGTCTATGGCCTTGGTATAGTTTGGGAGGAGCCGTACTACCG        1090

Qy  1208 GATCAAGGAAGTTGCTAAACTTCATCATGGCAGGAAACTATGAAGAGGCCTTGTGTTGTTG          1267
Db  1091 GTTCTAAAAAATTCTTACGTGTCTCATTGTGGAAGAAAACTTTGCGAGAGAGCTTTGAGAAGTTG      1150

Qy  1268 CCAAAGTGCAGGTGGAAATGGGAGCCCAGGTCGTTGGAATGTCAACATGGATGATGGCATGC        1327
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Right column:

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Db  1151 CACAGCAGCAGGTTGAAGCTGGGCACAGAGATTATCGACATTAACATGATGAAGGGATGC           1210

Qy  1328 TAGATGGTCCAACTGCAACTGACCAGATTTTGCAACTTAATTGCTTCCAGCCAGACACATCG         1387
Db  1211 TCGATTCGCAAAATGCGATGGTGCATTTCTAAACCTTGTAGCATCCGAACCGGACATTT            1270

Qy  1388 CAAAGGTACCTTGTGCATCGACTCCTCCAATTTGCGTGATGAAGCTGGGTTAAAGT               1447
Db  1271 CACGTGTACCGATCATCATGACTACTGGTTCTTAAAAGGAAAATCATTGAAGCGGCTTAAAAT        1330

Qy  1448 GCTGCCAAGGAAGTGCATTGTCAATAGCATAGTCTGAAGGAAGAGAGAGACGACTTCT            1507
Db  1331 GGCTACAAGGTAAACCGGTTGTTAACTGAAATCATTTCCTTAAAAGAAGGGTTATGACGAGTTTG      1390

Qy  1508 TGGAGAAGGCCAGAAGATTAAAAAGTATGAGGAATGTGGTCATGTGGTCTATGGCTTTTGATG        1567
Db  1391 TTGAAAAAGGCCCGCCTCTGCCGTCAATATGGTCTGCAATTATTGTGATGGCCTTTGACG          1450

Qy  1568 AAGAAGGACAGGCAACAGAACAGACAAAAATCAGAGTGTGCACCCGGGCCTACCATC             1627
Db  1451 AAGTAGGTCAGGCCGACACTGCTGAACGTAAACGTAAACTGAAATCTGAAGCGCTCTTATGACA       1510

Qy  1628 TGCTTGTGAAAAATCTGGGCTTAATCCAAATGACATTATTTTGACCCTAATATCCTAA            1687
Db  1511 TTTTGGTTAACGAAGTAGGCTTTCCCTGCTAAGAAATCTGAAGACGAACGTGTTTG              1570

Qy  1688 CCATTGGGACTGAATGGAGAGAACAACTTGTATGCCATTAATTTATCCATGCAACAA             1747
Db  1571 CAGTTGCGACTCGTATTGAAGAACATAACTACGCCAGTGCAGTCGATTTTATTGAAGCAACGG       1630

Qy  1748 AAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGACGGAGTCTTCTCCAACTTGTCCT       1807
Db  1631 GCTGGATTAAACAGAACTTACCCGACCACGCAGATTCTGGTGTGTCTAACGTTTCGT              1690

Qy  1808 TCTCCTTCCGGACTGAATGGAAGCAATGCCGAGAGCAATGACTGCATGGCGTTTCCTTTACCATG      1867
Db  1691 TCTCATTCCGTGCAATGAACCAGTTCGTGAGCCATTCACTCGTATTCTTGTACCATG             1750

Qy  1868 CAATCAAGTCTCGGCTGCATGGAGATAGTGGAAACCTCCCCTGTGTATGATG                   1927
Db  1751 CCATCAAGCAAGGCATGACCATGGGTATTGTGAACGGCAGGTCAAATGCTATTTTATGATG         1810

Qy  1928 ATATCCATAAGGAACTTCTGCAGCTCTGTGCTGAATAATCTGCAATCTGGAATAAAGACCCTGAGG     1987
Db  1811 ATATTCCTACCGAGCTAAAAGAAGCCGGTTGAAGATGTGCATTTTCATTTTTAAACCAAAATCAAGGTG  1870

Qy  1988 CCACTGGAGAAGCTCTTCACGTTACGTGATGCCCAGCTCAAGGCACA-----                   2028
Db  1871 AGTCTGGTCAAGTCGCGACTGAGAAAACTACTTGAAGTTGCAGAAAAATACCGTGACAAG          1930

Qy  2029 --GGAGGGAAGAAGTCATTCAGACTGATGAGTGGAGAGAAATGGCCCGTCGTGAGAACACGCC        2086
Db  1931 GTGGTGCAACAGAAAGAGAGCCGGAACCTTGAATGGCGTAAGTCAGTTGAAAAACGTC            1990

Qy  2087 TTGAGTATGCCCGTGTGAAGGGCAAATTGCTGAAGCTGTGAAAAATCATTATTGAGGAAGCA        2146
Db  1991 TTGAATATGCCTTGGTTAAAGGTAACTTTATATTGGACCAAGACACCGGAGGAAGCCC           2050

Qy  2147 GGTTAAACCCAAAAAAATAATATCCCGACCTCTCAATATAATTGAAGAACTCTGATGAATG         2206
Db  2051 GCTTAAAATCAAA-------CGTCCTTTAGATGTAATTGGAAGGGCCACTGATGGGACG           2101

Qy  2207 GAATGAAAATTGTTGGTGATCTTTTGAGCTGGAAAAATGTTTCTACCTCAGTTATAA             2266
Db  2102 GCATGAACGTCGTGGTGACTTGTCGGTTCAGGCAAAATGTTTCTTGCCACAAGTGTAA            2161

Qy  2267 AGTCAGCCCGGGTTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAA         2326
Db  2162 AATCTGCCCAGTCATGAAACAAGCAAGCAGTAGCATGGCTACATCGGAGTCGAAGCTGAA          2221

Qy  2327 GAGAAGAAACCAGAGTGCTTAACGGACAGTAGAAGAAGAGACCCTTACCAGGGCACCA            2386
Db  2222 ----------------------------------AGACCGAAGGACAGTAGCTAAAGGTAAAG       2248
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Qy  2387  TCGTGCTGGCCACTGTTAAAGGCGACGTGCACGACACATAGGCAAGAACATAGTTGGAGTAG  2446
          ||  ||||||  ||||||||||||||
Db  2249  TCCTAATGCCAACGGTTAAAGGTGACGTACACGCATATTGGTAAAAAATATTGTAGGCGTAG  2308

Qy  2447  TCCTTGGCTGCAATAATTTCCGAGTATTGATTAGGAGTCATGACTCCATGTGATAAGA     2506
          |||||||||    |||
Db  2309  TACTTGGCGTGATGGCTATGACATTGTGACCTTGCCTTGGCGTAATGGTCCCTTGCGAGAAAA  2368

Qy  2507  TACTGAAAGCTGCTCTTGACCACAAGCAGATATAATTGGCCTGTCAGGACTCATCACTC    2566
          |  ||||||||||    |||||
Db  2369  TCTTACAAACTGCAATTGATGAAAAATGTACATCATTGGACTGTCTCGTCTGATCACCC     2428

Qy  2567  CTTCCCTGGATGAAATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTC    2626
          |||||    |||||||||||||    |||||
Db  2429  CATCTTTAGATGAAATGAAAATGTGTATTTGTTGCTAAAGAAATGCAGCGTAAAGGCTTTAACATTC  2488

Qy  2627  CATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAATAG---CTC    2683
          |||||||    ||||||    ||||||    |||||||
Db  2489  CTTTATTAATTGGTGGGCGGACTACTTCTAAAGCACATACAGCAGTAAAAATTGACCCTC    2548

Qy  2684  CGAGATACAGTGCACCTGTAATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTTGTT     2743
          |||    |||||    ||||||    |||||
Db  2549  AGTATCAAAACGATGCGGTAATTTATGTTGCCCGATGCTTCACGCGCTGTTGGTGTAGCGA   2608

Qy  2744  CCCAGCTGTGTTAGATGATGAAAATCTAAAGGATGAATACTTTGAGGAAAATCATGGAAGAATATG   2803
          |||    ||||||    |||||    ||||||
Db  2609  CAACCTTGCTTGTCTTTCGAAAGAAATGCGTGGAGCATTTATTGAAGACGAGCATCGTGCTGAATATG  2668

Qy  2804  AAGATATTAGACAGGACCATTATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTC    2863
          |||||    ||||||    ||||||
Db  2669  CCAAAATTCGTGGACGTTTAGCCAACAACAAACAGCAGCCAAACTGACTTATAAAG       2728

Qy  2864  AAGCCAGAAAAAGTGGTTTCAAATGATTGGTCTGTGAACCTCACCCAGTGAAGCCCA      2923
          |||    ||||||    |||||
Db  2729  AGTCGGTTGAAAATGGTTTAAAATTGATGAAAGCTACGTGCCAC------CAAAACCAA     2782

Qy  2924  CGTTTATTGGGACCCAGTCTTGAAGACTATGACCTGCAGAAGCTCGTGACTACATTG      2983
          ||||||    |||||    |||||
Db  2783  ATCTTTTTGGGAACACAAGTTTTAAAGAATTATCCGCTTGCTACACTCGTGGATTATTTTG   2842

Qy  2984  ACTGGAAGCCTTCTTTGATGTCTCGGCAGCTCCGGGCAAGTACCCGGAATCGAGGCTTCC    3043
          |||||    ||||||
Db  2843  ACTGGACGCCCATTCTTATTCTTGGGAGTTTAACTGGCAA----------ATTCC        2887

Qy  3044  CCAAGATATTTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCC    3103
          |||||    ||||||    |||||
Db  2888  CGAAAATTTTAGAGAGATGAAGTGGTCGCGGCAGCAGCAACTGACCTTTACAACAGGCAC    2947

Qy  3104  ACAATATGCTGAACACACTGATTAGTCAAAGAAAACTCCGGGCCCCGGGTGTGGTTCGGGT   3163
          |||||    |||||    |||||
Db  2948  AAGGCGATGTTGAAAGATATTATCGACAACAATCGTTTTGATGCTGCGTGCTGTATTTGGTA  3007

Qy  3164  TCTGGGCCAGCACAGAGTATCCAAGACGATCACCTGACTGTACGGCAGAGCGTGTGCCCC    3223
          ||||||    |||||
Db  3008  TGTTCCCTGCTGCTCAGCGTACAGATGCAGATGCAGTATTTGATGGAAGCTGGTCAAA     3067

Qy  3224  AGGCTGCGAGAGCCCATAGCCACTTTCATGTGGTTAAGGCAACAGGCTGAGAAGGACTCTG   3283
          |||||    ||||||
Db  3068  ATGTTACGCA---------TACTTTTGAGCACTTACGCCAGCAATCTGACAAGGTGACAG    3118

Qy  3284  CCAGCACGGAGCCATACTACTGCCTCTCACTGCCTCTCAGACTTCATCGTCGGCATCC     3343
          |||||    |||||
Db  3119  GCA------AACCAAATTTATCCTTGGCAGATTACAT---TCGAGCTGCAGCGAGCAGC    3169

Qy  3344  GTGACTACCTGGGCCTGTTGCCGTTGCCTGCTGTTGGGGTAGAAGAGCTGAGCAAGGCCT    3403
          ||||||    |||||
Db  3170  AAGAGTACTTGGGCCGGATTCACTGTATCGTATTTTGGTGCAGAAGAACTGGCAAATGAAT   3229

Qy  3404  ATGAGGATGATGGTGACGACTACACTGCAATTTAGTTGCAGTCATGATTAGTTCATTAATGAA   3463
          |||||    |||||
Db  3230  ACAAAGCCAAGGTGATGACTACTCTGCAATTTAGTGCAGTCATTCATTAATGAA         3289
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Qy  3464  CAGAGGGCCTTGAGAGAGCTCCATGAAAGAGTTCGCCGAGAACTGTGTGGCCTACTGTG    3523
          ||||||
Db  3290  CCGAAGCTTTGCCGAACACTTACATGACGTATTCGTAAGAGAGTTCGTAAAGAGCTTATAAAG  3349

Qy  3524  GCAGTGAGCAGCTGACGCTGCGACAGACCTGCGAAGGTTGCGGAAGGTTGCAAGGGCATCGCCCCG  3583
          ||||||
Db  3350  CTGATGAGCAGCTCAGCAATGAGAACTGATTAAAGAGAAATATGTCGGTATTCGCCCTG    3409

Qy  3584  CTCCTGGCTACCCCAGCCAGCCCACCGACACTCACCGAGACTCACCGTGAGACTCGCAG    3643
          ||||||    |||
Db  3410  CACCAGGCTACCCTGCCTGCCCAGAGCACTCGAAAAAGCAGTGTGTTCGACTGGTTAG    3469

Qy  3644  ACATCGAGCAGTCTACAGCGCATTAGGTTAACAGAATCATTAGCCAATGGCCACCTGCTTCAG   3703
          ||||||    |||
Db  3470  GTTCTACCGACAAAAATCGGCACCAAACTGACTGAGCACTTTGCAATGATGCCGCCATCTT    3529

Qy  3704  CAGTCTCAGGCCTCACTTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAAGATTT      3763
          ||||||
Db  3530  CAGTAAGTGGTTTCTATTATTCTCATCCTCAGAGTGAATACTTTAACGTGGTAAAATCT    3589

Qy  3764  CCAAGGATCAGGTTGAGGATTATGCATTGAGGAGAACATATCTGTGGCTGAGGTTGAGA    3823
          ||||||
Db  3590  CTCAAGACCAACTTGAAGATTATGCAAAACGTAAAGGTTGGACACTGGATGATGAAGCCGAAGC  3649

Qy  3824  AATGGCTTGGACCCATTTTGG    3844
          |||||
Db  3650  GTTGGTTAGCTCCGAATTTAG    3670
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CC   including anti-P. aeruginosa drugs, as templates for recombinant
CC   production of P. aeruginosa-derived peptides or polypeptides, as target
CC   components for diagnosis and/or treatment of P. aeruginosa-caused
CC   infection, and in detection of P. aeruginosa sequences or other sequences
CC   of Pseudomonas species using biochip technology. Sequences ABD01397-
CC   ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification but was obtained in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html
XX
SQ   Sequence 3762 BP; 548 A; 1172 C; 1294 G; 748 T; 0 U; 0 Other;

Query Match             23.0%;  Score 903;  DB 11;  Length 3762;
Best Local Similarity   55.2%;  Pred. No. 5.4e-246;
Matches 2074;  Conservative    0;  Mismatches 1580;  Indels 103;  Gaps  12;
```

```
Db   2861  AATACGACGAATCGCCGCGGAAATGGCCGGTCGTGTGGTCAACACAGCCGTGGTCGGATGTCGGGG  2802
                ||||| ||| | | | ||||  |||||     |||| |  | |   |||  ||||   |||||
Qy   3701  CCCGCCTGCCAAGCGCCTTCCAGCACGCCCTATCCTGATCCTGATGGCGCGCA                3642

Db   2801  TCCTCAATATGTCGGGTGCGCGCGGCCACACAGTTCCACCTGCTGCCACTGCTTTTGAAGGACATCGCCA  2742
            |||||||  |||| |  ||||| |||||   | |||||| | |  ||||||  ||  ||||||||||||
Qy   3641  TGGGACCATGATCAGCGGGGAGAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTA             3582

Db   2741  AAGCTGTGAAAAATTGTAAGCCTAGAGTTCACCTGCCACTGCTTTTGAAGGACATATGT            1129
            ||||    ||  |  |||    ||      |||||||||     |||||| ||  ||||
Qy   3581  AAGATCATGCCAGGCGCTGAAAGCCAACAATGACACATTT               1070

Db   1130  TACTGTCTGGTCTCAGAGCCCTTCAGGATTGGACCGTACCACCAACTTTGTTAACATTGGAG        1189
            | || || | || || | |||||| |  | ||| | | || |  |||| | | |||  | |||
Qy   1070  TGTCGGGCCGAGCCAGAGCTGTCGCTGGGCAGAGAATCATTGAAAACAAATA               1130

Db   2687  GCCTGTCCGGCCTTGGAGCCGTTCACCATGACCGCAGCTCGCTGTTCGTCAACGTCGCGCG        2628
            ||||| ||| |||| |||  | || | |||| |  | || || |||| |  | | | |||||
Qy   1130  CCTCCCGGACCGAGCTGGAGCGCTCTCGGTGGCCATCGTGCCCCACCCGTGCCATGGCCTG     1189

Db   1190  AGCGCTGTAATGTTGCAGGATCAAGGAGAGTTTGCTAAACTCATCATGGCAGGAAACTATG        1249
            | ||| | |  | | ||||| | | ||||| || || || |  |||| | |||  ||| |||
Qy   2627  AGCGCACCAACATCACCGGTTCGGCGGAACGTATCCTGACCGGGAACCCCGCCAACACTACG     2568

Db   1250  AAGAAGCCTTGTGTGTTGCCAAGTGCAGGTGAAATGGAGCCCAGTGTTGGATGTCA              1309
            ||||| |  | |||| ||||| | |||| | | | | |||  || | |||||
Qy   2567  CGGAAGCTCTCGAGGTCGCCCAGCAGCAGGTGAAGCGCCCAGTGATCGACATCA                2508

Db   1310  ACATGGATGATGGCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTG          1369
            |||| | ||||||| ||||| | | |||||  | | || || |  ||| ||
Qy   2507  ACATGGACGAAGGCATGCTGGACTCGGACGAAGGTGAGATCGTCACCTTCTCAACCTGATCG     2448

Db   1370  CTTCCGAGCCAGACATCCGCAAAGTACCTTTGTGCATCGACTCCTCCCAATTTTGTCGTTGA       1429
            |||| ||||| |||   || || | || | |||| |||| | ||| ||||  | | |||||
Qy   2447  CCTCCCGAGCCCGACATCTCGGCGTGCCTGTCCGATCATGATCGATCGTCCAAGTGGGAAGTGA    2388

Db   1430  TTGAAGCTGGGTTAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAGG          1489
            |  ||||| |||   ||||| || |||||||| || ||| ||||| || ||| ||||||
Qy   2387  TCGAGGGCCCGGCCTTGAAGTGCATCCAGGGCAAGGGCATCGTCAACTGATCTCGATGAAGG     2328

Db   1490  AAGGAGGAGGACACTTCTTGGAGAAGAACAGGACCAGAGAAGTCTTAATCCAAAATCAGAGTGT      1549
            |||| ||| | ||| | |||| ||||   | || | ||| | | || ||   |   |  |||
Qy   2327  AAGGCGTCGAGGCCTTCAAGCACCATGGTGCTGGCAACAGCCGCCAGGCGCTTGCAAGAAAATCAGAGTGG  2268

Db   1550  TGGTCATGGGCTTTTGATGAAGCTGGCTTGTGTGAAAAAACTGGGCTTAATCAGAAAATGAAAATCAGAGTGT   1609
            ||| |||||||  || ||||||||||| | | | | |||  |||||  | ||  |  |  ||||
Qy   2267  TGGTGATGGCGCTCCTACGACGCAGTCCTGCCGGCATGGGCGACTGGTGTGATCCTGATCGA         2208

Db   1610  GCACCCGGGCCTACCATCTGCTTGTGTGAAAAAACTGGGCTTAATGCATCAATTTATTT          1669
            ||| ||| || | ||| | || | ||||||||||| | || | |||   || |||||||
Qy   2207  GCAAGCGCTCCTACGACATCCTGTCGTCGACGAAGTCGGCTTCCCACGCGGCCGCTCATCT         2148

Db   1670  TTGACCCTAATATCCTAACCATTGGACTGGAATGGACGGAGGAGAACAACAACTTGTATGCCATTA     1729
            ||||  ||  |||||| |  ||||    || | | | ||| | ||| ||||  |||||| |||||
Qy   2147  TCGATGCGAACATCTTCGCCATCTGGATGGCATCGGCCCATCGCGATCGTGATCCTGACCGGGTG   2088

Db   1730  ATTTTATCCATGCAACAAAAGTCATTAAAGAAACATTACCGCCGCCTGCCTACGCCTGGGAG         1789
            || ||| || |||| |  |||||||   || |  |||| ||  |||| |||| |  ||||||
Qy   2087  ATTTCATCAACGCGTCCATCCGGCGGTCCCGTCCAGGGCGCTGTGCTGGAGCTGGAGGGAAC        2028

Db   1790  GTCTTCCAACTTGTCCTCTCCTTCCGCCGTCCAGGGGCCGTTCGGAGGAAGCCAATGCATG        1849
            || || || ||| |  | || || | | ||||| ||| | | || |||||| | ||||
Qy   2027  GGGTGTCCAACGTGTCCTTCTCGTTCCGGTGGGCCGCGGCAACACCCGGTGCGGAGGGCCGACTC      1968

Db   1850  GGGTTTTCCTTTACCATGCGAATCATCACCGACGCCTCCCGGGCGACTAGTGAATGCTGGAA         1909
            |||| ||||  | || | ||| || | | ||| ||||| |  | |||| ||  |  |  |
Qy   1967  CGGTGTTCCTCTACTACGGCCATGGACCATGGACCATGGCCTGACCAGGCGCATGGGCGGCC       1908

Db   1910  ACCTCCCTGTGTATGATGATATCATAAGGAACTTCATAAGGAATTGGAA                     1969
            | ||| |  | |||| | || ||| ||  |||| |  |||||  | ||
Qy   1907  AGCTGGAAATTCACGAGATTCCGACCTGGGCCGCGCGGCCGGTGGTGTGC                    1848

Db   1970  GGAATAAAGACCCTGAGGCCCACTGAGAGACTTTTATTGAAATAATTGGAA                   2026
            || | ||| |  |||| || |   | || |||    | | |  |  |||||
Qy   1847  TCAACCGCACGCCCGAGGCCCGGTGGCGATCGCGGATCGAGAATGGCCGTGTCAA---GGCA       1788

Db   2027  CAGGAGGAGGAAGAAGTCATTCAGACTGATGAGTTGCGCAAGAACGCC                      2086
            |||| |||| | ||  ||||| ||   ||||  | | | ||| || ||
Qy   2027  CCAAGGCGACCACTCATGTCTCGGCGCCACCCAAAGGACACCTAAAGGATTTTGCTATGGATGGCT   1009
```

Db 1787 GCGGCGCGGTCAAGGAGGAGGCCGAGGACGAGGAATGGCGCAGCTACAGTGTCGAGAAGCGCC 1728

Qy 2087 TTGAGTATGCCCTTGTCGCCAGCATTGAAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCA 2146
         ||||| ||| || || || |||| ||||| ||||
Db 1727 TCGAGCATGCGCTGGTCGGTCAAGGGCATCATCCGACCTGGATCGTCGTCGAGGACACCGAGGA---- 1673

Qy 2147 GGTTAACCAAGAAAAAATATCCCGCACCTCTCAATATAATTGAAGGACCCCTGATGAATG 2206
         ||| ||||| || || ||| || |||| |||| | |||
Db 1672 ----ATGCCGCCAGTCAGTGTGCGGCGTCCCATGCAGTGGTCATCGAGGTCATCGAAGTCCCG 1617

Qy 2207 GAATGAAAATTGTTGGTGATCTTTTTGGAGCTGGAAAAATGTTTCTTACCTCAGGTTATAA 2266
         | |||| | ||||| | ||||||||| || ||| |||| || || |||
Db 1616 GGATGAACGTGTCGGCGCACCTGTTCGGCCCGGCAAGATGTTCCTCCCGGCAGGTGGTCA 1557

Qy 2267 AGTCAGCCCGGGTTATGAAGAAGGCGTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAA 2326
         ||| || |||| ||||| || || ||||| |||||| || |||||| || || | |
Db 1556 AGTCCCGGCGAGTGATGATGAAAACAGGCGGTGGCCCCACCTGTGATTCCCTTCATCGAGGCCGAGA 1497

Qy 2327 GAGAAGAAACCAGAGTGCTTACGGCACAGTAGAAGAAGGACACCCTTACCAGGGCACCA 2386
                                              AGCCGGAAGCCAAGGGCAAGA 1467
Db 1496 AAGGCGGATA------------------AGCCGGAAGCCAAGGGCAAGA 1467

Qy 2387 TCGTCTGGCCACTGTTAAAGCGTCGACGTGCGACATAGGCACGACATAGTTGGAGTAG 2446
         || | ||||||| | ||||| ||| ||||| ||||| |||| ||| | ||
Db 1466 TCCTGATGGCCACGGTGAGGGCCACGACGTGCACGACATCGTCGGCGGTGG 1407

Qy 2447 TCCTTGGCTGCAATAAATTTCCCGAGTTATTGATTTAGGAGTCATGACTCATCGTGATAAGA 2506
         | | |||||||| | | | || | || ||| | ||||| || ||| | | |||
Db 1406 TGTCTCGGCTGCAACGGCTATGACGTGGTCGAACCTGGTCGCCGGCGGGAGAAGA 1347

Qy 2507 TACTGAAAGCTGCTCTTGACCACAAGCACAGATATAATTGGCCTGTCAGGACTCATCACTC 2566
         | || | | ||| |||||||| | || ||| | | |||||||| |||| ||| | |
Db 1346 TCCCTGCGAGACCGCCATCGCCGGGAGAAATGCGACATCGGCGGCCTGTCGCCGATCACGC 1287

Qy 2567 CTTCCCTGGATGAAATGATTTTTTGTTGCCAAGGCAGATTAGCTATAAGGATTC 2626
         | | |||| || | || | || | ||| | |||| || || |||||| |
Db 1286 CGTCGCTGGACGACGATGGTCCACGTCGCCACGTCCGCAGAATTTCCAGTTGC 1227

Qy 2627 CATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACAGTTAAAATAGTCCGA 2686
         | |||| || || | ||||||||||| | | || | |
Db 1226 CGCTGATGATCGGCGCCGCCACTTCACCTACCTCGGTGGATCGAATCCGC 1167

Qy 2687 GATACAG---TGCACCTGTAATCCATGTCCTTGACGCGCTCCAAGAGTGTGTGGTCGTGTT 2743
         | ||| | ||| | || || || | | |||| | | | | |||| | |
Db 1166 AGTACGACAACGACGACGCGGTGGCTTACCTCACCGACGGCCGCCGTAGGCGTGCGCA 1107

Qy 2744 CCCAGCTGTTAGATGAAGATGAAAATCTAAAGGATGAATACTTTGAGGAAGAATATG 2803
         || ||||| || | || ||||| | ||| || || |||| ||||| ||
Db 1106 CCAAGCTGCTGCTCGTCCAAGGAGCTGAAGGCCGACTGCAGGAGCTGGCTGCTGGCTACG 1047

Qy 2804 AAGATAT------TAGACAGGACCAATTATGATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTT 2858
Db 1046 CGGTGGTTCCGCGGCAACGCACGGCCCAACCGCAGGCGCCCAGCCGGCTGAGCTACGAAC 987

Qy 2859 AAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGATTGGCTGTCTGAAACCTCACCAGTGAA 2918
         ||| ||||||| ||| |||| | | || ||| |||| ||| || || |||| || ||
Db 986 AGGGCGGATCGCCGCCAACAAGCCGGGCGTTCGACTGGCCGCGGGTTACCAGGCCCGAC------ 935

Qy 2919 GCCCACGTTTATTGGGACCCCAGTCTTGAACTGTGGAGAGACTGACCTGCAGAAGCTGGTGGACTA 2978
         ||| || || || || | ||||| || || | ||| || ||| || || ||||| | || ||
Db 934 GCCTTCCTTCACCGGCGGTCAGGGTGCTCGACGAGATCGACACCTCGCGCGGTCGCCGAGCTA 875

Qy 2979 CATTGACTGGGAAGCCTTCTTCTTTGATGTCGTCGGCAGCTCCGGGGCAAGTCGCGGGCAAGAATCCGAGG 3038
         ||| |||||| || ||||||| | | ||| ||| |||| |||| | ||| ||| |
Db 874 CATCGACTGGACGCGTTCTTCATTTCCTGGGACCTTGGCCCTGGCCGGGACCAAGTTACCCG------ 823

Qy 3039 CTTCCCCAAGATATTTAACGACAAAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGA 3098
         | | || || || |||| | || | | || || || |||||||| | |||| |
Db 822 ------CGCATCCTCCACCGGACGAAGTGTCGCGGCGAGGAGGCCGCCGCCACCGTCGTTGTTCAACGA 770

Qy 3099 TGCCCACAATATGCTGAACACACTGATTGGTCGAACAGTAGTCAAAGAAACTCCGGGCCCGGGGTGTGT 3158
         |||||| | | |||| || || || || || | ||||| ||||| | |||| || |||| | ||
Db 769 CGCCCAGCGAGCTGATGCTGAGAGCTGCTGAAGAGAAGTCGATCGACGAGAACGTGATCAAGGCCGCCGGTGTT 710

Qy 3159 TGGGTTCTGGCCAGCACAGAGTATCCAAGACGACATTCACCTGTACGCGAGAGGCTGCTGT 3218
         || ||||||| || | ||| | ||| |||| | ||| ||| | || |||| |
Db 709 CGGCTTCTGGCGGCCGCCAACCAGTCGAGCAGCGACGACCTGGAGGTCTACGGCGCCGATGG 650

Qy 3219 GCCCCAGGCTGCAGAGCCCATAGCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAGGA 3278
         || | || | | ||| | || ||| | ||| | | || | ||| || ||| ||
Db 649 C--------GAGACCCTGCCAGATCACTACTGCCACCACCTGCTGCAGCAGCGATCAAGCC 602

Qy 3279 CTCTGCCAGCACAGGAGCCATATCACTACTGCCTCTCAGACTTCATCGCTCCTTGCATTCTGG 3338
         | | |||||| ||| | || | || ||||| ||||| || || || | |||
Db 601 GGACGGCA------AGCCGAACCTGCCTGGCCGATTTCGTCGCCGATGGGAAGAAAGCCG 548

Qy 3339 CATCCGTGACTACCTGGGCCTGTTTG---CCGTTGCCTGCTTGTGGGTAGAAGAGCTGAG 3395
         ||| | |||||| | ||| | | | | | | | | ||| || ||| | |
Db 547 CGTGCGGCGACTACATCGGCGCGGCTTCATCACCACCGGGATCGGCGCCGAGGAAGTGGC 488

Qy 3396 CAAGGCCTATGAGGATGGTGCAGACGTCGCAGACTACAGCAGCATCATGGTCAAGGCGCTGGGGGA 3455
         |||||| || || | | || || ||| ||||||||||||||||||||||||||| || |
Db 487 CAAGGCGTACGAAGCCAAGGGCACGACTACAGCAGCATCATGGTCAAGGCGCTCGCCGA 428

Qy 3456 CCGGCTGCAGAGACCTTTGCAGAACATCCATGAAAGAGTTCGCCGAGAACTGTGGGC 3515
         || | || | | | || | ||| | | | || | | | ||| || || |||||
Db 427 CCCCTCCCGGAAGCCTGCGCGCCGAGCTGCGTCGCGAACGAGCGGGTCGCAAGGAGTACTGGGG 368

Qy 3516 CTACTGTGGCAGTGAGCAGCTGGAGCGTCGCAGACGCTGGAAGTTGCCGTACAAGGGCAT 3575
         |||| | | ||||| | | | || || | | | | || || | || || |||||
Db 367 CTACGCCCCGGACGAGCACCTCGACAACGAGGCCTTGATCAAGGAGCAATACGTCGGCAT 308

Qy 3576 CCGCCCGGCTCCTGGCTACCCCAGCCAGCCCGACCACCGAGAAGCTCACCATGTGGAG 3635
         ||||||||| || || ||||| || | ||||| |||| || ||| | | |||| ||
Db 307 CCGCCCGGCACCCGGGCTACCCGGCGCTACCCGGCCCATACCGACGAAAAGCCACCCTGTTCGA 248

Qy 3636 ACTCGAGACATCGAGCAGTCTACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACC 3695
         ||| | |||| | | | || | || | || || |||||| || | || ||
Db 247 ACTGCTCGATCCCGCAGGGCGTGTCGCCGTCAGCCTGACCGCGCACTACGCGATGTTCCC 188

Qy 3696 TGCTTCAGCAGTCTCAGGCCCTCACTTCTCCAATTGAAGTCCAAATATTTTGCTGTGGGG 3755
         ||| | || | |||||| || | | |||| || | | || || | || | | ||
Db 187 CGCCGCGGCGGTTCAGCGGTTGGTATTTCGCCCACCCGGCCGAGTACTTCGCGGGTCGG 128

Qy 3756 GAAGATTTCCAAGGATCAGGTTGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGA 3815
         ||||| | | |||| |||||| ||| | ||||| ||||||||| || || | |
Db 127 CAAGATCGACACAGGACCAGGTGAACGGTGAACGCCAGGGCCAGAAGGGCCCAGGAAGCCCAGCGT 68

Qy 3816 GGTTGAGAAATGGCTTGGACCCATTTTGGGATATGAT 3852
         | || | | | || ||| | || ||| |||||
Db 67   CAGCGAGCGCTGCTGCGCGCCGCGAACCTTGGCTACGAT 31

RESULT 11
ABD15089
ID   ABD15089 standard; DNA; 3795 BP.
XX
AC   ABD15089;
XX
DT   29-JUL-2004 (first entry)
XX
DE   Pseudomonas aeruginosa polynucleotide #13693.
XX
KW   Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW   antibacterial.
XX
OS   Pseudomonas aeruginosa.
XX
PN   US6551795-B1.
XX
PD   22-APR-2003.
XX
PF   18-FEB-1999;   99US-00252991.
XX
PR   18-FEB-1998;   98US-0074788P.
PR   27-JUL-1998;   98US-0094190P.

XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Delougherty C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; AB081518.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 13693; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polyepeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 3795 BP; 751 A; 1307 C; 1177 G; 560 T; 0 U; 0 Other;

Query Match   23.0%; Score 903; DB 11; Length 3795;
Best Local Similarity 55.2%; Pred. No. 5.5e-246;
Matches 2074; Conservative 0; Mismatches 1580; Indels 103; Gaps 12;

Left alignment block (query/database pairs with positions):

```
Db  1733 ...  1792
Qy  1790 ...  1849
Db  1793 ...  1852
Qy  1850 ...  1909
Db  1853 ...  1912
Qy  1910 ...  1969
Db  1913 ...  1972
Qy  1970 ...  2026
Db  1973 ...  2032
Qy  2027 ...  2086
Db  2033 ...  2092
Qy  2087 ...  2146
Db  2093 ...  2147
Qy  2147 ...  2206
Db  2148 ...  2203
Qy  2207 ...  2266
Db  2204 ...  2263
Qy  2267 ...  2326
Db  2264 ...  2323
Qy  2327 ...  2386
Db  2324 ...  2353
Qy  2387 ...  2446
Db  2354 ...  2413
Qy  2447 ...  2506
Db  2414 ...  2473
Qy  2507 ...  2566
Db  2474 ...  2533
Qy  2567 ...  2626
Db  2534 ...  2593
Qy  2627 ...  2686
Db  2594 ...  2653
Qy  2687 ...  2743
Db  2654 ...  2713
Qy  2744 ...  2803
Db  2714 ...  2773
Qy  2804 ...  2858
```

Right alignment block (query/database pairs with positions):

```
Db  2774 ...  2833
Qy  2859 ...  2918
Db  2834 ...  2885
Qy  2919 ...  2978
Db  2886 ...  2945
Qy  2979 ...  3038
Db  2946 ...  2997
Qy  3039 ...  3098
Db  2998 ...  3050
Qy  3099 ...  3158
Db  3051 ...  3110
Qy  3159 ...  3218
Db  3111 ...  3170
Qy  3219 ...  3278
Db  3171 ...  3218
Qy  3279 ...  3338
Db  3219 ...  3272
Qy  3339 ...  3395
Db  3273 ...  3332
Qy  3396 ...  3455
Db  3333 ...  3392
Qy  3456 ...  3515
Db  3393 ...  3452
Qy  3516 ...  3575
Db  3453 ...  3512
Qy  3576 ...  3635
Db  3513 ...  3572
Qy  3636 ...  3695
Db  3573 ...  3632
Qy  3696 ...  3755
Db  3633 ...  3692
Qy  3756 ...  3815
Db  3693 ...  3752
Qy  3816 ...  3852
Db  3753 ...  3789
```

RESULT 12
ACA44722

```
ID   ACA44722 standard; DNA; 3669 BP.
XX
AC   ACA44722;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #26379.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Proteus sp.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,   Zamudio C,   Malone C,   Haselbeck R,   Ohlsen KL,   Zyskind JW;
PI   Wall D,   Trawick JD,   Carr GJ,   Yamamoto R,   Forsyth RA,   Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU40852.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 32592; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 3669 BP; 1075 A; 686 C; 889 G; 1019 T; 0 U; 0 Other;
```

```
Query Match             23.0%;  Score 902.6;  DB 8;  Length 3669;
Best Local Similarity   55.0%;  Pred. No. 7e-246;
Matches 2046;  Conservative   0; Mismatches 1574;  Indels  99;  Gaps  10;

Qy        145 AAGAGGATTATGTGTCTGATGGAGGGATGGGGACCATGATCGATCCAGCGGGAGAAGCTAAAC 204
              |||  |||| | |||  ||  | |||||  | | |||||| ||||||  || |||| || ||||
Db         34 AAACGGATCTTAGTCCTTGATGCGCAATGGGAACCATGATCGATCCAGCAATATCAGCTGGCA 93

Qy        205 GAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATGCGCAGGCCGCTGAAAGGCAACAAT 264
              |||||  |||||||||||||  |||  ||||| |||||||||||||  |||||| ||||| |
Db         94 GAAGAAGATTACCGAGGTGAACGTTTTGCCCATTGATGTGATTTAAAGGGAATAT 153

Qy        265 GACATTTTAAGTATAACTCAGCCTGATGTCATTTACCAAATCCATAAGGAATACTTGCTG 324
              |||||||| ||| |||||| ||||  ||||||| | | | | ||||||  ||||||||
Db        154 GACCTTTTAGTCTTGACGCAGCCGCAGATCATTTACTGAAATTCATAATGCTTATTTTGAA 213

Qy        325 GCTGGGGCAGATATCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCCAAGCTGAC 384
              || | ||| | |||| || ||||||| || |  | |||| || || | |||| ||||  ||
Db        214 GCCGGTGCAGATATCGTGGAACAAACACCTTTAATGCAAGCTTCTATTGCCATGGCTGAT 273

Qy        385 TATGGCCTGAACACTTGCCTCCGATGAACATGTGCTCTGCAGGAGTGGCCAGAAAA 444
              ||| ||| |||| ||  | | ||| |  | | ||||||||||
Db        274 TATCAGATGGAAGGGTATGTGCAGAATTGAATGAAGAGGCTGCTAAACTTGCCAGAGCC 333

Qy        445 GCTGCCGAGGA---GGTAACTCTCCAGACAGGAATTAAGAGGTTTGTGGCAGGGGCTCTG 501
              ||| | ||||   |||| |   ||  |||  ||| ||||| | || |||| |||| ||
Db        334 TGTGCTGATAAATGGAGTGCATTAACGGCCAGATAAACCACGTTATGTTGCAGGGTATTA 393

Qy        502 GGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGGAAAGGCGGATTATAGGAAC 561
              || | | |    ||| | |||  || | || ||
Db        394 GGGCCGACCAATAGAACAGCATCCATTTCTCCTGATGTTAACGATCCCGGTTTCGTAAT 453

Qy        562 ATCACATTTGATGAGCTTGTGTTGAAGCATACCAAGAGCAGGCCAAAGACTTCTGGATGGC 621
              |||  ||| ||| | ||||  |||||
Db        454 ATCTCATTTGATACATTGGTGATGGCTTATCGAGAGGCGATCTGCGGACTCATTAAAGA 513

Qy        622 GGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTGCCAATGCCAAGCAGCCTTG 681
              |||| || |||| | || |||| | | |||  | ||| |
Db        514 GGGGTGGATTTAATTATGCGTGGAAACCATTTTGCACCCTAAATGCTAAAGCGGCTATT 573

Qy        682 TTTGCACTCCAAAATCTTTTTGAGGAGAAAATATGCTCCCCGGCCTATCTTTATTTCAGG 741
              ||| | |||||||||||| |
Db        574 TTTGCGATTAAATGTGAGTTTGATAATCTTAAATTGAATTACCGGTGATGATCTCAGGG 633

Qy        742 ACGATCGTTGATAAAAGTGGGGCGGACTCTTCCGGACAGACAGGAGAGGGGATTTGTCATC 801
              ||| |||| |||| | || | | | ||  |  | ||
Db        634 ACTATCACTGATGCGTCAGGTAGAACATTAACAGGGCAAACCACAGAAGCCTTTTATCAC 693

Qy        802 AGCGTGTCATCGAGAACCACCTCTGCATTGGAAATAAAATGTGCTTTGGGGTGCAGCTGAG 861
              || | |  | |||||  ||  | | | |||
Db        694 TCACTACGTCATCGCCGACGCGTTATCATTGGTTTAAATTGTGCGTGCCAAAAGAA 753

Qy        862 ATGAGACCTTTATTGAAATAATTGGAAAATGTACACAGCCTATGTCCTCGTTATCCC 921
              || | |  |  |||| |  ||| |||| || || || | |  ||
Db        754 TTACGCCAATATATTCAAACTCTCTCCCAAATATCAGAAACTCAGAAACTTATGTCAGTGCTCACCCT 813

Qy        922 AATGCAGGTCTTCCCAACACCTTTGGTACTATGATGAGAACGGCCTTCTATGATGGCCAAG 981
              |||| ||  |  |  |||  ||||| |||| |  | | | |  || ||
Db        814 AATGCTGGCTACCTAATGCCTTTGGCGGATAGATTTAGATGCCAATGAGATGGCGGAA 873

Qy        982 CACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAGTTGGAAGGATGCTGTGGGTCA 1041
              |   |||| | | | || || | |  || |||||  | | |||
Db        874 CAAATCAAGGAGTGGGGCCCAAGCTGGGTTTCTTAATTTGTCGGTGGTTGTTGTGTGGCACA 933

Qy       1042 ACACCAGATCATATCAGGGAAAATGCTGAAGCTGTGAAAAATTGTAAGCTAGAGTTCCA 1101
              || || |   |||| |||| ||| | |||| |||| | |  | ||| || | ||  ||
Db        934 ACCCCTGCCCATATTCAGGCTATTGCTCAAGCGGTTGATGGCATAGCACCTAGAACATTA 993

Qy       1102 CCTGCCACTGCTTTGAAGGACATATATGTTACTGCTCGGTCTCAGCCCCTTCAGGATTGGA 1161
              |   ||  |  |||||  |||  ||  | ||| || || || ||| |
Db        994 CCTGTCA-----TTAAAAAGCCTGCACTCTTCAGGTCTTGAGCCTTTGGTCATTGAT 1047

Qy       1162 CCGTACACCAACTTTGTTAACATTGGAGAGCGCGTAAATGTTGCAGGATCAAGGAAGTTT 1221
```

Db 1048 | 2119 GAAGGTAAAATGTTTTTACCCCAAGTAGTAAAAATCGGCACGGGTGATGAAACAGGCCGTA 2178

Qy 1107 | 2296 GGCCACCTTATCCCTTCATGGAAAAGAGAGAAACAGAGAACCAGAGTGCTTAACGGCACA 2355

Db 1222 | 2179 GCTTACCTTGAACCTTATATTCAAGCGACAACAAAAAGCAGGCAG------ 2222

Qy 1281 | 2356 GTAGAAGAAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTTAAAGGCGACGTG 2415

Db 1108 | 2223 ------CTCGGCAGGAAAAAGTGTTACTGGCGACAGTAAAGGGAGATGTT 2265

Qy 1341 | 2416 CACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCCGAGTTATT 2475

Db 1167 | 2266 CACGACATTGGCAAAATATTGTGGAGTGGTTGCAGTGTAATAACTATGAAAATTATC 2325

Qy 1401 | 2476 GATTTAGGAGTCATGACTCCATGTCATGTGATAAGATACTGAAAGCTGCTCCTGACCACAAAGCA 2535

Db 1227 | 2326 GATCTCGGGAGTCATGGTACCTTGCGATAAATCTTGCAAACAGCCATTGATGAACATGTT 2385

Qy 1461 | 2536 GATATAATTGGCCTGTCAGGACTCATCACTCCTCCCTGGATGAAATGATTTTTGTTGCC 2595

Db 1287 | 2386 GATATTATTGGATGTGTCTGGATTGATCATCCCCATCACTGGATGAGATGGTGAATGTTGCT 2445

Qy 1521 | 2596 AAGGAAATGGAGAGATTAGCTAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCA 2655

Db 1347 | 2446 AAAGAGATGGGAAAGACGGCGGTTTTCCTTAATGATTGGTGTGGGACAACATCG 2505

Qy 1581 | 2656 AAAACCCACAGACAGTTAAAATAGCTTCCGAGATACAGTGCTCTGTAATCCATGTCCTG 2715

Db 1407 | 2506 AAAGGCCACACCGCAGTAAAATTGAGCCTAAATTGTGAAATTACAGACCGTTTATGTGCAG 2565

Qy 1641 | 2716 GACGCGTCCAAGAGTGTGGTGTGTTAGATGTGAATCTCAAAGGATGAA 2775

Db 1467 | 2566 AATGCGTCAAGGACGGTGGTCGTTGGGGTGTGCTCATTATCGGCCGTGAT 2625

Qy 1701 | 2776 TACTTTGAGGAAATCATGGAAAATCATGAAGAATATGAGAACAGAGACCATTATGAGTCTCTC 2835

Db 1527 | 2626 TTTGTCGCTAAAAACACGCCGTGAATATGAAGTTCAGCGAGTGGCGAGAAAAAAAA 2685

Qy 1761 | 2836 AAGGAGAGGAGTACTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCAAATGGATTGG 2895

Db 1587 | 2686 CCGCGTACGCCTTCCGTTTCCTTAGCGAAAGTCGTGCCAATGCAGCTTGACTGG 2745

Qy 1821 | 2896 CTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGTCTTTGAAGACTAT 2955

Db 1647 | 2746 CAACACTATACGCACCTAAGGCGACAACAATTAGGGTACACAAGTTACAGCCAATATT 2805

Qy 1881 | 2956 GACCTGCAGAAGCAGTGGTGGACTACACATTGACTCAAGGGAGAAGCTTTCTTCTTGATGTGTCTGCAGCTC 3015

Db 1767 | 2806 GAA------ACTTACGTGAGTATGACTGAGTGGGGAGATGG 2859

Qy 1941 | 3016 CGGGGCAAGTCACCCGAATCGAATCGAGCTCTCCCCAAGATATTTAACGACAAACAGTAGGTGA 3075

Db 1827 | 2860 GCGGGGAAATATCCACGT------ATATTAGAAGAGATGAGGAGGTGTCGGAGAA 2904

Qy 2001 | 3076 GAGGCCAGGAAGGTCTACGAGTGATGCCACAATAGCCTGAACACACTGATTAGTGAACTAGGTCAAAAG 3135

Db 1887 | 2905 GAGGTAAGACGGCGTTTTGCAGATGCGAATGGCATGTGCATGTTGGATAAACTCAGCCGTGAAAAA 2964

Qy 2055 | 3136 AAACTCCGGGCCCCGGGGTGTGGTTCTGGCCAGACAGAGTATCCAAGACGACATT 3195

Db 1947 | 2965 TTACTGACACCGAAAGGTATCGTTGGTTATTCCCTGCTAATCGCCTTGGTGATGACATT 3024

Qy 2115 | 3196 CACCTGTACGCAGAGGCTGCGTCTGCGCCCATAGCCTGCAGAGCCCCATAGACCTT 3255

Db 2007 | 3025 TTACTGACACCGAAAGTGAAACGGCACAGCATG------AGTTATTACGTTGTTGCCAT 3075

Qy 2175 | 3256 TTAAGGCAACAGGCTGAGAAGGACTCTGCCGAGCCACCGAGCCATCCATCTTTCTATGGG 3315

Db 2058 | 3076 TTACGCCTAACTATTGCTTAGCAGAC------GTACCCTAACTATTGCTTAGCAGAC 3126

Qy 2235 | 3316 TTCATCGCTCCCTTGCATTCTGCTATCCGTGGATAGTCGTCTTGCTGACTATTTTGGTGCTTTTGCAGTTACCGGC 3375

Db 2295 | 3127 TTTATTGCCCCCTGGGATAGTCGCTTGCTGACTATTTTGGTGCTTTTGCAGTTACCGGC 3186

Db 1048 | ...

Qy 1107 | ...

[Remaining sequence alignment columns on the left side of the page contain additional Db/Qy aligned DNA sequences with position numbers 1048–2295 and corresponding alignment bars.]

PS   Claim 14; SEQ ID NO 30149; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening strains homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 3705 BP; 737 A; 1269 C; 1161 G; 538 T; 0 U; 0 Other;

Query Match   23.0%; Score 901.4; DB 8; Length 3705;
Best Local Similarity   55.2%; Pred. No. 1.5e-245;
Matches 2073; Conservative 0; Mismatches 1581; Indels 103; Gaps 12;

Qy   113 CCCTGCGGGATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGA 172
            ||| ||| ||||||| ||| ||||||| |||||||||| |||||| ||||||| ||
Db   29 CCCGCCTGCAAGGCCCTCCAGCACGCCCTCAGGGAACGTATCCTGATCCTCGATGGCGGCA   88

Qy   173 TGGGGACCATGATCAGCGGGAGAAGCTAAAGCAAGAGAACACTTCCGAGGTCAGGAATTTA 232
            ||| |||||| |||| || ||| || ||| |||||||| || ||| |||||| |
Db   89 TGGGCACCATGATCCAGCTACAAGCTGGAAGAGCAACAACGAGCGACTACCGCGCCGCTTCG 148

Qy   233 AAGATCATGCCAGGCCGCTGAAAGCAACAATGACATTTAAGTATAACTCAGCCTGATG 292
            || ||| ||||| || || ||| |||| ||| ||| || || |||||||| ||
Db   149 CCGACTGGCGAGCGACGTGAAAGCAACAACGAGCAACAACGAGCCGCCCGGACG 208

Qy   293 TCATTTACCAAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATA 352
                     |||| | ||||| || || || ||| |||| || ||| ||| ||||| ||
Db   209 TGATCCAGGCCATCGAGAGGGCCGCATCCTCGAGACCAACA 268

Qy   353 CTTTTAGCAGCACTAGTATTGCCCAAGTGACTAGTGGCTTGGCCTTACCGGA 412
            ||| || ||| ||| ||| ||||||| |||||||| || |||||| |||
Db   269 CCTTCAACGCCACCACCCAGTGTCCCAGGCCGACTACGGCATGTCGGCCTACGAAC 328

Qy   413 TGAACATGTGCTCTGCAGGAGTGCCAGAAAGCTGCCGAGGAGTAACTCTCCAGA---- 469
            || |||| ||| |||| |||| |||||| || || ||| || ||| |||
Db   329 TCAACGTCGAAGGGCCCTGCCCTGGCCCCAGGTGGCCGACGGGGAAGACCGGAGAGACCC 388

Qy   470 CAGGAATTAAGAGGTTTGTGGCAGGGGCTTCTGGGTCCAGCTAATAAGACACTCTCTGTGT 529
                  ||||||| ||| ||| |||||| ||| ||||| ||||| ||| |||||| |||||
Db   389 CGGACAAGCCGCGTTCGTCCGCCGGTGCTCCGGCCCGACCCAGCCGCACCCTGCTCGATTT 448

Qy   530 CCCCATCTGTGGAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCAT 589
            || |||||||| ||||| ||| |||||||| ||||| || |||| ||| ||||
Db   449 CCCCGGACGTGAACAACCCCGCTACCGGACGTCACCTTGACGAACTGGTGGAGAACT 508

Qy   590 ACCAAGAGCAGGCCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTA 649

Qy   3376 TTTGGGGTAGAGA---GCTGAGCAAGGCCTATGAGAGGATGATGGTGTGACGACTACAGCAGC 3432
            || ||| ||| ||||| | | ||| ||||| || || |||||||| ||
Db   3187 GGTCTAGAAGAGAGATGCACTCGCTAATGGGTATGATAATGCTCATGATGATTACAATAAA 3246

Qy   3433 ATCATGGTCAAGGCGCTCGGGGGACCCGCTGGCGAGAGGCCTTTGCAGAGAGCTCCATGAA 3492
            || ||| |||| || ||| ||| || |||| || || ||||| ||| || || ||
Db   3247 ATTATGTAAAGCGCTATCCGATCGTCTTGCAGAGATATTTGCCGAATATTTGCATCAA 3306

Qy   3493 AGAGTTCGCCGAGAACTGTGGGCCTACTGTGCCAGTGAGCAGCTGGACGTCCGAGACCTG 3552
            ||| ||| | ||| || || || ||| |||| |||| || |||| |||| |
Db   3307 CAAGTGAGAACCAAGATTTGGGTTACAGTCCTACAGCTCCTAATGCAGCCGTCTCCAAGGAGTTG 3366

Qy   3553 CGAAGGTTGCGTACAAGGGCATCCGCCCGGCTCCTGCTACCCCAGCCAGCGACCAC 3612
            ||| ||| | || | || |||| | | ||||| ||| ||| ||| |||| ||
Db   3367 ATTAGAGAAAATATCAAGGAACACGGACCTGCACCGGGGATATCCGGCTTGCCCAGAGCAC 3426

Qy   3613 ACCGGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGACCAGTAGTCTACAGGCCATTAGGTTA 3672
            ||| || ||| | || || || | || || |||| | || ||| | || ||| |||
Db   3427 ACAGAAAAAGCAAAAATTTGGCAACTGTTAAATGTAGAAAATCGCATTGGTATGGAGCTT 3486

Qy   3673 ACAGAATCATTAGCAATGGCAACTGCTTCAGCAGTCCACCTGCTTCGGGGGCTTCGGTATTTGG 3732
            ||| ||||| | | || ||||| || ||||| || || | ||| ||| || |||| |||
Db   3487 ACTGATGCTTACGCGATGTGGCCGGAGCTTCGGTATCGGGGGGCTTGGTATTTTTAGTCATCCT 3546

Qy   3733 AAGTCCAAATATTTGCTGTGTGGGGACAGATTTCCAAGGATCAGGTTGAGGATTATGCATTG 3792
            || |||| | | ||| || ||| || ||| ||||| || || || |||| |||
Db   3547 GAAAGTAAATATTTTTGCCGTCGTCAAATTCAAAAAGATCAGTAGGATCAGTGAAGATTACGGCCAAA 3606

Qy   3793 AGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCCATTTTGGGATATGA 3851
            ||| || ||| | | ||| ||||| ||| |||| |||| || || ||| |||| |||
Db   3607 CGTCGTCGGTATGAGTGTGAGAGTGGTGAAGTTGAGCGTTGGTTAGCCCCTAATTTAGGTTATGA 3665

RESULT 13
ACA42279
ID   ACA42279 standard; DNA; 3705 BP.
XX
AC   ACA42279;
XX
DT   19-JUN-2003 (first entry)
XX
DE   Prokaryotic essential gene #23936.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Pseudomonas aeruginosa.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-042292P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI   Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsych RA, Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU38409.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX

(Nucleotide sequence alignment — Query (Qy) and Database (Db) sequences)

```
Db  509  ...ACGTCGAGGCGACCCGAGGCCTGATCGAAGGCGCTTGTCCGACCTGATCCTGATCGAGGACCA  568
Db 1583  TCGATCGGAACATCTTCGCCATCGACCGGCATCGAGGAGAACACAACTACGCGTCG 1642

Qy  650  TTTTTGATACTGCCAAGGCAGCTTGTTTGCACTCGACAAATCTTTTGAGGAGA  709
Qy 1730  ATTTTATCCATGCAACAAAAGTCATTAAAGAACATTACCTGAGCCAGAATAAGTGAG 1789

Db  569  TCTTCGACACCTCAACGCGGCGATCTTCGCCGTGTTCGCGAGGAAC  628
Db 1643  ATTTCATCAACGCCTGCGCCTACATCCGGCACTCCCCTACGCCTGAGCTCGGCG 1702

Qy  710  AATATGTCTCCCGGCCTATCTTATTTCAGGGAGCGATCGTTGATAAAAGTGGGCGACTC  769
Qy 1790  GTCTTTCCAACTTGTCCTTCTCCTTCCGAGAATGAAGCCATTCGAGAAGCAATGCATG 1849

Db  629  TCGGGCGTGGAGCTGCCGATCATGATCATCTCCGAACCATCACCGACGCCTCCGGCACCCC  688
Db 1703  GGGTGTCAACGTGTCCCTTCTGTTCCGGGGCAACACCCGGTACGCGGAGGCGATCCACT 1762

Qy  770  TTTCCGGACAGACAGGAGGAGGGATTTGTCATCAGCGGTGTCTCATGGAGAACCACTCTGCA  829
Qy 1850  GGGTTTTCCTTTACCATGCAATCAAGTCTGGCACATGGGAGAGAGTGAATGCTGAA 1909

Db  689  TGTCGGGCCAGACCACCGAGGCCTTCGGAACTCGGTGCGGGCATGCCCGGCCGATCTCGG  748
Db 1763  CGGTGTTCCTCTACTACGGCGATCCGAACGGCCATCGTCAACGCGCCGCC 1822

Qy  830  TTGGATTAAATTGTGTCTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAA  889
Qy 1910  ACCTCCCTGTATGATGATATCCATGAAGACTTCTGCAGCTCTGTGAAGATCTCATCT 1969

Db  749  TAGGCCTGAACTGCGCGCCCTCGGCGGCCAAGGGAATTGCGGCCCGTACATCGAGGAACTGTCGA  808
Db 1823  AGCTGGAAATCTACGACGAGATTCCGAAAAGCGGCTGCGGGACGTGTGTGC 1882

Qy  890  AATGTACAAACAGCCTTATGTCCTCTGTTATCCCATGACGAGTCTTCCCAACACCTTTGGTG  949
Qy 1970  GGAATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTTACGTATGCCCAGACTCAA---GGCA 2026

Db  809  CCAAGGCCGACACTCAGTCTCGGGCGGAAATGCCGGTCGTGTGGTCGTCGAACGCCTTCGGCG  868
Db 1883  TCAACCGCACGCCCGAGGCCACCGAGGCCCTGGCCGATCGGCGATCACGACTACAAGGGCG 1942

Qy  950  ACTATGATGAAACGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCT  1009
Qy 2027  CAGGAGGGAAGAAAGTCATTCAGACTGATGAGTGAGGAAATGGCCCTTGTCGAAGAACGCC 2086

Db  869  AATACGACGAATCGCCGGCGAAATGCCGGTCGTGTGGTCGTCGAGGAATTCGCCGCTGCCGGGCT  928
Db 1943  GCGGGCGCGGTCAAGGAGGCCGGAGGATGGCGCAGCTACAGCGGTCGAGAAGCGGCC 2002

Qy 1010  TGGTCAATATAGTTGGAGGATGCTGTGTGGGTCAACACCAGATCATATCAGGAGAAATTGCTG  1069
Qy 2087  TTGAGTATGCCCTTGTGAAGGGCATTGAAAAACATATATTGAGGATACTGAGGAAGCA 2146

Db  929  TCCTCAATATCGTCGGCGGCGTCGTCGCGGCACACACCCCGCGACATCGAGGCGGCATCGGCCA  988
Db 2003  TCGAGCATGCGCTGGTCAAGGGCATCACCGTCGATCGTCGAGGACACCGAGGA---- 2057

Qy 1070  AAGCTGTGAAAAATTGTAAGCCTAGAGTTCCACCTGCCACCTGCCTGCTGTTTTGAACGACATATGT  1129
Qy 2147  GGTTAAACCAAAAAAATATCCCGACCTTCTCAATATAATTGAAGACACCCCTGATGAATG 2206

Db  989  AGGCAGTGGCCAAGTACCCGCGCGGCATCCCGGAGATTCCCCGGGCCTGTC------  1042
Db 2058  ----ATGCCGCCAGCAGTGTGCGCGTCCGACCTGCTGCGTCATCGAGGTGTCATGTGTCCG 2113

Qy 1130  TACTGTCTGGTCTGGAGTGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAG  1189
Qy 2207  GAATGAAAATTGTTGGTGATCTTTTTGGAGTGGAGCTGCGGCGCCCAGATGTTCTACCTCAGGTTATAA 2266

Db 1043  GCCGTGTCCGGCGGAGCCGGTGTTCACCATCGACCGCAGCTCCGAGGCGAACGTCGGGGCG  1102
Db 2114  GGATGAACGTGGTCGGCGACCTGTTCGCGGCGAGTGTTCCTCCGCCAGGTGGTGTCA 2173

Qy 1190  AGCGCTGTAAATGTTGCAGGGATCAAGAAGTTGCTAAACTCATCATGGCAGGAAACTATG  1249
Qy 2267  AGTCAGCGCGGGTTATGAAGAGGCTGTTGGCCACCTATTCCCTTTCATGGAAAAGAAA 2326

Db 1103  AGCGCACCACAACATCACCGGTTCGGCGCAAGTTCGCCCCGGCTGATCCGGCTGATCATGATTACG  1162
Db 2174  AGTCCGCGGGCGAGTGATGAAGCAGGAGGCGTGGCCCACCTGACCTTCATCGAGGCGGAGA 2233

Qy 1250  AAGAAGCCTTGTGTGTTGCCAAAGTGCAGGTGGAAATGGAGCCCAGGTGTTGGATGTCA  1309
Qy 2327  GAGAAGAAACCAGAGTGCTTAACGGACACAGTAGAGAGAGACCCTTACCAGGGCCACCA 2386

Db 1163  CGGAAGCTCTCGAGTGGTCGCCCAGCAGCAGGTGGAAGCCGGCGGCCAGAGTGATCGACATCA  1222
Db 2234  AAGGCGGACA----------------AGCCGGAGCCAAGGACAAGA 2263

Qy 1310  ACATGATGATGGCATGCTAGATGCTCGAAGTGCAATGACCAGATTTGCAACTTAATTG  1369
Qy 2387  TCGTGCTGGCCACTGTTAAAGGCGCAGGTGCACGACGTACGGCAAGAACAACATAGGTGGAGTAG 2446

Db 1223  ACATGGACGAAGGCATGCTGGACTCGAAGGCGGCGCCATGGTCACCTGCGAGGCCATGATCG  1282
Db 2264  TCCTGATGGCCACGGTGAAGGGCGACGTGCACGACATCGCAAGAACATCGTCGGCGTGG 2323

Qy 1370  CTTCCGAGCCAGAGCAATCGCGAAAGGTACCTTTGTGCATCGACTCCTCCCAATTTTGCTGTGA  1429
Qy 2447  TCCTTGGCTGCAATAATTCCAGTTATTGATTAGGAGTCATGACTCCATGTGATAAGA 2506

Db 1283  AGCGCCGAGCCGACATCTCGCGCGTTCGGCCGATCATGATGACGACTCGTCCCAAGTGGGGAAGTGA  1342
Db 2324  TGCTCGGCGTGAGTGATGAAGCTATGACGTGTGCGCGGCCGGAGAGA 2383

Qy 1430  TTGAAGCTGGGTTAAAGTGCTGCCAAGGGAGTGCATTGTCAATAGCATTAGTGCTGAAGG  1489
Qy 2507  TACTGAAAGCTGCTCTTGACCACAAGCAGTATAATTGGCTGCCTGTGCAGGACTCATCACTC 2566

Db 1343  TCGAGGCCGGCGGCCTTGAGATCGCAAGCCAGGGCAAGGGCATCGATCTCGATGGAAGG  1402
Db 2384  TCCTGCAGACCGGCCATCGCCGAGAAATGCGCACATCATCGGCCTGTCTGCCTGATCACGC 2443

Qy 1490  AAGGAGGAGACGACTTCTTGATGAAGAAGATTAAAAAGTATGGAGCGTGCTATGG  1549
Qy 2567  CTTCCCTGGATGGAAATGATTTTTGTTGCCAAGGAAATGGCCCAGAGTTAAAATAGCTTCCGA 2626

Db 1403  AAGGCGGATGGCCTTGCAGGCCCTTGTGTCCAAGCGCGACACCGGCCGGCGCAAGGAGAAATCT  1462
Db 2444  CGTCGCTGGACGAGATCGTGTCCCACGTCGAAGGCGGCATACCGCGTGAAGATCGATCCGC 2503

Qy 1550  TGGTCATGGCCTTTGATGAAGAGAACAGAGCAACAGACACAAAATCAGAGTGT  1609
Qy 2627  CATTGTTGATTGGAGGACGAACAACACTTCAAAAACCCACAAAAATAGCTTCCGA 2686

Db 1463  TGGTGATGGCCTTGACGAGGAGGCGGCGGCACTCCAGGAAGAGAAATCT  1522
Db 2504  CGCTGATGATCGAGGCGGCGCCACTACCTGCAAGGCGCATACCCGCGTGAATCGATCGCC 2563

Qy 1610  GCACCCGGCCTACCATCGTCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTT  1669
Qy 2687  GATACAG---TTGCACCTGTATCCAATGCATTCCTGAGCCGTGATAATGACATTATTT 2743

Db 1523  GCAAGCGCTCCTACGACACATCCTGGTCGTCGAACGAAGTCGGCTTCCCACCCGAGAGCATCATCT  1582
Db 2564  AGTACAGCAACGACGCGGTGGTCACCGACGGATGATAACTTGGCGTAGGCGGTGGCCA 2623

Qy 1670  TTGACCCTAAATATCCTAACCATTGGGACTGGAATGCAGAGGAGAACAACTTGTATGCCATTA  1729
Qy 2744  CCCAGCTGTTAGATGATGAAAATCTAAAGGATGAAATCTTTGAGGAGAATCATGGAAGAAATATG 2803

Db                                                                    
Db 2624  CCAGCCTGCTGTCCAAGGAGCTGGAATGCAGACTGGAGCTGAGGGAGCGGTGGCCA 2683
```

RESULT 14
ADI39093
ID   ADI39093 standard; DNA; 3705 BP.
XX
AC   ADI39093;
XX
DT   22-APR-2004 (first entry)
XX
DE   Pseudomonas aeruginosa metH DNA.
XX
KW   fermentation; methionine; Coryneform bacterium; methionine synthase;
KW   MetH; animal feed additive; sulphur; human nutrition; animal nutrition;
KW   cosmetic; pharmaceutical; gene; ds.
XX
OS   Pseudomonas aeruginosa.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..3705
FT   /*tag= a
FT   /product= "metH"
XX
PN   WO2003087386-A2.
XX
PD   23-OCT-2003.
XX
PF   16-APR-2003; 2003WO-EP004010.
XX
PR   17-APR-2002; 2002DB-01017058.
XX
PA   (BADI) BASF AG.
XX
PI   Kroeger B, Zelder O, Klopprogge C, Schroeder H, Haefner S;
XX
DR   WPI; 2003-877106/81.
DR   P-PSDB; ADI39094.
XX
PT   Fermentative production of sulfur-containing compounds, particularly L-
PT   methionine, useful as feed additives, by using Coryneform bacteria that
PT   overexpress methionine synthase.
XX
PS   Claim 5; SEQ ID NO 27; 304pp; German.
XX
CC   This invention describes a novel method for the fermentative production
CC   of methionine by growing a sulphur-producing Coryneform bacteria that
CC   expresses at least one heterologous nucleic acid encoding a protein with
CC   methionine synthase (MetH) activity. Methionine accumulates in the medium
CC   or the cells. The method can be used to produce an L-methionine-
CC   containing animal feed additive by culturing an L-Met-producing
CC   microorganism, removing water from the resulting broth, removing 0-100%
CC   of the biomass formed and drying the product to produce the feed additive
CC   in powdered or granular form. The nucleic acid encoding MetH has sequence
CC   homology less than 100% with respect to the metH coding sequence of
CC   Corynebacterium glutamicum ATCC 13032. Optionally at least one other gene
CC   in the methionine biosynthesis pathway (e.g. aspartate kinase,
CC   glyceraldehyde-3-phosphate dehydrogenase or 3-phosphoglycerate kinase) is
CC   also amplified or mutated so that it is not affected by metabolites. Also
CC   at least one metabolic pathway that reduces production of methionine is
CC   at least partly switched off (e.g. homoserine kinase, threonine
CC   dehydratase or threonine synthase). The method is especially used to
CC   produce L-methionine, useful as an additive for animal feeds. More
CC   generally sulphur-containing fine chemicals are useful in human and
CC   animal nutrition, cosmetics and pharmaceuticals. This sequence encodes a
CC   metH protein described in the disclosure of the invention.
XX
SQ   Sequence 3705 BP; 737 A; 1269 C; 1161 G; 538 T; 0 U; 0 Other;

Query Match   23.0%; Score 901.4; DB 10; Length 3705;
Best Local Similarity   55.2%; Pred. No. 1.5e-245;
Matches 2073; Conservative   0; Mismatches 1581; Indels 103; Gaps 12;

Qy   113 CCCTGCGGGATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGA 172
                  ||||| |||||||||||||||| | ||| | | |||||| ||||||

```
Qy         AAGAAGCCTTGTCTGTGTTGCCAAAGTGCAGGTGGAAATGGAGCCCGCCAGTGTTGGATGTCA  1309
      1250                                                                   
Db         CGGAAGCTCTCGAGGTCGCCGAGCAGCAGGTGAAAGCGCCGGCCAGTGATCGACATCA  1222
      1163                                                                   

Qy         ACATGATGATGGCATGCTAGATGTCTAGAGTGGTCCAAGTGCAATGCACAGATTTGCAACTTAATTG  1369
      1310                                                                   
Db         ACATGGACGAAGGCATGCGACTCTGGACTCGAGAGGCCGCCCATGTCACCTTCCTCAACCTGATCG  1282
      1223                                                                   

Qy         CTTCCGAGCCAGACATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGTCTGTGA  1429
      1370                                                                   
Db         CCTCCGAGCCCGACATCTCCGGCGTGCCGACATCATGATCGACTCCTCCAAGTGGGAAGTGA  1342
      1283                                                                   

Qy         TTGAAGCTGGGGTTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCAGTTAGTCTGAAGG  1489
      1430                                                                   
Db         TCGAGGGCCGGCCTCGAAGTGCATCCAGGCAAGGGCATCGTCAACTCGATGATGAGAGG  1402
      1343                                                                   

Qy         AAGGAGAGGACGACTTCTTGGAGAAGGCCAGGAAGAGATTAAAAAGTATGGAGCTGCTATGG  1549
      1490                                                                   
Db         AAGGCGTCGAGGCGTTCAAGCACCATGCCCGAGCACCGGCCTCGCTTCCACCGGAAGACCACCATGC  1462
      1403                                                                   

Qy         TGGTCATGGCTTTTGATGAAGGAGAACAGGCAGCAACACAGAAGACAGAACAACAAATCAGAGTGT  1609
      1550                                                                   
Db         TGTGATGGCCTTCGACGAGGACACTGCCTCAGGGGAACAGCAACAACTACACGCGGTCG  1522
      1463                                                                   

Qy         GCACCCGGCCTACCATCTGCTTCCTCTCCTTCCGAGAAGCCATTCGAGAGAACAATGCATG  1669
      1610                                                                   
Db         GCAAGCGCTCCTACGACATCTGGTCGCGACGAGTCGGCGCTTCCGCGGCGGGCAACAGCATCATCT  1582
      1523                                                                   

Qy         TTGACCCTAATATCCTAACCATTGGACTGGAATGGAAACGTGTATGCCATTA  1729
      1670                                                                   
Db         TCGATGGAACATCTTCGCCATCGCCGGGGTTACCACCGGCATGGCGGTCG  1642
      1583                                                                   

Qy         ATTTTATCCATGCAACAAAAGTCATTAAAGAAACATTACCTGAGCCAGAATAAGTGAG  1789
      1730                                                                   
Db         ATTTCATCAACGCCTGCGCCTACATCCGCGACAACCTCCCCTACGCCCTGAGCTCGGGGCG  1702
      1643                                                                   

Qy         GTCTTTCCAACTTGTCTCTCCTTCCGAGAGCCATTCGAGAGAAGCAATGCATG  1849
      1790                                                                   
Db         GGGTGTCCAAGTGTCTTCTCGTTCTCGCGGCCAACACCCGGTACGGCGAGGCGGATCCACT  1762
      1703                                                                   

Qy         GGGTTTCCTTTCATGCAATCAAGTCTCGGCATGGAACGATGGAGTGAATGCTGGAA  1909
      1850                                                                   
Db         CGGTGTTCCTTCCTCTACTACGGCGGCATGGCCTGACTCCAACGGCGTCAACGCCGGCC  1822
      1763                                                                   

Qy         ACCTCCGTGTATGATGATGTATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCT  1969
      1910                                                                   
Db         AGCTGGAAATCTACGACGAGATTCCGAAGGCGTCGCGGAGGCGGTCGACGTGGTGC  1882
      1823                                                                   

Qy         GGAATAAAGACCCTGAGGCCACTGAGGAAGCGCTCTTACGTTATGCCCAGACTCAA---GGCA  2026
      1970                                                                   
Db         TCAACCGCACGCCCGAGGCCACGGAGAATGCGGCCGATCGCGAGGACTACACAAGGGGCG  1942
      1883                                                                   

Qy         CAGGAGGGGAAGAGAAGTCATTCAGACTGATGAGTGGAGGAAATGGCCTGCGAAGAACGGCGC  2086
      2027                                                                   
Db         GCGGGCGCGGTCAAGGAGGGCGAGGACGAGGAATGGCCGGCTACAGCCGGGAGAAGCCGCC  2002
      1943                                                                   

Qy         TTGAGTAGTGCCTTGTGAAGGGCATTGAAAAACATATTATTGAAGGAGAAGCCA  2146
      2087                                                                   
Db         TCGAGCATGCGCTGGTTCAAGGGCATCACCACCTGGATCGTCGATGGTGGTGC-----  2057
      2003                                                                   

Qy         GGTAAACCAAAAAAAAATATCCCAATAATAATTGAAGAATGAATG  2206
      2147                                                                   
Db         ----ATGCCGCAGCAGTGTGCGGTCCCATCGGAGTTCATCGAGGTTCGTGATGTCCG  2113
      2058                                                                   

Qy         GAATGAAAATTGTTGGTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAA  2266
      2207                                                                   
Db         GGATGAACGTGGTCGGGCGACCTGTTCGCCGGCAAGATGTTCCTCCCGCAGTGGTCA  2173
      2114                                                                   

Qy         AGTCAGCCCGGGTTATGAAGAAGAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAA  2326
      2267                                                                   
Db         AGTCCCGCGGAGTGATGAAGAAGCAGCAGCGCGGTGCCCACCTTCCCTTCATGCCGATTCCTTCATCCGGTGATGGAGGCGGAGA  2233
      2174                                                                   
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Db         CCCGCGCTGCAAGCCCTCCAGCACGCGCCCTCAGGGAACGTATCCTGATCCTCGATGGCGGCA  88
      29                                                                    
Qy         TGGGGACCATGATCAGTGATCTCAGCGGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTA  232
      173                                                                   
Db         TGGGCACCCATGATCGATCCAGAGCTACAGAGCTGGAAGAGGCCGACTACCGGCCGAGCGCTTCG  148
      89                                                                    

Qy         AAGATCATGCCCAGGCCCGCTGAAAGCTGAAAGGCAACAATCAATTTAAGTAGTATAACTCAGCCTGATG  292
      233                                                                   
Db         CCGACTGGCCGAGCGACGTGAAAGGCAACAACGACCTCTTGCTGCGGCCGCCCGGACG  208
      149                                                                   

Qy         TCATTTACCAAATCCATAAGGATATACTTGCTGCTGGCGCAGATATCATTGAAACAAATA  352
      293                                                                   
Db         TGATCCAGGCCATCGAGAAGGCCTACCCTCGACCTCGAGAACATCCTCGAGACCAACA  268
      209                                                                   

Qy         CTTTTAGCAGCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGACCTCCGA---  412
      353                                                                   
Db         CCTTCAACGCCACCACCAGGTGTCCCAGGCCGCCATACGGCGCCGACCACGGCCTGCGCCTACCGGCAAC  328
      269                                                                   

Qy         TGAACATGTGCTTCTGCAGGAGTTGGCCAGAAAGCTGCCGAGAGGTAACTCTTCCAGA  469
      413                                                                   
Db         TCAACGTCGAAGGGGCGGCGCTTTCGTTCGCCGGGCGCTCGGCGTGTGCCGGCGCCGAGGACCCC  388
      329                                                                   

Qy         CAGGAATTAAGAGGTTGTGGCGGAGGTTGCTGCGAGGGGCTCTGGTGGGGTTCATTCATTGATATCTCTGT  529
      470                                                                   
Db         CGGACAAGCGCCGGCTTTCGTCGGCGTCGCGGCGGCCTGGTGATCGAAGGCCGCACCGTGTCGCACCC  448
      389                                                                   

Qy         CCCCATCTGTGAAAGCTGCCGGATTATAGGAACATCATTGATGAGCTTGTGAAGCAT  589
      530                                                                   
Db         CCCCGGACGTGAACACCCCGGCTCACCTTCGACGAACGTACCACCGGCCTGCCGCCGCCACCC  508
      449                                                                   

Qy         ACCAAGAGCAGGACAGCAGAGAGGAGGACTTCTGGATGGCGGGGTTGGATATCTTACTCATTGAAACTA  649
      590                                                                   
Db         AGGTCGAGGGCGGACGCCGGGGCCCGAGGCCTGATCGGAAGCGCGCGGCCCGATCCTCGG  568
      509                                                                   

Qy         TTTTTGATACTGCCAATGCCAAGGCCAGCAGCCTTGTGTTTGCACTTGGAAGTGAAAATCTTTTTGAGGAGA  709
      650                                                                   
Db         TCTTCGACACCCTGAACACGGGCGCGATCTTCGCCGGTGCGGGGAATGCCTGCGCGGTGTTCGAGGAAC  628
      569                                                                   

Qy         AATATGCTCCCCGGCCTATCTTTATTTCAGGGACGATGTCGTTGATAAAAGTGGGCGGACTC  769
      710                                                                   
Db         TCGGGGTTGCCAGCCACCCCGGCGCCGATCATGATGTCGGCGTCTGCGTGGCCGCCACCC  688
      629                                                                   

Qy         TTTTCCCGACAGCAGAGGAGGATTTGTCATCAGCTGTCTCATGAGGAACCACTCTGCA  829
      770                                                                   
Db         TGTCGGGGCCAGACAGGGCGTTCTGAACTCGGTGCGGCGGCATGCCCGCCGGCCGGTCGG  748
      689                                                                   

Qy         TTGGATTAAATTGTGCTTGGGTGGCAGCTGCAGCTGAGGTCAACACTTATTGTTGAAAATAATTGGAA  889
      830                                                                   
Db         TAGGCCTGAACTGCGCGCCCTCGCGGCCCAAGGAATTGCGGCCGCCACATCGAGGCGAACTGTCGA  808
      749                                                                   

Qy         AATGTACAACAGCCTATGTCCTCTGTTATCCCAATGCAGAGGTCTTCCCAACACCTTTGGTG  949
      890                                                                   
Db         CCAAGGCCGACACTGTCTCGGCGCCCAGCGGCCTTCGGCGG  868
      809                                                                   

Qy         ACTATGATGAAACGCCTTCTATGATGAGCCAAGCACCTAAAGGATTTTGCTATGGATGGCT  1009
      950                                                                   
Db         AATACGACGAATCGCCGGCTGTGTGCGGCGAAATTCGCCCGCCGGCT  928
      869                                                                   

Qy         TGGTCAATATAGTTGAAGGATGGATGCTGTGGTCGGTCAACACCAGATCATATATGT  1069
      1010                                                                  
Db         AGGCAGTGCAAGTACCCGCCGGCGGCCATCCCGGAGATTCCCGGCCTGTC------  988
      929                                                                   

Qy         AAGCTGTGAAAATGTAAGCCTAGAGTTCACCTGCCACTGCTTTTGAAGGACATATGT  1129
      1070                                                                  
Db         AGGCAGTGGCCAAGTACCCGGCGGCCATCCCGGAGATTCCCGGCCTGTC------  1042
      989                                                                   

Qy         TACTGTCTGGTCTAGAGCCTTCAGGATTGGACCGTACCACCAACATTGTTAACATTGGAG  1189
      1130                                                                  
Db         GCCTGTCCGGCGGCCGTTCACCGACGACCGTCGCTTCGTCGTCGTGTTCGTCGGCG  1102
      1043                                                                  

Qy         AGTCAGCGCTGTAATGTTGCAGGATCAAGGAAGTTTGCTAAACTCATGGCAGGAAACTATG  1249
      1190                                                                  
Db         AGCGCACCACCAACATCACCCGGTTCGGCCAAGTTCGCCCCGCTTGATCCCGGTGATGAAGAAGAAAACTACG  1162
      1103                                                                  
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Qy   2327 GAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAAGAGACCCTTACCAGGCACCA 2386
             |||      |                          ||||||||
Db   2234 AAGGCGACA------------------------AGCCGGAAGCCAAGGGCCAAGA     2263

Qy   2387 TCGTGCTGGCCACTGTTAAAGGCAAGAACATAGTTGGAGTAG                  2446
          ||    ||  ||||    ||  |||||||||| |||  ||||
Db   2264 TCCTGATGGCCCACGGTGAAGGGCGACGTGCACGACAATCGGCAAGAACATCGTCGGCGGTGG 2323

Qy   2447 TCCTTGGCTGCAATAATTTCCGAGTTATTAGGACTCCATGTGATAAGA            2506
             |||||||||||  || |  ||   |||  |||| ||||||
Db   2324 TGCTCGGCTGCAACGGCTATGACGTGGTCGACCTCGGCGTGATGGTCCGGCGGAGAAGA     2383

Qy   2507 TACTGAAAGCTGCTCTTGACCACAAGCAGATATAATTGGCCTGTCAGGACTCATCACTC    2566
               |    ||||  |   ||       ||||  ||||         ||||||||||
Db   2384 TCCTGCAGACCCGCCATCGCCGAGAAATGCAATCATCCGCTGTCTGGCCTGATCACGC     2443

Qy   2567 CTTCCCTGGATGAAATGATTTTTGTTGCCAAGGAAATTAGAGATTAGCTATAAGGATTC   2626
          ||||||||||      |    ||  ||||||||  ||||||  ||||   ||| ||||
Db   2444 CGTCGCTGGACGAGATGTCCACGTCGTCGGCCAGTGAAGATCCAGCGGCAGAATTTCCAGTTGC 2503

Qy   2627 CATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGA   2686
            ||||||||||||||    |||  ||    |     ||     |||||    ||||| |
Db   2504 CGCTGATGATCCGGCGCGCCACTACCTCGAAGATGCGGTGAAGATCGATCCGC        2563

Qy   2687 GATACAG---TGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGGTGTT     2743
          |||||||      ||   ||  |||| || ||  || ||||||||||||
Db   2564 AGTACAGCAACGACGCGGTGGTCTACGTGCCGCGCTCGCCGCGCGTAGGCGTGGCCA      2623

Qy   2744 CCCAGCTGTTGATGAAATCTAAAGATGAATACTTTGAGGAAGAATATG            2803
          |||  |||  |   | |  ||    ||  |  ||||||||||    |
Db   2624 CCAGCCTGCTGTCCGAAGGAGCTGCAAGGCGCCGACTACG                   2683

Qy   2804 AAGATAT-----TAGACAGGACCATTATGAGTCTCTCAAGGAGGAGGATACTTACCCTT    2858
          ||| |||        ||||||  ||||||  || |   ||||||||| ||||| ||
Db   2684 CGGTGGTCCGCGAACGACGCGGCCAACCGGCCGCCGCAGCGGCTGAGCTACGAAC       2743

Qy   2859 AAGTCAAGCCAGAAAAGTGGTTTCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAA   2918
           |||| | ||  || ||||||     |||||  ||||| |  |||| |||||||  |
Db   2744 AGGCGATCGCACCAACAAGCCGGTTGCGTTCGACTGGCCGGTCACCAGGCCCGAC---   2795

Qy   2919 GCCCACGTTTATTGGGACCCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTCGTGGACTA 2978
           |||  ||| |||||||    ||| |  ||||  |  |||||||| ||||| ||||| ||
Db   2796 GCCTTCCTTCACCGGCGTGCAGGGTGCTCGACGGGTGCTCGCCGGTA                2855

Qy   2979 CATTGACTGGAGAGCCGTTTTCTTTGATGTCGGAGCTCCCGGGGCAAGTACCCGAATCGAGG 3038
          |||||||||||| |||       ||| |     ||   |||||| |||| |||||  | ||
Db   2856 CATCGACTGGACGACGCCGTTCTCATTCCTGGGAACCTGGCCCGGCCGAAGTACCCAAGTACCCG- 2907

Qy   3039 CTTCCCCAAGATATTTAACGACAAAAACAGTAGGTGAGAGGTCTCACGATGA          3098
          |||||      |   || ||| ||   |   |||  ||||||| || |||
Db   2908 CATCGAGTGGGACCGCGTTCTTCATTTCCTGGGACCTGGCCGGCCAAGTACCCG-     2907

Qy   3099 TGCCCACAATATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGGT   3158
              |||||  |||| |||||  ||||||||||||||||| |  ||||||   |||||
Db   2961 CGCCCAGGCGATCGTGAGGAAGCTGATCGACGAGAAGCTGATCAAGGCCGGCGGTGTT     3020

Qy   3159 TGGGTTCTGGCCAGCAGCACAGATCCAAGAGGACAGCATTCACCTGTACGGCAGAGAGGCTGTGT 3218
          |||||||||||||||||||          |   | | ||  |||||
Db   3021 CGGCTTCTCTGGCCGCCAACCAGTCGAGGCTGGAGGTCTACGGCGCCGATGG           3080

Qy   3219 GCCCCAGGCTGCAGAGCTCTGCCGCAGAGGCTGAGGCTGCTGAGAAGGCTGAGAAGGA     3278
              |   ||   |      |||||||||||||||| |||| ||  |||| |||||
Db   3081 C-----------GAGACCCTGCGCACCACCTGCGCAGCAGACGATCAAGCC            3128

Qy   3279 CTCTGCCACGACGGAGCCATACTACTGGCCTCTCAGACTTCATCGGCTCCATTCTGG    3338
            | ||||  ||     | ||  |||| |||  ||||||  |||||||    |
Db   3129 GGACGGCA------AGCCGAACCTGTCGCCGAGCCGATTTCGTCGCGCCGGATTTCGCGCCGGCGTTT 3182

Qy   3339 CATCCGTGACTACCTGGGCCTGTTTG---CCGTTGCCTGCTTTGGGTGTAGAAGAGCTGAG 3395
          |||||||||| || |||||    |||     ||| |||  |||||
Db   3183 CGTGCGCGACTACATCGGCGGCTTCATCACCACCACCGGGATCGGCGATCGGCGGCGAGGAAGTGGC 3242

Qy   3396 CAAGGCCTATGAGGATGAGGATGGTGACGACTACACAGCGACTACATCGTTCAAGGCGCTGGGGGA 3455
              |||  |||||||| ||||||||| |||| |||  |||
Db   3243 CAAGGCTACGAAGCCAAGGGCGACGACTACAACAGCATCATGGTCAAGGCGCTCGGCCGA    3302

Qy   3456 CCGGCTGCAGAGGCCTTGCAGCAGCTCCATGAAAGAGAGTCCGCCGAGAACTGTGGGC   3515
          |||  ||||| |||| |  |||| ||  |||  || |||||||||||| |||||
Db   3303 CCGCCTCGCCGAGCCTGCGCGCCAGTGCTGCTGCGACGTGCGACGACTGGGG        3362

Qy   3516 CTACTGTGGCAGTGAGCAGCTGCAGACCTCGCAGACTGCGAAGGTTGCCGGTACAAGGGCAT 3575
          |  ||||||||||| |||     | ||  |||||| |||  |||||  ||||
Db   3363 CTACGCCCGGACGAACACCTCGACACAACGAGGCCTTGATCAAGGAGCAATACGTCGGCAT   3422

Qy   3576 CCGGCCGGCTCCTGGCTACCCCGGACGCGTCCAAGCTCGAGGAGCTCACCATGTGAG     3635
          ||||||||| |||||| || ||||||  | ||||||||
Db   3423 CCGCCCCGGCCACCGGGCTACCCGCCCCGACCATCCGGAGAAAAGGCACTCTGTTCGA   3482

Qy   3636 ACTCGCAGACATCGAGCAGTCTACAGGCAGCATTAGTTAACAGAATCATTAGCAATGGCACC 3695
             |||||| || ||||| | |   |||| |   | ||||
Db   3483 ACTGCTCGATCCGCAGAGGGCGCCTGCGCCTGACCGACCGCATCACGCGATGTTCCC      3542

Qy   3696 TGTTCAGCAGTCTCAGGCCTCTACTTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGG    3755
          |||| | | |  || |||  | |  |  ||     |||||||  ||| | |||  |||
Db   3543 GGCCGGCGCGGGTCAGCGTGGGTTGTATTTCGCCCACCCGAGCGCCAGTACTTCGCGGTCGG 3602

Qy   3756 GAAGATTTCCAAGGATCAGGTTGAGATTATGTCATTGGAGGAGAACACATATCTGGGCTGA   3815
          |||  | ||| ||| |||   | |||||||    |||||||| |  |
Db   3603 CAAGATCGACAACGACCAGGTGAACGTGCTACGACGCCCAGGAGCCCAGGAAGCCCAGCGCT 3662

Qy   3816 GGTTGAGAAATGGCTTGGACCCATTTGGGATATGAT                        3852
            |||||||| | ||   || | ||||||||
Db   3663 CAGCGAGCGCTGCTGGCGCCGCCGACCTTGGCTACGAT                      3699
```

RESULT 15
ADF02792
ID   ADF02792 standard; DNA; 3750 BP.
XX
AC   ADF02792;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Bacterial polynucleotide #3077.
XX
KW   Proteus mirabilis infection; bacterial infection; antibacterial;
KW   immunostimulant; gene; ds.
XX
OS   Proteus mirabilis.
XX
PN   US6605709-B1.
XX
PD   12-AUG-2003.
XX
PF   05-APR-2000; 2000US-00543681.
PR   09-APR-1999; 99US-0128706P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Breton GL;
XX
DR   WPI; 2003-895291/82.
DR   P-PSDB; ADF06964.
XX
PT   New Proteus mirabilis polypeptides and polynucleotides, useful as
PT   reagents for diagnosis of bacterial disease, as components of
PT   antibacterial vaccines, as targets for antibacterial drugs, or as
PT   biocontrol agents for plants.
XX
PS   Disclosure; SEQ ID NO 3077; 870pp; English.
XX
CC   The invention relates to new Proteus mirabilis polypeptides and
CC   polynucleotides. The invention also relates to antibodies against the
CC   polypeptides, methods for producing the polypeptides, a method of
CC   generating vaccines for immunising an individual against P. mirabilis, a

```
CC   method for evaluating a compound for the ability to bind a P. mirabilis
CC   polypeptide and a method for screening test compounds for anti-bacterial
CC   activity. The polypeptides and polynucleotides are useful as molecular
CC   targets for diagnosing, preventing and treating pathological conditions
CC   resulting from bacterial infection, as reagents for diagnosis of
CC   bacterial diseases, as components of antibacterial vaccines, as targets
CC   for antibacterial drugs or as bio-control agents for plants. This
CC   sequence represents a Proteus mirabilis polynucleotide of the invention.
XX
SQ   Sequence 3750 BP; 1124 A; 696 C; 895 G; 1035 T; 0 U; 0 Other;

Query Match             23.0%;  Score 901;  DB 10;  Length 3750;
Best Local Similarity   55.0%;  Pred. No. 2e-245;
Matches 2045;  Conservative    0;  Mismatches 1575;  Indels   99;  Gaps   10;
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```
  145 Qy  AAGAGGATTATGGTGCTGGATGAGGGACCATGATCCAGCGGGAGAAGCTAAAC     204
  112 Db  AAACGTTTAGTCCTTGATGCGCAATGGGAACCATGATCCAGCAATATCAGTTCGGCA  171

  205 Qy  GAAGAACACTTCCGAGTCAGGAATTTAAAGATCATGCCAGGCCGCTGAAAGGCAACAAT  264
  172 Db  GAAGAAGATTACCGAGGTGAACGTTTTGCCCATTGGCAATGTGATGTTAAAGGGAATAAT  231

  265 Qy  GACATTTAAGTATAACTCAGCTGATGTCATTTACCAAATCCATAAGGAATACTTGCTG     324
  232 Db  GACCTTTTAGTCTTGACGCAGCCGCAGATCATTACTACCTTTCATAAATGCTTATTTTGAA  291

  325 Qy  GCTGGGGCAGATATCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCCAAGCTGAC  384
  292 Db  GCCGGTGCAGATATCGTAGAAACAAACAACCTTTAATGCAACTCTATTGCCATGGCTGAT  351

  385 Qy  TATGGCCTTGAACACTTGGCCTCTGCTGGAGTGGCCAGAAAA                    444
  352 Db  TATCAGATGGAAGGGTTATGTGCAGAATTGAATGAAGAGAGGCTGCTAAACTTGCCAGAGCC  411

  445 Qy  GCTGCCGAGGA---GGTAACTCTCCAGACAGGAATTAGAGGTTTGTGCAGGGGCTCTG     501
  412 Db  TGTGCTCGATAAAATGGAGTGCATTAAGCGCCAGATAAACCACGTTATGTTGCAGGGGTATTA 471

  502 Qy  GGTCCGACTAATAAGACACTCTCTGTGTCCCCATCGTGTGGAAAGGCCGATTATAGGAAC  561
  472 Db  GGGCCAACCAAATAGAACAGACGATCCATTTCTCCTGATGTTAACGATCCCGCATTTCGTAAT  531

  562 Qy  ATCACATTGATGATGAGCTTGTTGTGAAGCATACCAAGAGGCAGCAGAGGCCCAAAGGC  621
  532 Db  ATCTCATTTGATACATTAGTGACATGCTTATCGCAGAGGCGATCTGCGGACTCATTAAAGA  591

  622 Qy  GGGGTTGATATCTTACTCATTGAAAACTATTTTTGATACTGCCAATGCCAAGGCAGCCTTG  681
  592 Db  GGGGTGGATTTAATTATGTGGAAACCTAAATGCGGGCTAGGGCAAATGCTGGCTATT      651

  682 Qy  TTTGCACTCCAAAATCTTTTTGAGGAGAAAATGCTCCCCGGCTATCTTTATTTCAGGG    741
  652 Db  TTTGCGATTAAGTGAGTTTGATAATCTTATAATTTGAATTACCGGTGATGATCCTCAGGG  711

  742 Qy  ACGATCGTTGATAAAGTGGGGCGACTCTTTCCGGACAGACAGGAGGGATTTGTCATC     801
  712 Db  ACTATCACTGATCGCTCAGGTAGAACATTAACAGGGCAAACCACAGAAGCGTTTTATCAC  771

  802 Qy  AGCGTGTCTCATGGAGAACCACTCGCATTGGCTTTGGGTGCTCAGCTGAG           861
  772 Db  TCACTACGTTACGCGACGCGTTATCATTTGGTTAAATTGTGCGCAGGGCCAAAAGAA    831

  862 Qy  ATGAGACCCTTTATTGAAATAAATTGGAAAAATGTACAAACGCCTTCTCCTCGTTATCCC   921
  832 Db  TTACGCCAATATATTCAAACTCTCCCCAAATACGAGAACTTATGTCAGTGCTCACCCCT   891

  922 Qy  AATGCCAGTTCTTCCCAACACCTTTGGTGACTATGAAAACGCCTTCTCATGATGGCCAAG  981
  892 Db  AATGTGCTTACCTTAATGCCTTTGGCGGATAAGTTTAGATCGCCAATGAGGGGCCGGAA   951

  982 Qy  CACCTAAAGGATTTTGCTATGGAATGGTCGTCAATATAGTTTGGAGAGTGGGTGTGGGTCA 1041
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  952 Qy  CAAATCAAGGAGTGGGCGCAAGCTCGGGTTTCTTAATATTGTCGGTGGTGGTTGTGTGGCACA 1011
 1042 Db  ACACCAGATCATATCACGGGAAATTGCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCCA  1101
 1012 Qy  ACCCCTGCCCATATTCAGCGTATTGCTCAAGCGGTTGATGGGCATAGCACCTAGAACATTA  1071

 1102 Db  CCTGCCACTGCTTTGAAGGACATATGTTACTGTCGTCGTGCTCTAGAGCCCTTCAGGATTGGA 1161
 1072 Qy  CCTGTCA------TTAAAAAAGCCTGTCGACTTCTCAGGTCTTGAGCCTTTGGTCATTGAT  1125

 1162 Qy  CCGTACACCAACTTGTTAACATTGGGAGAGCCGTCTATATGTCGCAGATCAAGGAAGTT   1221
 1126 Db  GATAATTCGCTGTTCGTCAATGTGGGGGAACGAACGATGTGACAGGTTCGGCTAAATTT   1185

 1222 Qy  GCTAAACTCATCATGCCAGGAAACTATGAAGAAGCCTTGTCTGTGTTGCCCAAAGTGCAGGTG 1281
 1186 Db  AAACGTTTAATAAAGAGAGGTAATTACCAAGAGCCCTTGATGTTGTCGTCGTCAGCAAGTT  1245

 1282 Qy  GAAATGGGAGCCCAGGTGTTGAATGTCAACATGGATGATGGCATGCTAGATGGTCCAAGT  1341
 1246 Db  GAAAACGGTGCTCAAATCATCGATATCAATATGGATGAAGGCATGTTAGATGCGATAGAA  1305

 1342 Qy  GCAATGACCAGATTTGCAACTTAATGCTTCCGAGCCAGCAGACTCGCAAAGTACCTTTG  1401
 1306 Db  GCAATGACAACGTTTTCTTAATCTTATTGCGGGTGAACCCGATTATTGCCAAAGTCCCGATT  1365

 1402 Qy  TGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTCGGTTAAGTGCTGCCAAGGGAAG    1461
 1366 Db  ATGATTGACTCGTCAAAATGCCAAGTCATTGAGGAAGGATTGAAATGTATTCAGGGTAAG  1425

 1462 Qy  TGCATTGTCAATAGCATTAGTGTCGAAGGAGGAGGACGACTCTTCCTTGGAGAGGCCAGG  1521
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 1522 Qy  AAGATTAAAAAGTATGAGCGTGCTCATGCGTGGTCATGGCTTTGATGAAGAAGACAGCA   1581
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 1582 Qy  ACAGAAACAGACACAAAAATCAGATGTGCACCCGGGCTACCACTCGCTGTGTGAAAAAA  1641
 1546 Db  GATACTCGAGCGCCAGAATAAGTGGAGGTCTTTGTCGGCGGTGTGCTATCTATCATCATTGAAAAA 1605

 1642 Qy  CTGGGCTTTAATCCAAATGACATTATTTTTGACCCTGTATAATCCTAACCATTGGGACTCGA 1701
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 1702 Qy  ATGGAGGAACACAACTTGTATGCCATTAATTTTATCCTGCAACAAAAGTCATTAAAGAA  1761
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 1822 Qy  ATGGAAGCCATTCGAGAAGCAATGCATCGTGGGGTTTTCCTTACCAAGTCAAGTCTGGC  1881
 1786 Db  AATGATCCCGGTTCGGGAAGCGGAGCCGATCCACTCCGTTTTCTTCTATTACGCGTGAAAAAATGT 1845

 1882 Qy  ATGGACATGGAGATAGTGAATGCTGAAATGCTGGGAAACCTTCCTGTATGATATCCATAAGGAA 1941
 1846 Db  ATGGATATGGGGATTGTCAATGTTGCAACTCGCTATTTATGACTCATTAGCGGATGAA    1905

 1942 Qy  CTTCTGCAGCTCGTGCTCGTCGTGAGATCTCATCGTGGAATAAAGACCCTGAGGCCACTGAGAAGCTC 2001
 1906 Db  CAACTGCTGTAGCGGATGTTTATTTTAAATCGCCATCGGCATGCACTGATAATTTA     1965

 2002 Qy  TTACGTTATGCCCAGACTCAAGGC-------ACAGGAGGAAGAAAGTCATTCAGACTGAT 2055
 1966 Db  CTTGGCACTGCAGGGAGCGTTATCGTGGCTACTAAAAGTGGTACTAAGAGTACTGATAATTTA  2025

 2056 Qy  GAGTGGGAAATGGCCCCTGTCGAAGAACGCCTTGAAGTAATGCCCTTGTGAAGGGCATTGAA 2115
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Qy  2116 AAACATATTATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAAAATATCCCGACCT 2175
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Db  2086 GAATTTATCATTGAAGATACAGAAG--------CGTGTCGCCAACAAGCTTCGAGTCCT 2136

Qy  2176 CTCAATATAATTGAAGACCCCTGATGAAATGAAATGTTGTGATCTTTTTGGA 2235
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Db  2137 ATCGAAGTGATAGAAGGGCCATTAATGAACACAGTGGCGATCTGTTTGGT 2196

Qy  2236 GCTGGAAAAATGTTTCTACCTTCAGGTTATAAAGTCAGCCCGGGTTATGAAGAAGGCTGTT 2295
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Db  2197 GAAGGTAAAAATGTTTTTTACCCCAAGTAGTAGTAAAAATCGGCAACAGGCCGTA 2256

Qy  2296 GGCCACCTTATCCCTTTCATGAAAAAGAAAGAGAGAAACCAGAGTGCTAAACGGCACA 2355
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Db  2257 GCTTAACCTTGAACCTTATATTCAAGCGACAAAAAAAGCAGGCAG------ 2300

Qy  2356 GTAGAAGAGAGGACCCTTACCAGGCGACCACCATCGTGCGCCACTGTTAAAGGCGACGTG 2415
         -----------CTCGGCAGGAAAAGTGTTACTGGCGACAGTAAAGGGAGATGTC
Db  2301 -----------CTCGGCAGGAAAAGTGTTACTGGCGACAGTAAAGGGAGATGTC 2343

Qy  2416 CACGACATAGGCAAGAACACATGAGTGGAGTAGTCCTTGGCTGCAATAATTTCCGAGTTATT 2475
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Db  2344 CACGACATTGGCAAAAAATATTGTCGGAGTGTGTTTGCAATGTAATAACTATGAAATTATC 2403

Qy  2476 GATTTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGACCACAAGCA 2535
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Db  2404 GATCTGGGGGTCATGGTACCTTGCGATAAAATCTTGCAAACAGCCATTGACGAAAATGTT 2463

Qy  2536 GATATAATTGGCCTGTCGAGACTCATCACTCCTTCCCTCCGGATGAAATGATTTTGTTGCC 2595
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Db  2464 GATATTATTGGATTGTCTGGATTGATCACTCCATCACTGGATGAGATGGTGAATGTTGCT 2523

Qy  2596 AAGGAAATGGGAGAGATTAGCTATAAGATTCCATTGTTGATTGTGGAGGAGCAACCACTTCA 2655
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Db  2524 AAGGAGATGGAAAGACGCGGTTTTTTCTTCCCTTAATGATTGGTGTGCCGACAACATCG 2583

Qy  2656 AAAACCCACACAGCAGTTAAAATAGTTCCGAGATACAGTGCACCTGTAATCCATGTCCTG 2715
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Db  2584 AAAGCGCACACGCAGTAAAAATTGAACCTATTAAGATTATTATCGGCCCAACAAAAGGCTGAT 2643

Qy  2716 GACGCGTCCAAGAGTGTGGTGTCGTGTTCCCAGTCGTGTTAGAGTATGAAAATCTAAAGGATGAA 2775
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Db  2644 AATGCGTCAAGAACGGTCGGGGGTGGTCGCTCGGGGTGGTTGGTTAGCCCTAATTTAGGTTATGA 2703

Qy  2776 TACTTTTGAGGAGAAATCATCGGAAGAATATGAAGATATTAGACAGGACCATTATGAGTCTCTC 2835
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Db  2824 CAACACTATACGGCCACCTCAAGCCGAACCAAATTAGGGTACAACAAGTTACAGCCAATATT 2883

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Db  2884 GAA------ACTTTACGTGGCTATATCGTGACTGATGAGCCGCCTTTTTCTTTATGATGTCATTG 2937

Qy  3016 CGGGGCAAGTCCAGGAAGGTCTTACGATGTCTACGATGATCCCAACAATATGCTGAAGCTC 3075
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Qy  3076 GAGGGCAAGTCCAGGAAGGTCTTTTGCAGATGCGAATGCCATGTTTTGAAGACTCTGAAAAG 3135
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Qy  3136 AAACTCCCGGCCCCGGGGGTGTGGTTTGGGTTGGGTTCTGCGCCAGCAGAGTATCCAAGAGACGACATT 3195
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Qy  3256 TTAAGGCAACAGCTGAGGAAGGACTCTGCCAGCACGGAGCCAATACTACTGCCTCTCCAGAC 3315
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Db  3205 TTTATTGCCCCTGTGATAGTCGTCTTGCTGACTATTTTGGTGCTTTGCAGTTACCGGC 3264

Qy  3376 TTTGGGGTAGAAGA---GCTAGCAAGGCCATGAGGATGATCGTGACGACTACAGCAGC 3432
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Db  3265 GGTCTAGAAGAAGATGAATGCGCTAATGGGTATGGTATAATGCTCATGATGATTACAATAAA 3324

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Search completed: March 6, 2006, 16:12:40
Job time : 1510 secs

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                  GenCore version 5.1.7
            Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:     March 6, 2006, 14:48:07 ; Search time 9723 Seconds
                                       (without alignments)
                                       18858.231 Million cell updates/sec

Title:       US-10-607-712-1
Perfect score: 3919
Sequence:    1 ggtcacctgtggagcacg.........ctcaaggaaatacaacctag 3919

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched:    41078325 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters:       82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
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             2: gb_est2:*
             3: gb_est3:*
             4: gb_htc:*
             5: gb_est4:*
             6: gb_est5:*
             7: gb_est6:*
             8: gb_est7:*
             9: gb_gss1:*
            10: gb_gss2:*
            11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
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Result No.	% Score	Query Match	Length	DB	ID	Description
1	3632.4	92.7	3711	11	DQ037675	DQ037675 Homo sapi
2	2977.6	76.0	3677	11	DQ037676	DQ037676 Pan trogl
3	2282.6	58.2	4888	4	CR859882	CR859882 Pongo pyg
4	1435.6	36.6	2150	4	AK037599	AK037599 Mus muscu
5	819.2	20.9	1788	9	AK085987	AK085987 Mus muscu
6	814.8	20.8	863	3	BM450887	BM450887 AGENCOURT
7	814	20.8	1043	3	BQ062840	BQ062840 AGENCOURT
8	797.4	20.3	871	5	BX390174	BX390174 BX390174
9	791.2	20.2	943	5	BU189680	BU189680 AGENCOURT
10	718.4	18.3	961	3	BX332266	BX332266 BX332266
11	707.4	18.1	721	4	AL598311	AL598311 DKFZp313F
12	672.4	17.2	698	7	CN414972	CN414972 170004180
13	611.4	15.6	715	8	DN280822	DN280822 1161963 M
14	598.8	15.3	758	8	CX228713	CX228713 MBM08606
15	591.2	15.1	623	7	CR629973	CR629973 DKFZp469I
16	591.2	15.1	626	5	BX485695	BX485695 DKFZp686C
17	578.8	14.8	582	3	BP336015	BP336015 BP336015
18	578.8	14.8	582	3	BP336553	BP336553 BP336553
19	570.4	14.6	583	3	BP313585	BP313585 BP313585
20	570.4	14.6	583	3	BP337383	BP337383 BP337383
21	568.8	14.5	997	2	BG258321	BG258321 602379766
22	561.2	14.3	618	7	CV356711	CV356711 MR4-RT002
23	558.2	14.2	915	5	BQ954233	BQ954233 AGENCOURT
24	555.2	14.2	560	3	BP220649	BP220649 BP220649
25	554.6	14.2	668	1	AI872333	AI872333 wm57h11.x
26	549.2	14.0	806	1	AJ724455	AJ724455 AJ724455
27	537.8	13.7	581	3	BP336596	BP336596 BP336596
28	534.2	13.6	937	5	BQ960377	BQ960377 AGENCOURT
29	531.2	13.6	657	9	CC249505	CC249505 RRF186 Ba
30	530.2	13.5	874	2	BB879762	BB879762 60491666
31	527.8	13.5	727	6	CB600441	CB600441 AGENCOURT
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33	520.6	13.3	527	7	BX470290	BX470290 DKFZp779J
34	517.8	13.3	574	7	CV344680	CV344680 MR1-HN006
35	505	12.9	617	8	CK620511	CK620511 ml13b08.y
36	503	12.8	581	8	DN279755	DN279755 1160811 M
37	502.4	12.8	658	6	CB455191	CB455191 712318 MA
38	501.8	12.8	885	6	CF548421	CF548421 AGENCOURT
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                         ALIGNMENTS

RESULT 1
DQ037675
LOCUS       DQ037675                3711 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Homo sapiens MTR gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ037675
VERSION     DQ037675.1  GI:66888884
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3711)
AUTHORS     Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE       A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
JOURNAL     (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED      15869325
REFERENCE   2  (bases 1 to 3711)
AUTHORS     Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL     Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment. Translation starts at the beginning of
            alignment.
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                     /gene="MTR"
                     /locus_tag="HC7587"
ORIGIN

Query Match           92.7%;  Score 3632.4;  DB 11;  Length 3711;
Best Local Similarity 98.0%;  Pred. No. 0;
Matches 3636; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
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Qy    64  ATGTCACCCGCCTCCAAGACCCTGTCGCAACCCGAGGTCTGAAGAGAAACCCTGCGGGAT  123
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Db     1  ATGTCACCCGCGCCTCCAAGACCCTGTCGCAACCCGAGGTCTGAAGAGAAACCCTGCGGGAT   60

Qy   124  GAGATCAATGCCATTCTGCAGAAGAGAGGATTATGTGCTGGATGTGGGGATGGGGACCATG  183
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Db    61  GAGATCAATGCCATTCTGCAGAAGAGAGGATTATGTGCTGGATGGGGATGGGGACCATG  120

Qy   184  ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAATTTAAAGATCATGCC  243
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Db   121  ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAATTTAAAGATCATGCC  180

Qy   244  AGGCCCGCTGAAAGGCAACAATGACAATTTAAGTATAACTCAGCCTGATGTCATTTACCAA  303
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Db   181  AGGCCCGCTGAAAGGCAACAATGACAATTTAAGTATAACTCAGCCTGATGTCATTTACCAA  240

Qy   304  ATCCATAAGGAATACTTGCTGGGTCGGGGCAGATATCGCAGAAACAAATACTTTTAGCAGC  363
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Qy   364  ACTAGTATTGCCCAAGCTGACTATGGCCTTGGCCTTACCGGATGAACATGTGC  423
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Qy   424  TCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGAGAG  483
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Db   361  TCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGAGAG  420

Qy   484  TTTGTGGCAGGGGCTCTGGGTCCGACTAATAGAGACACTCCTGTGTCCCATCTGTGTGAA  543
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Db   421  TTTGTGGCAGGGGCTCTGGGTCCGACTAATAGAGACACTCCTGTGTCCCATCTGTGTGGAA  480

Qy   544  AGGCCAAGGCAGCCCTTGTTGTTGAGAACATCACATTTGATGAGCTTGACTACTATTTTGATACTGCC  603
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Db   481  AGGCCAAGGCAGCCCTTGTTGTTGAGAACATCACATTTGATGAGCTTGACTACTATTTTGATACTGCC  540

Qy   604  AAAGGACTTCTCGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTGCC  663
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Qy   664  AATGCCAAGGCAGCCCTTGTTGCACTCGAAGCTTGATGAGCTTGTTGAGAACATGTGCTCCCGGACAGCA  723
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Db   601  AATGCCAAGGCAGCCCTTGTTGCACTCGAAGCTTGATGAGCTTGTTGAGAACATGTGCTCCCCGG  660

Qy   724  CCTATCTTTATTGGATGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGACA  783
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Db   661  CCTATCTTTATTGGATGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGACA  720

Qy   784  GGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGT  843
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Qy   904  TATGTCCTCTGTTATCCCAATGCCAATGCCAATGCCTTTGGTGACTATGATGAAACG  963
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Db   841  TATGTCCCTCTGTTATCCCAATGCCAATGCCTTTGGTGACTATGATGAAACG  900

Qy   964  CCTTCTATGATGCCAAGCACCTAAAGATTTGCTATGGAGNNNNNNNNNNNNNNNNNNN  1023
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Db   901  CCTTCTATGATGCCAAGCACCTAAAGNNNNNNNNNNNNNNNNNNNNNNNN  960

Qy  1024  GCGAGGATGCTGTGGGTCAACACCAGATCATATCGGGGAAATTGCTGAGCTGTGAAAAAT  1083
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  1020

Qy  1084  TGTAAGCCTAGAGTTCCACCTGCTTTTGAAGGACATATGTTACTGTCTCGGTCTA  1143
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Db  1021  TGTAAGCCTAGAGTTCCACCTGCTTTTGAAGGACATATGTTACTGTCTCGGTCTA  1080
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Qy  1144  GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATGTT  1203
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  1081  GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTGTTAACATTGGAGAGCGCTGTAATGTT  1140

Qy  1204  GCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAGAAGAAGCCTTGTGT  1263
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAGAAGAAGCCTTGTGT  1200

Qy  1264  GTTGCCAAAGTGCAGGTGGAAATGGGACGCCAGGTGTGTGGATGTCAACATGGATGATGGC  1323
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Db  1201  GTTGCCAAAGTGCAGGTGGAAATGGGACGCCAGGTGTGTGGATGTCAACATGGATGATGGC  1260

Qy  1324  ATGTCTAGATGGTCCAAGTGCAATGACAGATTTGCAACTTAATTGCTTCCGAGCCAGAC  1383
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Db  1261  ATGTCTAGATGGTCCAAGTGCAATGACAGATTTGCAACTTAATTGCTTCCGAGCCAGAC  1320

Qy  1384  ATCGCAAAGGTACCTTTGTGCATCGACTCCTCGACTCCCAATTTGCTCGTCGGAAGCTGGGGTTA  1443
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Db  1321  ATCGCAAAGGTACCTTTGTGCATCGACTCCTCGACTCCCAATTTGCTCGTCGGAAGCTGGGGTTA  1380

Qy  1444  AAGTGCTGCCAAGGGAGTGCAGTGCATTGTGCAATGACATTAGTCTGAAGGAGGAGGACGACAC  1503
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Db  1381  AAGTGCTGCCAAGGGAGTGCAGTGCATTGTGCAATAGCATTAGTCTGAAGGAGGAGGACGAC  1440

Qy  1504  TTCTTGGAGAAGGCCAGGAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTCATGGCTTTT  1563
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Db  1441  TTCTTGGAGAAGGCCAGGAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTCATGGCTTTT  1500

Qy  1564  GATGAAGAAGGACAGGCAACACAGAAAATCAGAGTGTGCACCCGGGCCTAC  1623
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Db  1501  GATGAAGAAGGACAGGCAACACAGAAAATCAGAGTGTGCACCCGGGCCTAC  1560

Qy  1624  CATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACACATATTTTTGACCCTAAATATC  1683
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Db  1561  CATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACACATATTTTTGACCCTAAATATC  1620

Qy  1684  CTAACCATTGGGACTGGAATGGAGGAACAACAACTTGTATGCCATTAATTTATCCATGCA  1743
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  CTAACCATTGGGACTGGAATGGAGGAACAACAACTTGTATGCCATTAATTTATCCATGCA  1680

Qy  1744  ACAAAAGTCATTAAAGAACATTACCTTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTG  1803
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  ACAAAAGTCATTAAAGAACATTACCTTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTG  1740

Qy  1804  TCCTTCTCCTTCCGGAGAATGGAAGCCAATGCAATGCATGGGGTTTTCCTTTAC  1863
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Db  1741  TCCTTCTCCTTCCGGAGAATGGAAGCAATGCATGGGGTTTTCCTTTAC  1800

Qy  1864  CATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAAGATCTCATCTGAAGATCTCATCTGTGTAT  1923
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Db  1801  CATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAAGATCTCATCTGTGTAT  1860

Qy  1924  GATGATATCCATGACTTCTGCAGCTTCTGGAAGATCTGAAGAATAAGACCCCT  1983
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Db  1861  GATGATATCCATGACTTCTGCAGCTTCTGGAAGATCTGAAGAATAAGACCCCT  1920

Qy  1984  GAGGCCACTGAGAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAGTC  2043
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Db  1921  GAGGCCACTGAGAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAGTC  1980

Qy  2044  ATTCAGACTGATGAGTGAGTGAAAATGGCCCGTGAGTATGCCCTGTGTG  2103
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Db  1981  ATTCAGACTGATGAGTGAGTGAAAATGGCCCGTGAGTATGCCCTGTGTG  2040

Qy  2104  AAGGGCATTGAAAAACATATTATTGAGGAATACTGCCAGGTTAAACCAAAAAA  2163
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Db  2041  AAGGGCATTGAAAAACATATTATTGAGGAATACTGCCAGGTTAAACCAAAAAA  2100

Qy  2164  TATCCCCGACCTTCTCAATATAATGAAGGACCCCGATGAATGAAATTGTTGGT  2223
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Db  2101  TATCCCCGACCTTCTCAATATAATGAAGGACCCCGATGAATGAAATTGTTGGT  2160

Qy  2224  GATCTTTTTGGAGCTGGAAAATGTTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTTATG  2283
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Qy    3241 TGCCTCTCAGACTTCATCGCTCCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTT 3300
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Db    3364 GCCGTTGCCTGCTTGGGTAGAAGAGCTGAGCAAGGCCTATGAGGCCTATGAGGATGGTGACGAC 3423

Db    3301 GCCGTTGCCTGCTTGGGTAGAAGAGCTGAGCAAGGCCTATGAGGCCTATGAGGATGGTGACGAC 3360

Qy    3424 TACAGCAGCATCATGGTCAAGGCGCGTCGGGGACCGGCTGGGCAGAGGCCTTTGCAGAAGAG 3483
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Db    3361 TACAGCAGCATCATGGTCAAGGCGCGTCGGGGACCGGCTGGGCAGAGGCCTTTGCAGAAGAG 3420

Qy    3484 CTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGGCAGCTGGACGTC 3543
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Db    3421 CTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGGCAGCTGGACGTC 3480

Qy    3544 GCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGCCAG 3603
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Db    3481 GCAGACCTGCGCAGGCGTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGCCAG 3540

Qy    3604 CCCGACCACACCGAGAGCTCACCATGTGGAGACTCGCAGACATCGAGACAGTCTACAGGC 3663
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Db    3541 CCCGACCACACCGAGAGCTCACCATGTGGAGACTCGCAGACATCGAGACAGTCTACAGGC 3600

Qy    3664 ATTAGGTTAACAGAATCATTAGCAATGCAATGGCACCTGCTTCAGGAGTTCTCAGGCCCTCACTTC 3723
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Db    3601 ATTAGGTTAACAGAATCATTAGCAATGCAATGGCACCTGCTTCAGGAGTTCTCAGGCCCTCACTTC 3660

Qy    3724 TCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGAATTTCCAAGGATCAG 3774
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Db    3661 TCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGAATTTCCAAGGATCAG 3711
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RESULT 2
DQ037676
LOCUS           DQ037676               3677 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION      Pan troglodytes MTR gene, VIRTUAL TRANSCRIPT, partial sequence,
                genomic survey sequence.
ACCESSION       DQ037676
VERSION         DQ037676.1  GI:66888885
KEYWORDS        GSS.
SOURCE          Pan troglodytes (chimpanzee)
  ORGANISM      Pan troglodytes
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Pan.
REFERENCE   1  (bases 1 to 3677)
  AUTHORS       Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
                Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
                White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE         A Scan for Positively Selected Genes in the Genomes of Humans and
                Chimpanzees
  JOURNAL       (er) PLoS Biol. 3 (6), E170 (2005)
  PUBMED        15869325
REFERENCE   2  (bases 1 to 3677)
  AUTHORS       Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
                Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
                White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE         Direct Submission
  JOURNAL       Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
                Rockville, MD 20850, USA
COMMENT         This sequence was made by sequencing genomic exons and ordering
                them based on alignment. Translation starts at the beginning of
                alignment.
FEATURES            Location/Qualifiers
     source         1..3677
                    /organism="Pan troglodytes"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9598"
     gene           <1..>3677
                    /gene="MTR"
                    /locus_tag="HC7587"
ORIGIN

Query Match    76.0%;   Score 2977.6;  DB 11;  Length 3677;
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Db    2161 GATCTTTTGGAGCTGAAAAATGTTCTACCTCAGTTATAAAGTCAGCCCGGGTTATG 2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    2284 AAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAAGAGAAGAAACCAGAGTG 2343

Db    2221 AAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAAGAGAAGAAACCAGAGTG 2280

Qy    2344 CTTAAGCACAGTAGAGAGAGGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTT 2403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 CTTAAGCGGCACAGTAGAGAGAGGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTT 2340

Qy    2404 AAAGGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAAT 2463
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 AAAGGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAAT 2400

Qy    2464 TTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTT 2523
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 TTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTT 2460

Qy    2524 GACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTCCCTGGATGAAATG 2583
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 GACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTCCCTGGATGAAATG 2520

Qy    2584 ATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAGGATTCCATTGTTGATTGGAGGA 2643
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 ATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAGGATTCCATTGTTGATTGGAGGA 2580

Qy    2644 GCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCTCCGAGATACAGTGCACCTGTA 2703
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 GCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCTCCGAGATACAGTGCACCTGTA 2640

Qy    2704 ATCCATGTCCTGGACGCGTCCAAGACGTCGTGTGTGTGTGGTGTGGTTAGATGAAAAT 2763
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 ATCCATGTCCTGGACGCGTCCAAGACGTCGTGTGTGTGTGGTGTGGTTAGATGAAAAT 2700

Qy    2764 CTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATAGACAGGACCAT 2823
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Db    2701 CTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATAGACAGGACCAT 2760

Qy    2824 TATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGTTTC 2883
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Db    2761 TATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGTTTC 2820

Qy    2884 CAAATGGATTGGCTGTCTGCAACCTGCTCACCCAGTGAAGCCCAGTTTATTGGGACCCAGGTC 2943
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 CAAATGGATTGGCTGTCTGCAACCTGCTCACCCAGTGAAGCCCAGTTTATTGGGACCCAGGTC 2880

Qy    2944 TTTGAAGACTATGACCTGCAGAAGCTGTGTGGACTACATTGACTGGAAGCCTTTCTTTGAT 3003
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TTTGAAGACTATGACCTGCAGAAGCTGTGTGGACTACATTGACTGGAAGCCTTTCTTTGAT 2940

Qy    3004 GTCTGGCAGCTTCCGGGCAAGTACCCGAATCGAAGCTTCCCCAAGATATTTAACGACAAA 3063
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 GTCTGGCAGCTTCCGGGCAAGTACCCGAATCGAAGCTTCCCCAAGATATTTAACGACAAA 3000

Qy    3064 ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCACCAACAATGCTGAACACACTG 3123
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Db    3001 ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCACCAACAATGCTGAACACACTG 3060

Qy    3124 ATTAGTCAAAAGAAACTCCGGCAGGCTTGGGTGTGGTTCTGGCCAGCAGCAGAGTATC 3183
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Db    3061 ATTAGTCAAAAGAAACTCCGGCAGGCTTGGGTGTGGTTCTGGCCAGCAGCAGAGTATC 3120

Qy    3184 CAAGACGACATTCACCTGTACGCAGAGGCTGCTGCCCCAGGCTGCAGAGCCCATAGCC 3243
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121 CAAGACGACATTCACCTGTACGCAGAGGCTGCTGCCCCAGGCTGCAGAGCCCATAGCC 3180

Qy    3244 ACTTTCTATGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACTAC 3303
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181 ACCTTCTATGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACTAC 3240

Qy    3304 TGCCTCTCAGACTTCATCGCTCCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTT 3363
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Best Local Similarity   81.3%;   Pred. No. 0;
Matches 2989;  Conservative 0;  Mismatches 0;  Indels 688;  Gaps 0;

Qy    98 AAGGTCTGAAGAAAACCCTGCGCGGATGAGATCAATGCCATTCTGCAGAGAGGATTATGG  157
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Db     1 AAGGTCTGAAGAAAACCCTGCGCGGATGATCGATGCCATTCTGCAGAAGAGGATTATGG   60

Qy   158 TGCTGGATGGAGGGATGGGACCATGATCCAGCCGGGAGAAGCTAAACGAACAACACTTCC  217
         ||||||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Db    61 TGCTGGATGGAGGGATGGGACCATGATCCAGCCGGGAGAAGCTAAACGAACAACACTTCC  120

Qy   218 GAGGTCAGGAATTTAAAGATCATGCCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTA  277
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Db   121 GAGGTCAGGAATTTAAAGATCATGCCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTA  180

Qy   278 TAACTCAGCCTGATGTCATTTACCAAATCCATAAGGAATACTTGCTCGCTGGGGCAGATA  337
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TAACTCAGCCCGATGTCATTTACCAAATCCATAAGGAATACTTGCTCGCTGGGGCAGATA  240

Qy   338 TCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCCAAGCTGACTATGGCCTTGAAC  397
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Qy   398 ACTTGGCCTACCCGGATGAACATGTGCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGG  457
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Db   301 ACTTGGCCTACCCGGATGAACATGTGCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGG  360

Qy   458 TAACTCTCCAGACAGGAATTAAGAGTTGTGCGCAGGGGCTCTGGGTCCGACTAATAAGA  517
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Db   361 TAACTCTCCAGACACGGAATTAAGAGTTGTGCGCAGGGGCTCTGGGTCCGACTAATAAGA  420

Qy   518 CACTCTCTGTGTCCCCATCTGTGGAAAGGCCGGATTATAGGAACATCACATTGATGAGC  577
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Db   421 CACTCTCTGTGTCCCCATCTGTGGAAAGGCCGGATTATAGGAACATCACATTGATGAGC  480

Qy   578 TTGTTGAAGCATACCAAGAGCAGGCCAAAGGACTTCTCGGATGGCGGGGTGATATCTTAC  637
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Db   481 TTGTTGAAGCATACCAAGAGCAGGCCAAAGGACTTCTCGGATGGCGGGGTGATATCTTAC  540

Qy   638 TCATTGAAACTATTTTTGATACTGCCAAGGCAGCCGTTGTTTGCACTCCAAAATC  697
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Db   541 TCATTGAAACTATTTTTGATACTGCCAAGNNNNNNNNNNNNNNNNNNNNNNNNN  600

Qy   698 TTTTGAGGAGAAATATGCTCCCCGGCCTATCTTTATTTCAGGGACCGATCGTTGATAAAA  757
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Qy   758 GTGGGCCGGACTCTTCCCGGACAGAGAGAGGGATTTGTCATCAGCGAGATGCGTCATGAG  817
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Db   661 GTGGGCCGGACTCTTCCCGGACAGAGAGAGGGATTTGTCATCAGCGAGATGCGTCATGAG  720

Qy   818 AACCACTCTGCATTGGATTAAATTGTGCTTGGGTGCAGCTGAGATGACCTTTATTG  877
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Db   721 AACCACTCTGCATTGGATTAAATTGTGCTTGGGTGCAGCTGAAATGACCTTTATTG  780

Qy   878 AAATAATTGGAAAATGTACAACAGCGCCTTCTCTCGTTATCCCAATGCAGTCTTCCCA  937
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Db   781 AAATAATTGGAAAATGTACAACAGCGCCTTCTCCTCGTTATCCCAATGCAGNNNNNNN  840

Qy   938 ACACCTTTGGTACTATGATGAAACGCCTTCTGTTCATGGCCAAGCACCTGANNNNNNNNNN  997
         ||||||
Db   841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  900

Qy   998 CTATGGATGGCTTGGTCAATATAGTTGGAGGATGTCGTGGGTCAACACCAGATCATATCA 1057
         ||||||||||
Db   901 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  960

Qy  1058 GGGAAATTGCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTG 1117
         |||||||||
Db   961 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1020

Qy  1118 AAGGACATATGTTACTGTCTCGGTCTCTAGAGCCCTTCAGGAATTGGACCGTACACCAACTTTG 1177
         ||||||||||||
Db  1021 NNNNNNNNNNNNNNNNNNNNNNNGTCTAGAGCCCTTCAGGATTGGACCGTACACCAACTTTG 1080


Qy  1178 TTAACATTGGAGAGCGGCTGTAATGTGTGCAGGATCAAGGAAGTTGCTAAACTCATCATGG 1237
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Db  1081 TTAACATTGGAGAGCGGCTGTAATGTGTGCAGGATCAAGGAAGTTGCTAAACTCATCATGG 1140

Qy  1238 CAGGAAACTATGAAGAGCCTTGTGTGTTGCCAAAGTGCAGTGGAAATGGGAGCCCAGG 1297
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Db  1141 CAGGAAACTATGAAGAGCCTTGTGTGTTGCCAAAGTGCAGTGGAAATGGGAGCCCAGG 1200

Qy  1298 TGTTGGATGTCAACATGGCCATGCTAGATGTGTCCAAGTGCAATGACCAGATTTT 1357
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Db  1201 TGCTGGATGTCAACATGGCCATGCTAGATGTGTCCAAGTGCAATGACCAGATTTT 1260

Qy  1358 GCAACTTAATTGCTTCCGAGCCAGACATCGGCAAAGGTACCTTTGTGCATCGACTCCTCCA 1417
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Qy  1418 ATTTTGCTGTGATTGAAGCTGGGTTAAAGTGCCAAGGAAGTGCATTGTCAATAGCA 1477
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Qy  1478 TTAGTCTGAAGGAAGGAGAGGACGACTTCTTTGGAGAAGCTGGCGGAGGAGGAG 1537
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Db  1441 GAGCTGCTATGGTGGTCATGGCTTTTGTGCACCCGGGCCTACCATCTGCTTGTGAATCAGAG 1500

Qy  1598 AAATCAGAGTGTGCACCCGGGCCTACCATCTGCTTGTGATGAAGAAACAGCAACAGACACAA 1657
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Db  1501 AAATCAGAGTGTGCACGCGGGCCTACCATCTGCTTGTGATGAAGAAACAGCAACAGACACAA 1560

Qy  1658 ATGACATTATTTTGACCCTAATATCCTAACCATTGGGACTGAATGGGACTCATTAAATCCAA 1717
         |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db  1561 ATGACATTATTTTGACCCTAATATCCTAACCATTGGGACTGAATGGGACTCATTAAATCCAA 1620

Qy  1718 TGTATGCCATTAATTTTATCCATGCAACAACAAAAGTCATTAAGAAACATTACCTGGAGCCA 1777
         |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db  1621 TGTATGCCATTAATTTTATCCATGCAACAACAAAAGNCATTAAGAAACATTACCTGGAGCCA 1680

Qy  1778 GAATAAGTGGAGGTCTTTCCTTACCAACTTGTCCTTCCGAGGAATGGAAGCCATTGAG 1837
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 GAATAAGTGGAGGTCTTTCCTTACCAACTTGTCCTTCCGAGGAATGGAAGCCATTGAG 1740

Qy  1838 AAGCAATGCATGGGCGTTTTCCTTTACCATGCAATCAAGTCTCTGCCATGGACAGTAG 1897
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 AAGCAATGCATGGGCGTTTTCCTTTACCATGCAATCAAGTCTCTGCCATGGGGGATAG 1800

Qy  1898 TGAATGCTGGAAACCTCCCGTGTATGATGAATATCCCGACCTTCTGCAGCTCTGTG 1957
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 TGAATGCTGGAAACCTCCCGTGTATGATGAATATCCCGACCTTCTGCAGCTCTGTG 1860

Qy  1958 AAGATCTCATCTGAATAAAGACCCTGAGGCCACTGAGACTGATGAGTGGAAATGGCCCCTGTCG 2017
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AAGATCTCATCTGAATAAAGACCCTGAGGCCACTGAGACTGATGAGTGGAAGTGGCCCCTGTCG 1920

Qy  2018 CTCAAGGCACAGGAGGGAAGAAAGTCATTCAGACTGATGAAAACATATTATTGAGGATACTG 2077
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CTCAAGGCACAGGAGGGAAGAAAGTCATTCAGACTGATGAGTGGAGAAACATATTATTGAGGATATTG 1980

Qy  2078 AAGAACGCCTTGAGTGATGCCCTTGTGAAGGGCATTGAGAGGGCATTGAGATACTGAGGATACTCA 2137
         |||||||||||||||||||||||||||||||||||||||||
Db  1981 AAGAACGCCTTGAGTGATGCCCTTGTGAAGGGCATTGAGATATGAGGGATANTGG 2040

Qy  2138 AGGAAGCCAGGTTAAACCCAAAAAAATATCCCCGACCTCTCAATATAATTGAAGGACCCC 2197
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 AGGAAGCCAGGTTAAACCCAAAAAAATATCCCCGACCTCTCAATATAATTGAAGGACCCC 2100

Qy  2198 TGATGAATGGAATGAAAAATTGTTGGTGATCTTTTTGGAGCTGAAAAAATGTTTCTACCTC 2257
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Db  2101 TGATGAATGGAATGAAAAATTGTTTGGTGATCTTTTTGGAGCTGAAAAAATGTTTCNACCTC 2160
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Qy   2258  AGGTTATAAAGTCAGCCCGGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGG   2317
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Db   2161  AGGTTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN   2220

Qy   2318  AAAAAGAAAGAGAGAAACCAGAGTGCTTAACGCACAGTAGAGAGAGGACCCTTACC      2377
                                             ||||||||||||||||||||NACCCTTACC
Db   2221  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN   2280

Qy   2378  AGGGCACCATCGTGCTGCCCACTGTTAAAGGCGACGTGCACGACATAGGCAAGAACATAG   2437
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  AGGGCACCACCGTGCTGCGCCACTGTTAAAGGCGACGTGCACGACATAGGCAAGAACATAG   2340

Qy   2438  TTGGGAGTAGTCCTTGGCTGCAATAATTTCCGAGTTGATTGATTTAGGAGTCATGACTCCAT   2497
           ||||||||||||||||||||||||
Db   2341  TTGGGAGTAGTCCTTGGCTGCAATAATTTCCGNNNNNNNNNNNNNNNNNNNNNNNNNNNN   2400

Qy   2498  GTGATAAGATACTGAAAGCTGCTTCTTGACCACAAAGCAGATATAATTGGCCTGTCAGGAC   2557
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Db   2401  NNNNNNNNNNNNNNNNNNNNNNNNNATATAATTGGCCTGTCAGGAC   2460

Qy   2558  TCATCACTCCTTCCCTGATGAAATGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTA   2617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  TCATCACTCCTTCCCTGATGAAATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTA   2520

Qy   2618  TAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTAAAA   2677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  TAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTAAAA   2580

Qy   2678  TAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGTGG   2737
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Db   2581  TAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGTGG   2640

Qy   2738  TGTGTTCCCAGCTGTTAGATGAAAAATCTAAAGGATGAATACTTGAGGAAATCATGGAAG   2797
           ||||||||||||||||||||||||||||||||||||||||
Db   2641  TGTGTTCTCAGCTGTTAGATGAAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAG   2700

Qy   2798  AATATGAAGATATTAGACAGGACCATTAGAGTCTCTTCAAGGAGAGGAGATACTTACCCT   2857
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Db   2701  AGTATGAAGATATTAGACAGGACCATTAGAGTCTCTTCAAGGAGAGGAGATACTTACCCT   2760

Qy   2858  TAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGAATGGCTGTGTCTGAACCTCACCCAGTGA   2917
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Db   2761  TAAGTCAAGCCAGAAAAAGTGGTTTTCCAAATGAATGGCTGTGTCTGAACCTCACCCAGTGA   2820

Qy   2918  AGCCACACGTTATTGGGACCCAGGTCTTGAAGACTATGACCTGCGAAGCTGGTGGACT   2977
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Db   2821  AGCCACGTTTATTGGGACCCAGGTCTTGAAGACTATGACCTGCGAAGCTGGTGGACT   2880

Qy   2978  ACATTGACTGGAAGCCTTTCTTTGATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAG   3037
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Db   2881  ACATTGACTGGAAGCCTTTTCTTTGATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAG   2940

Qy   3038  GCTTCCCCAAGATATTTAACGACAAAACAGTAGGTGGACAAGGCTCCAGGAAGGTCTACGACTG   3097
           ||||||||||||||||||||||||||||||||||||||||||
Db   2941  GCTTTCCCCAAGATATTTAACGACAAAACAGTAGGTGGAGAAGGCTCCAGGAAGGTCTACGACATG   3000

Qy   3098  ATGCCCACCAAATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGCCGGGGGTGTGG   3157
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  ATGCCCACAATATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGCCGGGGGTGTGG   3060

Qy   3158  TTGGGTTCTGGCCAGCAGAGTATCCAAGACACATTCACCTGTACGCAGAGGCTGCTG   3217
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Db   3061  TTGGGTTCTCGGCCAGCAGCACAGAGTATCCAAGACACATTCACCTGTACGCAGAGGCTCGTG   3120

Qy   3218  TGCCCCAGGCTGCGAGAGCCCATAGCCACTTCTCTATGGTTAAGGCAACAGGCTGAGAAGG   3277
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Db   3121  TGCCCCAGGCTGCNNNGGCTGCGNNNGCCCATAGCCACCTTCTATGGGTTAAGGCAACANNNNNNNNNN   3180

Qy   3278  ACTCTGCCAGCACGGAGCCCATACTACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTG   3337
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Db   3181  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN   3240
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Qy   3338  GCATCCGTGACTACCTGGGCCTGTTGCCGGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCA   3397
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Db   3241  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN   3300

Qy   3398  AGGCCTATGAGGATGATGCTGACGACTACAGCAGCATCATGTCAAGGCGCCGCTGGGGACC   3457
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Db   3301  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN   3360

Qy   3458  GGCTGGCAGAGGCTTTGCAGAGAGAGTCCATGAAAGAGAGTTCGCCGAGAACTGTGGGCCT   3517
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Db   3361  NNNNNNNNNNGCCTTTGCAGAGAGAGTCCATGAAAGAGAGTTCGCCGAGAACTGTGGGCCT   3420

Qy   3518  ACTGTGGCAGTGAGCAGCTGGACGTGCCGAGACCTGCGAAGGTTGCGGTACAGGGCATCC   3577
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Db   3421  ACTGTGGCAGTGAGCAGCTGGACGTGCCGAGACCTGCGAGGGTTGCGGTACAAGGGCATCC   3480

Qy   3578  GCCCGGCTCCTGCTACCCCCAGCCAGCCGACCACCGAGAGCTCACCATGTGGAGAC   3637
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Db   3481  GCCCGGCTCCTGCTACCCCAGCCAGCCGACCACCGAGAGCTCACCATGTGGAGAC   3540

Qy   3638  TGCAGACATCGAGCAGTCTACAGAGTCATTAGGTTAACAGAATCATTAGCAATGCACCTG   3697
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Db   3541  TCCCAGACATCGAGCAGTCTACAGAGTCATTAGGTTAACAGAATCATTAGCAATGCACCTG   3600

Qy   3698  CTTCAGCAGTCTCAGGCCTCTACTTCTCCAATTGAGTCCAAATATATTTGCTGTGTGGGGA   3757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CTTCAGCAGTCTCAGGCCTCTACTTCTCCAATTTGAGTCCAAATATATTTGCTGTGTGGGA   3660

Qy   3758  AGATTTCCAAGGATCAG   3774
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Db   3661  AGATTTCCAAGGATCAG   3677
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RESULT 3
CR859882
LOCUS   CR859882   4888 bp   mRNA   linear   HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp469P1116 (from clone DKFZp469P1116)
ACCESSION   CR859882
VERSION   CR859882.1 GI:55730633
KEYWORDS   HTC.
SOURCE   Pongo pygmaeus (orangutan)
  ORGANISM Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1 (bases 1 to 4888)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE   Direct Submission
  JOURNAL   Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
  COMMENT   Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by Medigenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project.
            This clone (DKFZp469P1116) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469P1116
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES   Location/Qualifiers
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                     /clone="DKFZp469P1116"
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                     /dev_stage="adult"

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            YAQTGTGKKVIQTDEWRNGSVEERLEYALVKGIEKHIVEDTEARLNQEKYPRPLN
            IIEGPLMNGMKIVGDLFGAGKMFLPQVIKSARVMKKAVGHLIPFMEKEREETRVLNGT
            VEEEDPYQGTIVLATVKGDVHDIGKNIVGVLGCNNFRVIDLGVMTPCDKILKAALDH
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ORIGIN
Query Match         58.2%;   Score 2282.6;   DB 4;   Length 4888;
Best Local Similarity   92.6%;   Pred. No. 0;
Matches 2485;   Conservative  0;   Mismatches   39;   Indels  159;   Gaps   2;
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Db   1870 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TACAATTGACTGGAAGCCTTCTTCTTGATGTGTCTGGCAGCTCCGGCGGGCAAGTACCCGAATCGA

Qy   3037 GGCTTCCCAAGATATTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGAT
          ||||| |||||||||||||||||| ||||||||||||||||| ||| |||||||||||
Db   1930 GGCTTTCCAAGATATTAACGACACAAAACAGTAGGTGGAGAGCGCCAAAAAGTCTACGAT  1989

Qy   3097 GATGCCCACAATATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTG
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Db   1990 GATGCCCAAAATATGCTGAACACACTGATTAGTCAAAAGAAACTCCAAGCCCGGGGTGTG  2049

Qy   3157 GTTGGGTTCTGCCAGCACAGAGTATCCAAGACGACATTCACCTGTACGCAGAGGCTGCT
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Db   2050 GTTGGGTTCTGCCAGCACAGAGTATCCAAGACGATTCACCTCACCTGTACGCAGAGGGTGCT  2109

Qy   3217 GTGCCCCAGGCTGCAGAGCCCATAGCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAG
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Db   2110 GTGCCCCAGGCTGCAGAGCCCATAGCCACCTTCTATGGGTTAAGGCAACAGGCTGAGAAG  2169

Qy   3277 GACTCCTGCCAGCACGGAGCCCATACTACTGCCCTCCAGACTTCATCGTCCCTGCCATTCT
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Db   2170 GACTCCTGCCAGCACGGAGCCCATACTACTGCCCTTCCAGACTTCATCGTCCCTGCCATTCT  2229

Qy   3337 GGCATCCGTGACTACCTGGGGTTGCCGTGCCGTTGCCGTTGGGGTAGAGAGCTGAGC
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Db   2230 GGCATCCGTGACTACCTGGGGTTTGCCGTGCCGTTGCCGTTGGGGTAGAGAGCTGAGC  2289

Qy   3397 AAGGCCTATGGAGGATGATGGTGACGACTACAGCAGCATCATGGTCAAGGCGCTGGGGGAC
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Db   2290 AAGGCCTATGAGGATGATGGTGACGACTACAGCAGCATCATGGTCAAGGCGCTGGGGGAC  2349

Qy   3457 CGGCTGCAGAAGGCCTTTGCAGAAGAGTCCATGAAAGAGTTCGCGCGAGACTGTGGGCC
          ||||| |||| |||||||||||||||||||||||||||||||||| |||||| |||||||
Db   2350 CGGCTGGCAGAGGCCTTTGCAGAAGAGTCCATGAAAGAGTTCGCGCCGAGAACTGTGGGCC  2409

Qy   3517 TACTGTGGCAGTGAGCAGTCGACGTCGAAGGTTGCGGTACAAGGGCATC
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Db   2410 TACTGTGGCAGTGAGCAGTCGACGTCGCAGGTTGCGGTACAAGGGCATC  2469

Qy   3577 CGCCCGGCTCCTGGCTACCCGAGCCCAGCGCCCGACCACCAGAGAAGCTCACCATGTGGAGA
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Db   2470 CGCCCCGGCTCCTGGCTACCCGAGCCCAGCCTGACCACACTGAGAAGCTCACCATGTGGAGA  2529

Qy   3637 CTCGCAGACATCGAGCAGTCTACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCT
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Db   2530 CTCGCAGACATCGAGCAGTCTACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCT  2589

Qy   3697 GCTTCAGCAGTCTCAGGCCCTCTACTTCTCCAATTTGAAGTCCAAAATATTTTGCTGTGGGG
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Db   2590 GCTTCAGCAGTCTCAGGCCTCTCAGGCCCTCCAATCTGAAGTCCACATATTTTGCTGTGGGG  2649

Qy   3757 AAGATTTCCAAGGAACCAGGTTGAGGATTATGCATTGAGGAAGAACATATCTCGTGGCTGAG
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Db   2650 AAGATTTCCAAGGAACCAGGTTGAGGATTACGGTTGAGGAAGAACATATCTCGTGGCTGAG  2709

Qy   3817 GTTGAGAAATGGCTTGACCCCATTTGGGATATGATGATACAGACTAACTTTTTTTTTTTTT
          |||||||||||||||||||||||||||||||||||||||||||||||      ||||||||
Db   2710 GTTGAGAAATGGCTTGACCCCATTTGGGATATGATGATACAGACTAAC-----TTTTTTTT  2764

Qy   3877 TTGCCTTTTTTATCTTGATGATCCTCAAGGAAATACAACCTAG  3919
          | ||||||||| ||||||||||||||||||||||||||||||
Db   2765 TGCCTTTTTTTGTCTTGATGATCCTCAAGGAAATACAACCTAG  2807
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RESULT 4
AK037599

LOCUS   AK037599   2150 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus 16 days neonate thymus cDNA, RIKEN full-length
            enriched library, clone:A130029B16
            product:5-methyltetrahydrofolate-homocysteine methyltransferase,
            full insert sequence.
ACCESSION   AK037599
VERSION   AK037599.1 GI:26085945

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                  /dev_stage="16 days neonate"
     misc_feature 1..2150
                  /note="5-methyltetrahydrofolate-homocysteine
                  methyltransferase (MGD|MGI:894292, GB|AA415486, evidence:
                  BLASTN, 100%, match=222)"
ORIGIN

Query Match      36.6%;    Score 1435.6;   DB 4;   Length 2150;
Best Local Similarity   84.5%;   Pred. No. 0;
Matches 1669;   Conservative   0;   Mismatches 234;   Indels 73;   Gaps 2;
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Qy      72 CGCGCTCCAAGACCCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGGATGAGATCAA 131
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Db     232 CGCGTCGCCTGCGCGTGTCACTCGGACATACACCAACTTTGTTAACATTGGAAAGATGAGATGAGATTGA 291

Qy     132 TGCCATTCTCGAGAAGAGGATTATGGTGCTGAATGAGGGACCATGATCAGCCG 191
           |||  ||||| ||||  |||| |  |||||| | ||||||||||||||||||
Db     292 AGCCATTCTTCGGAAGAGGATCATGGTGCTGACGGTGGGATGGGGACCATGATCAGCCG 351

Qy     192 GGAGAGCTAAAGCGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATGCCAGGCGCT 251
           ||  ||    |||||||| ||||||| || |||||||||||||||||||||| ||||
Db     352 GTACAAACTAAGTGAAGAACACATTTCCAAGGTCAAGAGTTTAAAGATCATCAGCAGGCCACT 411

Qy     252 GAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACCAAATCCATAA 311
           ||||||||||||||||| |||  |  |  |  ||||| || |||||||||| || ||||
Db     412 GAAAGGCAACAACAATGACATCTTAAGTATATACTCAGCCTGATATTATTTACCAGATTCATAA 471

Qy     312 GGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCAGCACTAGTAT 371
           |||||||||||||||| | | | ||| || | || || | | | || || ||  ||||
Db     472 GGAATACTTGCTGGCTGGGCAGATATCATCGAAACAAACACTTTCAGCAGTACTACTAGTAT 531

Qy     372 TGCCCAAGCGACTATGGCCTTGAACACTTGGCCTACACCGGATGAACATGTGCTCTGCAGG 431
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Db     532 CGCCCAGGCTGACTATGGCCTTGAACACTT                                  561

Qy     432 AGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAAGAGGTTTGTGGC 491
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     562 ------------GGAGTCAAGAGAGGTTTGTGGC 581

Qy     492 AGGGGCTCTGGACTCGGTCCGACTAATAAGAACACTTCTCTGTCTCCCCATCTGTGGAAAGGCCGGA 551
           ||||||||||||||||||||||| |||||| | || | || |||| ||||||||||||||||||| ||||
Db     582 TGGAGCTCTGGGTCCGACTAATAAGAACACTTTCTGTGTCTCCCCATCTGTGGAAAGGCCAGA 641

Qy     552 TTATAGGAACAATCACATTTGATGAGCTTGTTGAAGCATACCAAGACAGCAGGCCAAAGAGACT 611
           |||||||||||||||||||||||| ||||||||||||||   |||  ||| || |||| |||
Db     642 TTATAGGAACAATCACATTTGATGAGCTTGTTGTTGACGCCATACCAAGGAGGCAGGCCAAGGGACT 701

Qy     612 TCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTGCCAATGCCAA 671
           ||||||| ||||||||||||||| |||||||| |||| || | |||  |  || |||||
Db     702 GCTGGATGGCAGGGTCAGGGTCGACATCTTACTCATTGAATCTGTATCAATTTTTGATACAGCTAATGCCAA 761

Qy     672 GGCAGCCTTGTTGCACTCCAAAATCTTTGAGGAGAAATATG---CTCCCCGGCCTAT 728
           ||| || ||||||  |    |||||| | ||||| || |||       |||| |||
Db     762 AGCAGCCTTTGTCACCAGGGTCCGGATCCAGAAACCTTTGAAGAGAATTATGCTCCTCCTCGGCCTAT 821

Qy     729 CTTTATTTCAGGGACGATCGTTCATGAGAAACCACTCTGCATTGGATTAAATTGTGCTTT 788
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Db     822 CTTTATTTCTGGGACCATTGTCCATTGGGAACTGGAAGAGCTCTTTTTCTGGGCACGGGAGA 881

Qy     789 GGGATTTGTCATCAGCGTGTCTCATGAGAAACCACTTCTGTCATTGGATTAAATTGTGCTTT 848
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Qy     849 TATCCATAAGGAACTTCTGCAGCTGAATGAGGCCTTTCATTGGAAAATGTACCAACAGCCTATGT 908
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Qy     909 CCTCTGTTATCCCAATGCAGGTCTTCCCAACACCCTTTGGTGACTATGATGAAACGCCTTC 968
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Qy     969 TATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGATGGCTTGGTCATATAGTTGGAGG 1028
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Qy    1029 ATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATTGTAA 1088
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Qy    1089 GCCTAGAGTTCCACCTGCCACTGCTTTTGAACGACATATGTTACTGTCTGGTCTAGAGCC 1148
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RESULT 5
AK085987
LOCUS   AK085987   1788 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
            library, clone:D830038K18 product:hypothetical Vitamin B12
            dependent methionine synthase activation domain containing protein,
            full insert sequence.
ACCESSION   AK085987
VERSION   AK085987.1 GI:26351896
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
PUBMED   10349636
REFERENCE   2

AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
PUBMED   11042159
REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
PUBMED   11076861
REFERENCE   4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 1788)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
            URL:http://fantom.gsc.riken.jp/.
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Matches 896; Conservative   0; Mismatches 128; Indels   0; Gaps   0;

Qy   2838 GGAGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGTTTCCAAATGGATTGGCT 2897
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Db   295 GGAGAGAAATACGTACCCCTAAGTCAAGCCAGAAAAACACGGTTTCCACATTGATTGGCT 354

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Db   355 CTCTGAACCTCATCCAGTGAAGCCCACGTTTATTGGGACCCAGGTCTTTGAGGACTACACA 414

Qy   2958 CCTGCAGAAGACGTGGTGAGACTACATTGACTGGAGCCTTTCTTGATGGTCGGCAGCTCCG 3017
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Qy   3138 ACTCCGGCCCCGGGGTTCTGGGTTCTGGCGTGGTTGGGTCTCGGCCACCAGAGTATCCAAGACGACCATTCA 3197
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                     Technologies."
ORIGIN

Query Match         20.8%;   Score 814.8;   DB 3;   Length 863;
Best Local Similarity  98.9%;   Pred. No. 3.2e-216;
Matches  841;   Conservative  0;   Mismatches  0;   Indels  7;   Gaps  2;

Qy    283  CAGCCTGATGTCATTTACCAAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATT  342
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Qy    343  GAAACAAATACTTTAGCAGCACTAGTATTGCCCAAGCTGACACTAGTATTGAACACTTG  402
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(left column continuation)

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RESULT 6
BM450887

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ACCESSION   BM450887
VERSION     BM450887.1  GI:18499927
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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Qy   1063  ATTGCTGAAGCTGTGAAAAATTGTAAG-CCTAGAGTTCCACCTGCCA-CTGCTTTGAAG 1120
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Db    791  ATTGCCTGAGCTGTGAAAAATTGTAAGCCCTAGAGTTCCACCTGCCACCTGCTTTGAAG  850

Qy   1121  GACATATGTT 1130
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Db    851  GACATATGGT  860
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RESULT 7
BQ062840
LOCUS   BQ062840   1043 bp   mRNA   linear   EST 02-APR-2002
DEFINITION AGENCOURT_6826659 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924378
            5', mRNA sequence.
ACCESSION   BQ062840
VERSION   BQ062840.1 GI:19890017
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1043)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2094 row: g column: 03
            High quality sequence start: 242
            High quality sequence stop: 479.
FEATURES   Location/Qualifiers
     source   1..1043
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5924378"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."

ORIGIN

Query Match   20.8%; Score 814; DB 3; Length 1043;
Best Local Similarity   98.2%; Pred. No. 5.8e-216;
Matches 876; Conservative   0; Mismatches 10; Indels 6; Gaps 5;

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Qy   2422  ATAGGCAAGAACAGTTGGAGTAGTCCTT-GGCTGCAATAATTTCCGAGTTATTGATTT 2480
                 |||  |||||| ||||||||||||||||| ||||||||||||||||||||||||||||
Db     56  ATAAGCAAGAACATAGTTGGAGTAGTCCTTAGGCTGCAATAATTTCCGAGTTATTGATTT  115

Qy   2481  AGGAGTCATGACTCATGTGATAAGATACTGAAAGCTGCTCTTGACCACAAAGCAGATAT 2540
                 ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    116  AAGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGACCACAAAGCAGATAT  175

Qy   2541  AATTGGCCTGCTCAGGACTCATCACTCCTTCCCTGGATGAAATGATTTTTGTTGCCAAGGA 2600
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Db    176  AATTGGCCTGCTCAAGACTCATCACTCCTTCCCTGGATGAAATGATTTTTGTTGCCAAGGA  235

Qy   2601  AATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAAC 2660
                 |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    236  AATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAAC  295

Qy   2661  CCACACAGCAGTTAAAATAGCTCCGAATACAGTGCACCTGTAATCCATGTCCTGGACGC 2720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    296  CCACACAGCAGTTAAAATAGCTCCGAATACAGTGCACCTGTAATCCATGTCCTGGACGC  355

Qy   2721  GTCCAAGAGTGTGTGGTGTTCCCAGCTGTTAGATGAAAATCTAAAGGATGAATACTT 2780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    356  GTCCAAGAGTGTGGTGTGGTGTTCCCAGCTGTTAGATGAAAATCTAAAGGATGAATACTT  415

Qy   2781  TGAGGAAATCATGGAAGAATATGAAGATTAGACAGGACCATTATGAGTCTCTCAAG-G 2839
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Db    416  TGAGGAAATCATGGAAGAATATGAAGATTATAGACAGGACCATTATGAGTCTCTCAAGAG  475

Qy   2840  AGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGATTGGCTGT 2899
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Db    476  AGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGATTGGCTGT  535

Qy   2900  CTGAACCTCACCCAGTGAAGCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATGACC 2959
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    536  CTGAACCTCACCCAGTGAAGCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATGACC  595

Qy   2960  TGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTCTTGATGTCTGGCAGCTCCGGG 3019
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    596  TGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTCTTGATGTCTGGCAGCTCCGGG  655

Qy   3020  GCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAACGACAAAACAGTAGGTGGAGAG 3079
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    656  GCAAGTACCCGAATCGAGGCTTTCCCAAGATATTTAACGACAAAACAGTAGGTGGAGAG  715

Qy   3080  CCAGGAGGTCTACGATGCGATGATGTCTTCGGCCAGCACAATATGCTGAACACACTGATT 3139
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Db    716  CCAGGAGGTCTACGATGCGATGATGTCTTCGGCCAGCACAATATGCTGAACACACTGATT  775

Qy   3140  TCCGGGCCCGGG--TGTGGTTGGGTTCTGGCCAGCACAGAGTATCCAAGACGACATTCAC 3198
                 ||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db    776  TCCGGGCCCGGGNTGTGGTTGGGTTCTGGCCAGCACAGAGTATCCAAGACGACATTCAC  835

Qy   3199  CTGTACGGCAGAGGCTGCTGTGCCCAGGCTGCAGAGCCCATGGCCACTTTCATGGGTTA 3258
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Db    836  CTGTACGGCAGAGTGCTGTGCCCAGGCTGCAGAGCCCATGGCCACTTTCATGGGTTA  895

Qy   3259  AGGCAACA--GGCTGAGAAGGACTCTGCCAGCACGG-AGCCATACTACTGCC 3307
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Db    896  AGGCAACAAGGGCTGAGAAGGACTCTGCCAGCACGCGGAACCATACTACTGCC  947
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RESULT 8
BX390174
LOCUS   BX390174   871 bp   mRNA   linear   EST 29-APR-2004
DEFINITION BX390174 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC010YO17 5-PRIME, mRNA sequence.
ACCESSION   BX390174
VERSION   BX390174.2 GI:46877980
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 871)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 8, 2003 this sequence version replaced gi:3046266.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
740.f.
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAG006ZC05_CS00515_1&c=740.f.

FEATURES
    source   Location/Qualifiers
                    1..871
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="CS0DC010YO17"
                    /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                    /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                    /note="1st strand cDNA was primed with a NotI-oligo(dT)
                    primer. Five prime end enriched, double-strand cDNA was
                    digested with Not I and cloned into the Not I and EcoR V
                    sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   20.3%;   Score 797.4; DB 5; Length 871;
Best Local Similarity 98.0%;   Pred. No. 2.5e-211;
Matches 837; Conservative   0; Mismatches 14; Indels   3; Gaps   3;

Qy   669 CAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGGCCTAT 728
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   19 CCAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGGCCTAT 78

Qy   729 CTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGACAGGAGA 788
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   79 CTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGACAGGAGA 138

Qy   789 GGGATTTGTCATCAGCGTGTCTCATGAGAACCACTCTGCATTGGATTAAATTGTGCTTT 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   139 GGGATTTGTCATCAGCGTGTCTCATGAGAACCACTCTGCATTGGATTAAATTGTGCTTT 198

Qy   849 GGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGT 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199 GGGTGCAGCTGAAATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGT 258

Qy   909 CCTCTGTTATCCCAATGCAGAGTCTTCCCAACACCTTTGGTGACTATGATGAAACGCCTTC 968
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259 CCTCTGTTATCCCAATGCAGAGTCTTCCCAACACCTTTGGTGACTATGATGAAACGCCTTC 318

Qy   969 TATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAGTTGGAGG 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   319 TATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAGTTGGAGG 378

Qy   1029 ATGCTGTGGGTCAACACCAGATCATATCAGGGAAAATTGCTGAGCGTGTGAAAAATTGTAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   379 ATGCTGTGGGTCAACACCAGATCATATCAGGGAAAATTGCTGAGCGTGTGAAAAATTGTAA 438

Qy   1089 GCCTAGAGTTCCACCTGCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTCTGAGCC 1148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   439 GCCTAGAGTTCCACCTGCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTCTGAGCC 498

Qy   1149 CTTCAGGATTGGACCGTACACCAACCTTTGTTAACATTGGAGGAGCGCGTGTAAGTTGCAGG 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   499 CTTCAGGATTGGACCGTACCACCAACCTTTGTTAACATTGGAGGAGCGCGTGTAAGTTGCAGG 558

Qy   1209 ATCAAGGAGTTTGCTAAACTCATCATGCAGGAAACTATGAGAAGCCTTGTGTTGTTGC 1268
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Db   559 ATCAAGGAGTTTGCTAAACTCATCATGCAGGAAACTATGAGAAGCCTTGTGTTGTTGC 618

Qy   1269 CAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGTGATGTCAACATGGATGATGGCATGCT 1328
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Qy   1329 AGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGACATCGC 1388
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Db   679 AGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTNCGAGCCAGACATCGC 738

Qy   1389 AAAGGTACCTTGTGCATCGACTCCTCCAATTTGCTGTGTGATTGAAGCTGGGTTAAAGTG 1448
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Db   739 ANAGGTACCTTTGTGCATCGACTCCTCCC-ATTTTGCTGTGTGATTTGAGCTGGGTTAAAGTG 797

Qy   1449 CTGCCAAGGGAGTGCATTGTCAATAGCATTAGTCTGAAGAGGAGGAGGAGACTTCTT 1508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   798 CTGCC-AGGGAGTGCATTGTC-ATAGCTTAGTCCTGAAGCAGTAGTCCTGAAGGAGGAAGGAGGAGGACGACTTCTT 855

Qy   1509 GGAGAAGGCCAGGA 1522
          ||||| || ||
Db   856 GGAGAAGCCANGA 869

RESULT 9
BU189680
LOCUS   BU189680   943 bp   mRNA   linear   EST 04-SEP-2002
DEFINITION AGENCOURT_7968068 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6170551
            5', mRNA sequence.
ACCESSION   BU189680
VERSION   BU189680.1 GI:22703664
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 943)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13537 row: h column: 08
            High quality sequence stop: 587.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6170551"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_67"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT;
                     Average insert size 1.75 kb. Library constructed by Life
                     Technologies."

ORIGIN

Query Match   20.2%;   Score 791.2; DB 5; Length 943;
Best Local Similarity 96.5%;   Pred. No. 1.4e-209;
Matches 830; Conservative   0; Mismatches 28; Indels   2; Gaps   2;

Qy   2155 CAAAAAAAATATCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAAA 2214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CAAAAAAAATATCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAAA 60

Qy   2215 ATTGTTGGTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTGGTTATAAAGTCAGCC 2274
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATTGTTGGTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTGGTTATAAAGTCAGCC 120

Qy   2275 CGGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAGAAGAAGA 2334
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAGAAGAAGA 180

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Qy   2335  ACCAGAGTGCTTAACGGCACAGTAGAAGAAGAGGACCCTTACCAGGCACCATCGTGCTG  2394
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ACCAGAGTGCTTAACGGCACAGTAGAAGAAGAGGACCCTTACCAGGCACCATCGTGCTG   240

Qy   2395  GCCACTGTTAAAGGCGACGTGCACGACATAGGCACGCAAGAACATAGTTGGAGTTCCTTGGC  2454
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GCCACTGTTAAAGGCGACGTGCACGACATAGGCACGCAAGAACATAGTTGGAGTTCCTTGGC   300

Qy   2455  TGCAATAATTCCGAGTATTGATTTAGGAGTCATGAGTCCATGTGATAAGATACTGAAA  2514
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  TGCAATAATTCCGAGTATTGATTTAGGAGTCATGAGTCCATGTGATAAGATACTGAAA   360

Qy   2515  GCTGCTTCCTGACCACAAAGCAGATATAATTGGCCTGCAGGACTCATCACTCCTTCCCTG  2574
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Db    361  GCTGCTCCTGACCACACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTG   420

Qy   2575  GATGAAATGATTTTTGTGCCAAGGAAATGAGAGATTAGCTATAAGGATTCCATTGTTG  2634
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GATGAAATGATTTTTGTGCCAAGGAAATGAGAGATTAGCTATAAGGATTCCATTGTTG   480

Qy   2635  ATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGT  2694
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  ATTGGAGGAGCAACCACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGT   540

Qy   2695  GCACCTGTAATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTA  2754
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GCACCTGTAATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTA   600

Qy   2755  GATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAGAGATATTAGA  2814
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Db    601  AATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAGAGATATTAGA   660

Qy   2815  CAGGACCATTATGAGTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAA  2874
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CAGGACCATTATGAGTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAA   720

Qy   2875  AGTGGTTTCCAAATGATTGGCTGTCGTCTGAACCTCACCCAGTGAAGCCCACGTTT-ATTGG  2933
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Db    721  AGTGGTTTCCAAATGATTGGCTGTCGTCTGAACCTCACCCAGTGAAGCCCACGTTTAATTGG   780

Qy   2934  GACCCAGGTCTTGAAGACATGACCTGC-AGAAGCTGGTGGCTGACTACATTGACTGGAAGC  2992
           |||||||||||||||||||||||||   |||||||||||||||||  ||||||||||||
Db    781  GACCCAGGTCTTGAAAACTAATACCTGCAAAAAAGCTGGGGGACTAAATTTGACTGGAAA   840

Qy   2993  CTTTCTTGATGTCTGCGCAG  3012
           |||||  || ||||| ||||
Db    841  CCCTTTTTCTTTTAATGGCTG   860
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RESULT 10
BX332266
LOCUS       BX332266              961 bp    mRNA       linear     EST 08-APR-2004
DEFINITION  BX332266 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC010YO17 5-PRIME, mRNA sequence.
ACCESSION   BX332266
VERSION     BX332266.2  GI:46280008
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 961)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 2, 2003 this sequence version replaced gi:30343109.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
```

```
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            740.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DC010AH09QP1&c=740.f.
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                     /clone="CS0DC010YO17"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a Noti-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
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Query Match          18.3%;    Score 718.4;  DB 5;    Length 961;
Best Local Similarity 92.4%;    Pred. No. 3.6e-189;
Matches 749;  Conservative  26;  Mismatches  33;   Indels  3;   Gaps  3;
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Qy     2  GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCCTCCTGCGCAAGGAGGAGGAGACTCGACA   61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   139  GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCCTCCTGCGCAAGGAGGAGGAGACTCGACA  198

Qy    62  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCGAAGTCTGAAGAGGTCTGATGGAGGAAACCCTGCGGG  121
          ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db   199  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCGAA-GTCTGAAGAGGTCTGATGGAGGAAACCCTGCGGG  257

Qy   122  ATGAGATCAATGCCATTCTGAGAAGAGAGATTATGGTGCTGGATGGAGGGGATGG-GGACC  180
          |||||||||:::||||||||||||||||||||||||||||||||||||||||||| |||||
Db   258  ATGAGATCMATSCCATTCTGAGAAGAGAGATTATGGTGCTGGATGGATGGGATGGCGGACC  317

Qy   181  ATGATCAGCGGAGAAGCTAAACGAGAGAGAAGAGACACTTCCGAGTCAGGAATTTAAAGATCAT  240
          |||||||||||||||:::|::|:|:||||:::|||||::||:||:||||||||||||||||||
Db   318  ATSMTCCASCGGAGAAGCTAAACSMASAACMCTTCCGMGGTCAGGAATTTAMAGMTCAT  377

Qy   241  GCCAGGCCGCTGAAAGGCCAACAAAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTAC  300
          ::|::|||||||||||||||||:||:||||||:|||||:|:||||:|||:::||::||::::|
Db   378  SCCASGCCGCTGAAAGGCAACMATGACMATGTTTAAGTATAACTCAGCCTSCTGTCMTTTMC  437

Qy   301  CAAATCCATAAGGAAATACTTGCTGGCTGGGCAGAATCATTGATGAGCTCATTCAAACAAATACTTTTAGC  360
          |||||:||:|: ||:|| ::|:||||||||||||||||||||||||||||||||||||||||
Db   438  CAAMTCCATMAGNCNTTNCTTNCTNNCTNNGGCCNNTNTCATTCAAACAAATACTTTTAGC  497

Qy   361  AGCACTAGTATTGCCCAAGCTGACTATGGCCTTGACACTTGGCCTACCGGATGAACATG  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   498  ACGCCTCGTATTGCCCAAGCTGCCCTCGCCCTTGACACTTGGCCTACCGGATGAACATG  557

Qy   421  TGCTCTGCAGGAGTGGCCAGAAAAGTGCCAGAAAAGTCTAACTCTCCGAGCAGGAATTAAG  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   558  TGCTCTGCAGGAGTGGCCAGAAAAGTGCCAGAAAAGTCTAACTCTCCGACAGCAGGAATTAAG  617

Qy   481  AGGTTTGTGGCAGGGGCTCTGGGTCTCTGGGTCTCCCCATCTGTGTCCCCATCTGTG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   618  AGGTTTGTGGCAGGGGCTCTGGGTCTCTGGGTCTCCCCATCTGTGTCCCCATCTGTG  677

Qy   541  GAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   678  GAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAG  737

Qy   601  GCCAAAGGACTTCTGGATGCGGGGTGATATCTTACTCATTGAAACTATTTTGATACT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   738  GCCAAAGGACTTCTGGATGCGGGGTGATATCTTACTCATTGAAACTATTTTGATACT  797

Qy   661  GCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATC-TTTTGGAGGAGAAATATGCTCC  719
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   798  GCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTTGGAGGAGAAATATGCTCC  857

Qy   720  CCGGCCATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGACA  779
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Db    241  CTTGAGTATGCCCTTGTGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGCC    300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2146  AGGTTAAACCAAAAAAAATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAAT   2205
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AGGTTAAACCAAAAAAAATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAAT    360

Qy   2206  GGAATGAAAAATTGTTCGTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTATA   2265
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GGAATGAAAAATTGTTGGTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTATA    420

Qy   2266  AAGTCAGCCCGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAA   2325
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  AAGTCAGCCCGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAA    480

Qy   2326  AGAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAAGAGGACCCTTACCAGGGCACC   2385
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AGAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAAGAGGACCCTTACCAGGGCACC    540

Qy   2386  ATCGTGCTGGCCACTGTTAAAGGCGACGTGCACGACGTGCACGACATAGGCAAGACATAGTTGGAGTA   2445
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  ATCGTGCTGGCCACTGTTAAAGGCGACGTGCACGACGTGCACGACATAGGCAAGAACATAGTTGGAGTA    600

Qy   2446  GTCCTTGGCTGCAATAATTCCGAGTTATTGATTTAGGAGTCATGACTCCCATGTGATAAG   2505
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GTCCTTGGCTGCAATAATTCCGAGTTATTGATTTAGGAGTCATGACTCCCATGTGATAAG    660

Qy   2506  ATACTGAAAGCTGCTCTTGACCACCAAAGCAGATATAATTGGGCTGT-CAGGACTCATCAC   2564
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  ATACTGAAAGCTGCTCTTGACCACCAAAGCAGATATAATTGGGCTGTCGTGCCCAGGACTCATCAC    720

Qy   2565  T   2565
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Db    721  T   721
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RESULT 12
CN414972
LOCUS       CN414972          1700041800817 GRN_ES Homo sapiens cDNA 5', mRNA sequence.   698 bp    mRNA        linear     EST 16-MAY-2004
DEFINITION  17000418008177 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN414972
VERSION     CN414972.1  GI:47402566
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 698)
AUTHORS     Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
TITLE       Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
JOURNAL     Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED      15146197
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 698    Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1..698
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, cell lines H1, H7, and
                     H9"
                     /clone_lib="GRN_ES"
                     /note="oligo dT primed, full-length enriched cDNA library
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Db    858  CGGGCCTATCTTTATTTCAGGGAGGATTGTCATCAGCGTGTCT   917
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Qy    780  GACAGGAGAGGGATTGTCATCAGCGTGTCT   810
            |||||||||||| ||: || :|:|| ||:|
Db    918  GACASGAGAGAGRTTKTCATCRCGTGTCTCMT   948
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```
RESULT 11
AL598311
LOCUS       DKFZp313F151_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone     721 bp    mRNA       linear     EST 04-SEP-2003
DEFINITION  DKFZp313F151 5', mRNA sequence.
ACCESSION   AL598311
VERSION     AL598311.1  GI:15161002
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 721)
AUTHORS     Poustka.A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
TITLE       EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and
            Wiemann,S.)
JOURNAL     Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp313F151) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1..721
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp313F151"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="313 (synonym: hlcc2)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

Query Match     18.1%;   Score 707.4;  DB 1;  Length 721;
Best Local Similarity  99.7%;   Pred. No. 4e-186;;
Matches  719;  Conservative  0;  Mismatches  1;  Indels  1;  Gaps  1;
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Qy   1846  CATGGGGGTTTCCTTACCATGCAATCAAGTCTGGCATGGACATGGACATGGAGATGGAGTAGTGAATGCT   1905
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CATGGGGGTTTCCTTACCATGCAATCAAGTCTGGCATGGACATGGACATGGAGATGGAGTAGTGAATGCT     60

Qy   1906  GGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTC   1965
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTC    120

Qy   1966  ATCTGGAATAAAGACCCTGAGGCCACTGGAGAAGCTCTTACGTTATGCCCAGACTCAAGGC   2025
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ATCTGGAATAAAGACCCTGAGGCCACTGGAGAAGCTCTTACGTTATGCCCAGACTCAAGGC    180

Qy   2026  ACAGGAGGGAAGAAAGTCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGC   2085
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ACAGGAGGGAAGAAAGTCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGC    240

Qy   2086  CTTGAGTATGCCCTTGTGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGCC   2145
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ORIGIN

from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

JOURNAL   Unpublished (2003)
COMMENT   Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: RLK8011 row: D column: 8
            Seq primer: GTAATACGACTCACTATAGGG.

FEATURES   Location/Qualifiers
     source   1..715
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 7BOV"
                     /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including ovary, hindbrain, uterus, and day-30 whole
                     embryos."

ORIGIN

Query Match   15.6%;   Score 611.4;   DB 8;   Length 715;
Best Local Similarity   92.0%;   Pred. No. 3.3e-159;
Matches   656;   Conservative   0; Mismatches   56;   Indels   1; Gaps   1;

Qy   1977 AGACCCTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGACACAGGAGGGAA 2036
            ||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||
Db   2 AGACCCTGAGGCCACCGAGAGCTCTTACACTACACACGCCCAGACTCAGGCAAAGGAGGAA   61

Qy   2037 GAAAGTCATTCAGACTGATGAGTGAGTGGGAGGGAAATGGCCTTGTCGAAGAACGCCTTGAGTATGC 2096
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 GAAAGTCATCCAGACTGATGAGTGGAGTGGGAGGGAAATGGCCGTGTCGAAGAACGCCTTGAGTACGC   121

Qy   2097 CCTTGTGAAGGCCATTGAAGAACATATATTGAGGATACTGAGGAGAACTGAGGAGTTAAACCA 2156
            |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Db   122 TCTTGTGAAGGGCCATTGAAGAACATTATTGAAGATACTATTGAAGATACTGAGGAGTTAAACCA   181

Qy   2157 AAAAAAATATCCCGACCCTCTCAATATAATTGAAGACCCCTGATGAATGGCATGAAAAT 2216
            |||||||||||||||||||||| |||||| ||| |||| |||||| ||||| |||||
Db   182 GGAAAAAATATCCCGACCCTTCTGAATATAATTGAAGGGCCCGCGCTGATGAATGGCATGAAAAT   241

Qy   2217 TGTTGGTGATCTTTTGGAGCTGGAAAAAATGTTCTACCTCCAGGTTATAAAGTCAGCGCCG 2276
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 TGTTGGTGATCTTTTGGAGCTGGAAAAAATGTTCTACCTCCAGGTTATAAAGTCAGCCTCG   301

Qy   2277 GGTTATGAAGAGAGGCGTGTTGGCCACCTTTCATGGAAAAAGAAAGAGAGAAGAAGAAAC 2336
            ||||||||||||||| |||||||||||||||||||| || ||||||||||||||||||||
Db   302 GGTCATGAAGAAGAGGCCGTGGGTCACCTTATTCCCTTCATGAAAAAGAAAGAGAGAAGAAGAAAC   361

Qy   2337 CAGAGTGCTTAAACGGACACAGTAGAAGAAGACGACCCTTACCAAGGACCACCATCGTGCTGGC 2396
            ||||||||||||| ||||| |||| ||||||||||| |||||||||||||||||||||||||
Db   362 CAAAGTGCTTTACTGGCAAAATAGAACATAGGAAGATGAGAGACAACATAGTTGGAGTAGTGCTTCCTTGGCTG   421

Qy   2397 CACTGTTAAAGGCGACGTGCACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTAGTCCTTCGGCTG 2456
            || |||||||||| ||||| |||||| || ||||||||| |||||||||||||||||||||
Db   422 TACTGTTAAAGGTGACGTACGCGGCCAAGAACATAGTTGGAGTGGTTCTTCGGCTG   481

Qy   2457 CAATAATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGC 2516
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   482 CAATAATTCCAGAGTTATTGATTTAGGAGTCATGACTCCATGTGACTGACAAGATACTGAAGGC   541

Qy   2517 TGCTCTTGACCACAAAGCACAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGA 2576
            |||||||||| |||||||||||| ||| |||||||||||||||||||||||||||||||||
Db   542 TGCTCTAGACCACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGA   601

Qy   2577 TGAAATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGAT 2636
            |||||||||||||||||| |||||||||||||||| |||||||||||||||||||| |||
Db   602 TGAAATGATTTTTGTCGCCTAAGGAAATGGAGGACTAGCTATAAAGATCCCATTGTTGAT   661

ORIGIN

Query Match   17.2%;   Score 672.4;   DB 7;   Length 698;
Best Local Similarity   99.9%;   Pred. No. 2.6e-176;
Matches   673;   Conservative   0; Mismatches   0;   Indels   1; Gaps   0;

Qy   1006 GGCTTCGTCAATATAGTTGGAGGATGCGTGTGGTCAACACCAGATCATATCAGGGAAATT 1065
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   25 GGCTTGGTCAATATAGTTGGAGGATGCGTGTGGTCAACACCAGATCATATCAGGGAAATT   84

Qy   1066 GCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACAT 1125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85 GCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACAT   144

Qy   1126 ATGTTACTGTCGTCGGTCTAGAGCCCTTCAGGATTGGACGTACACCAACTTGTTAACATT 1185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   145 ATGTTACTGTCTGGTCTAGAGCCCTTCAGGATTGGACGTACACCAACTTGTTAACATT   204

Qy   1186 GGAGAGCGCGTGTAATGTTGCAGGATCAAGAAGTTTGCTAAACTCATCATGGCAGGAAAC 1245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   205 GGAGAGCGCGTGTAATGTTGCAGGATCAAGAAGTTTGCTAAACTCATCATGGCAGGAAAC   264

Qy   1246 TATGAAGAAGCCTTGTCGTTGTGTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCCAGGTGTTGGAT 1305
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265 TATGAAGAAGCCTTGTCGTTGTGTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCCAGGTGTTGGAT   324

Qy   1306 GTCAACATGGATGATGCGTCTAGATGGTCTAGAGTGGTCCAAGTGCAATGACCAGATTTGCAACTTA 1365
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   325 GTCAACATGGATGATGCGTCTAGATGGTCTAGAGTGGTCCAAGTGCAATGACCAGATTTGCAACTTA   384

Qy   1366 ATTGCTTCCGAGCCAGACATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCT 1425
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385 ATTGCTTCCGAGCCAGACATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCT   444

Qy   1426 GTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTG 1485
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445 GTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTG   504

Qy   1486 AAGGAAGGAGGAGGACGACTTCTTGGAGAAGGCCAGGAAGTAAAAAGTATGATGGAGCTGCT 1545
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505 AAGGAAGGAGGAGGACGACTTCTTGGAGAAGGCCAGGAAGTAAAAAGTATGATGGAGCTGCT   564

Qy   1546 ATGGTGGTCATGGCTTTGATGAAGAAGGACAGGCAACAGAAAATCAGA 1605
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   565 ATGGTGGTCATGGCTTTGATGAAGAAGGACAGGCAACAGAAAATCAGA   624

Qy   1606 GTGTGCACCCGGGCCTACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATT 1665
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625 GTGTGCATCCGGGCCTACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATT   684

Qy   1666 ATTTTTGACCCTAA 1679
            ||||||||||||||
Db   685 ATTTTTGACCCTAA   698

RESULT 13
DN280822

LOCUS   DN280822   715 bp   mRNA   linear   EST 02-MAR-2005
DEFINITION 1161963 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   DN280822
VERSION   DN280822.1   GI:60449432
KEYWORDS   EST.
SOURCE   Bos taurus (cow)
  ORGANISM Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 715)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE   A second set of bovine ESTs from pooled-tissue normalized libraries

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Qy   2871  AAAAAGTGGTTCCAAAATGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTAT  2930
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Db    241  AAAACACGGTTCCACATTGATTGGCTTCTGAACCTCATCCAGTGAAGCCCACGTTTAT   300

Qy   2931  TGGGACCCAGGTCTTTGAAGACTATAGACCTGCGAAGCTGGTGGACTACATTGACTGAA  2990
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    301  TGGGACCCAGGTCTTTTGAGGACTACAACCTGCAAAAGCTGGTGGACTACATTGACTGAA  360

Qy   2991  GCCTTTCTTTGATGTCGGCAGCTCCGGGCCAAGTACCCGGATTCGAGGCTTCCCCAGAT  3050
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Db    361  GCCTTTTCTTTGACGTCGGCAGCTCCGGGCCAAGTACCCGAACCGAGGATTTCCCAAGAT  420

Qy   3051  ATTTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCACACATAT  3110
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  ATTTAATGACAAAGCAGTAGGTGAAGAGCCAGGAAAGTGTATACAATGATGCTCAGAATAT  480

Qy   3111  GCTGAACACACTGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGGTTCTGGCC  3170
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    481  GCTGAACATACTGATTAGTCAAAAGAAACTGCAGGCCCAGGGGTGTGGTTGGATTCTGGCC  540

Qy   3171  AGCACAGAGTATCCAAGACGACATTCACCTGTACGACGA-GGCTGCTGGTCGCCAGGCTG  3229
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    541  AGCACAGAGTGTCCAGATGACATCACCACCTGTATGCAGAGAGGGGGGGGGGTGCCCAGGCCG  600

Qy   3230  CAGAGCCCATAGCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCA  3289
           |||||||||| |||||||||||||||||||| | |||||||||||||||||||||| ||||
Db    601  CTGAGCCCATAGCCACTTCTATGGGTAGGCAGCAGGCTGAGGAAGGACTCTTCTAGTA   660

Qy   3290  CGGAGCCATACTACTGCCTCTCAGACTTCATCGTCCCTTGCATTCTGGCATCCGTGACT  3349
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Db    661  CAGACCCCTACCACTGCCTCTCAGACTTCATTGCTCCTTTGCATTCTCTGGGGTCTGTGACT  720

Qy   3350  ACCTGGGGCTGGTTGCCGTTGCGTTGCTGCCTTGGGGTAGAA  3387
           ||||| ||||||||||||||||||||||||||||||||||||
Db    721  ACTTGGGGTCTGTTGTTGCTGGTGCCGTTGGGGCTTGAA   758
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RESULT 15
CR629973
LOCUS       CR629973                 623 bp    mRNA    linear    EST 11-AUG-2004
DEFINITION  DKFZp46910922_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
            DKFZp46910922 5', mRNA sequence.
ACCESSION   CR629973
VERSION     CR629973.1  GI:51126053
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
ORGANISM    Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1  (bases 1 to 623)
AUTHORS     Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
TITLE       Pongo pygmaeus mRNA (Bahr,A., Lauber,J., Mewes,H.W., et al.)
JOURNAL     Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
            (Hilden/Germany) within the cDNA sequencing consortium of the
            German Genome Project. This clone (DKFzp46910922) is available at
            the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
            Berlin, Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFzp46910922
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
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ACCESSION   CX228713
VERSION     CX228713.1  GI:56684005
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
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REFERENCE   1  (bases 1 to 758)
AUTHORS     Williams,C., Wirta,V., Richter,K., Karlsson,C., Lundeberg,J. and
            Carlsson,L.
TITLE       Expressed sequence tags of cDNA clones from a hematopoietic stem
            cell line expressing Lhx2
JOURNAL     Unpublished (2005)
COMMENT     Contact: Williams, C.
            Molecular Biotechnology
            Institution of Biotechnology
            AlbaNova University Center, KTH-Royal Institute of Technology, 106
            91 Stockholm, Sweden
            Tel: +4685537832
            Fax: +4685537481
            Email: cecilia.williams@biotech.kth.se
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ORIGIN

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Matches 599;  Conservative    0;  Mismatches  14;  Indels    0;  Gaps    0;

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Job time : 9732 secs
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             Copyright (c) 1993 - 2006   Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table:  IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched:       1303057 seqs, 888780828 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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2	3884.8	99.1	7122	3	US-09-318-448-2	Sequence 2, Appli
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9	3851	98.3	3856	3	US-08-980-326-75	Sequence 75, Appl
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ALIGNMENTS

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; Sequence 1, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3919
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (1)...(3919)
; OTHER INFORMATION: Entire cloned cDNA encoding wild type methionine
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US-08-980-326-1

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Qy   1081 AATTGTAAGCCTAGAGATGTCCACCTGCCTGCTTTTGAAGGACTTGTAACATTGAAGGACATATTGGAGAGGCGCTGTAAT 1140
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Qy   1381 GACATCGCAAAGTACCTTGTGCATGCAGTCCTCCAATTTTGCTGTGATTGAAGCTGGG 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GACATCGCAAAGTACCTTGTGCATGCAGTCCTCCAATTTTGCTGTGATTGAAGCTGGG 1440

Qy   1441 TTAAAGTGCTGCCAAGGAAGTGCATTGTCAATGACATTAGTCTGAAGGAAGGAGAGAGAGAC 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTAAAGTGCTGCCAAGGAAGTGCATTGTCAATGACATTAGTCTGAAGGAAGGAGAGAGAGAC 1500

Qy   1501 GACTTCTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGTGCATGGCT 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GACTTCTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGTGCATGGCT 1560

Qy   1561 TTTGATGAAGAAGGACAACAGGCAACAGAAATCAGACAAAATCAGAGTGTGCACCCGGGCC 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TTTGATGAAGAAGGACAACAGGCAACAGAAATCAGACAAAATCAGAGTGTGCACCCGGGCC 1620

Qy   1621 TACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCCTAAT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCCTAAT 1680

Qy   1681 ATCCTAACCATTGGAACTCGGCTGGCCATTGAGGAGAACACAACTTGTATGCCATTAATTTTATCCAT 1740
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Db   1681 ATCCTAACCATTGGAACTCGGCTGGCCATTGAGGAGAACACAACTTGTATGCCATTAATTTTATCCAT 1740

Qy   1741 GCAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGTCTTTCCAAC 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGTCTTTCCAAC 1800

Qy   1801 TTGTCCTTCCTCTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTTCTT 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTGTCCTTCCTCTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTTCTT 1860

Qy   1861 TACCATGCAATCAAGTCTCGGCTGGCATGGACATGGAGATAGTGAATGCTGAAAACCTCCCTGTG 1920
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Db   1861 TACCATGCAATCAAGTCTCGGCTGGCATGGACATGGAGATAGTGAATGCTGAAAACCTCCCTGTG 1920

Qy   1921 TATGATGATCCATAAGGAACTTCGTGTGAAGATCTCATCTGGAATAAAGAC 1980
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Db   1921 TATGATGATCCATAAGGAACTTCGTGTGAAGATCTCATCTGGAATAAAGAC 1980

Qy   1981 CCTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGCACAGGGAAGAA 2040
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Db   1981 CCTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGCACAGGGAAGAA 2040

Qy   2041 GTCATTCAGACTGACTGATGAGTGAGAAATGGCCCTTGTCGAAGAACGCCTTGAGTATGCCCTTT 2100
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Db   2041 GTCATTCAGACTGACTGATGAGTGAGAAATGGCCCTTGTCGAAGAACGCCTTGAGTATGCCCTTT 2100

Qy   2101 GTGAAGGGCATTGAAACATATATTATTGAGGAGTTAAACCAAAAA 2160
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GTGAAGGGCATTGAAACATATATTATTGAGGAGTTAAACCAAAAA 2160

Qy   2161 AAATATCCCGACCTCTCAATATAATTGAAGGACCCTGATGAATGGAATGAAAATTGTT 2220
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Db   2161 AAATATCCCGACCTCTCAATATAATTGAAGGACCCTGATGAATGGAATGAAAATTGTT 2220

Qy   2221 GGTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGGTT 2280
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Db   2221 GGTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGGTT 2280

Qy   2281 ATGAAGAAGGCTGTTGGCCACCTTCATCCCTTTCATGGAAAAGAAGAAAGAGAAGAACCAGA 2340
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Db   2281 ATGAAGAAGGCTGTTGGCCACCTTCATCCCTTTCATGGAAAAGAAGAAAGAGAAGAACCAGA 2340

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Qy  2341 GTGCTTAACGGCACAGTAGAAGAAGAGACCCTTACCAGGCACCATCGTGTGCTGGCCACT 2400
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Qy  2401 GTTAAAGGGCGACGTGCACGTGCGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAAT 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GTTAAAGGGCGACGTGCACGTGCGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAAT 2460

Qy  2461 AATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGCT 2520
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Db  2461 AATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGCT 2520

Qy  2521 CTTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCTGATGAA 2580
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Db  2521 CTTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCTGATGAA 2580

Qy  2581 ATGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAACGGATTCCATTGTTGATTGA 2640
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Db  2581 ATGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAACGGATTCCATTGTTGATTGA 2640

Qy  2641 GGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATACAGTGCACCT 2700
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Db  2641 GGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATACAGTGCACCT 2700

Qy  2701 GTAATCCATGTCCTGACGCGTCCAAGAGTGTGGTGTGTTCCCAGCTGTTAGATGAA 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2761 AATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAAATGAAGATATTAGAGAGGAC 2820
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Db  2761 AATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAAATGAAGATATTAGAGAGGAC 2820

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Db  2821 CATTATGAGTCTCTCAAGGAGGAGACTACCCTTAAGTCAAGCCAGAAAAAGTGGT 2880

Qy  2881 TTCCAAATGGATTGGCTGTGTCTGAACCTCACCCAGTGAAGCCACGTTTATTGGGACCCAG 2940
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Db  2881 TTCCAAATGGATTGGCTGTGTCTGAACCTCACCCAGTGAAGCCACGTTTATTGGGACCCAG 2940

Qy  2941 GTCTTTGAAGACTATGACCTGCAGAGAGCTCGGTGGTGGACTACAGGCTGTGATGGGAAGCCTTTCTTT 3000
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Qy  3001 GATGTCTGGCAGCTCCGGGGCAAGTACCGGAATCGAGGCTTCCCCAAGATATTTAACGAC 3060
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Db  3001 GATGTCTGGCAGCTCCGGGGCAAGTACCGGAATCGAGGCTTCCCCAAGATATTTAACGAC 3060

Qy  3061 AAAACAGTAGGTGGAGAGGCCAGGAGGTCTACGATGATGCCCACAATATGCTGAACACA 3120
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Db  3061 AAAACAGTAGGTGGAGAGGCCAGGAGGTCTACGATGATGCCCACAATATGCTGAACACA 3120

Qy  3121 CTGATTAGTAGTCAAAAGAAAACTCACCGGGCGTGTTGGGTGTTGGGGTTCTGGCCAGCACGAGT 3180
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Db  3121 CTGATTAGTAGTCAAAAGAAAACTCACCGGGCGTGTTGGGTGTTGGGGTTCTGGCCAGCACGAGT 3180

Qy  3181 ATCCAAGACACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATA 3240
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Db  3181 ATCCAAGACACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATA 3240

Qy  3241 GCCACTTTCTATGGGTTAAGGCAACAGCTGAGAAGGACTCTGCGCACGGAGCCATAC 3300
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Db  3241 GCCACTTTCTATGGGTTAAGGCAACAGCTGAGAAGGACTCTGCGCACGGAGCCATAC 3300

Qy  3301 TACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGCATCGTGTAGCTACCTGGGCCTG 3360
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Db  3301 TACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGCATCGTGTAGCTACCTGGGCCTG 3360

Qy  3361 TTTGCCGTTGGCTGCTTTGGGTTAGAGAGCTGAGCAAGGCCTATGAGGATGATGGTGAC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TTTGCCGTTGGCTGCTTTGGGTTAGAGAGCTGAGCAAGGCCTATGAGGATGATGGTGAC 3420

Qy  3421 GACTACAGCAGCAGCATCATGTGCTGGCCACT 3480
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Db  3421 GACTACAGCAGCAGCATCATGTGCTGGCCACT 3480

Qy  3481 GAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGTGAGCAGCTGGAC 3540
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Db  3481 GAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGTGAGCAGCTGGAC 3540

Qy  3541 GTCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCGCCCGCGTCCTCGGCTACCCCAGC 3600
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Db  3541 GTCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCGCCCGCGTCCTCGGCTACCCCAGC 3600

Qy  3601 CAGCCCCACCACACCGACAGAAGCTCACCATGTCGAGACTCGCGACAATCGAGCAGTCACA 3660
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Qy  3661 GGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGCCTCTAC 3720
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Db  3661 GGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGCCTCTAC 3720

Qy  3721 TTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAG 3780
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Db  3781 GATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATT 3840

Qy  3841 TTTGGGATATGATACAGACTAACTTTTTTTTTTTTGCCTTTTTATCTTGATGATCC 3900
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Db  3841 TTTGGGATATGATACAGACTAACTTTTTTTTTTTTTTGCCTTTTTATCTTGATGATCC 3900

Qy  3901 TCAAGGAAATACAACCTAG 3919
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Db  3901 TCAAGGAAATACAACCTAG 3919
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RESULT 2
US-09-318-448-2
; Sequence 2, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 7122
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-2

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  Query Match          99.1%;  Score 3884.8;  DB 3;  Length 7122;
  Best Local Similarity 99.6%;  Pred. No. 0;
  Matches 3904;  Conservative  0;  Mismatches 12;  Indels  2;  Gaps  1;

Qy    2 GTCAACCTGTGGGAGCAGCACGTCTTCTCTGCCGCCAAGGAGGAGGACTCGACA 61
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Db  225 GTCAACCTGGGAGCAGCACGTCTTCTCTGCCGCCAAGGAGGAGGACTCGACA 284

Qy   62 ACAGTCACCCGCGTCCAAGACCTGTCGCAACCCGAGTCGAAGAAGTCTCGACGTCGAAGAAACCCTGCGGG 121
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  285 ACAGTCACCCGCGTCCAAGACCTGTCGCAACCCGAGTCGAAGAAGTCTCGACGTCGAAGAAACCCTGCGGG 344

Qy  122 ATGAGATCAATGCCATTCTGCAGAAGAGATTATGGTGCTGATGGGAGGGATGGGGACCA 181
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Db  345 ATGAGATCAATGCCATTCTGCAGAAGAGATTATGGTGCTGATGGGATGGGGACCA 404

Qy  182 TGATCCAGCGGGAGAAGCGGCTCAAACGCAAGGGAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 241
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Db  1485 GTGTTGCCAAAGTGCAGGTGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATG 1544

Qy  1322 GCATGCTAGATGGTCCAAGTGCAATGCAACCAGATTTGCAACTTAATTGCTTCCGAGCCAG 1381
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Db  1545 GCATGCTAGATGGTCCAAGTGCAATGCAACCAGATTTGCAACTTAATTGCTTCCGAGCCAG 1604

Qy  1382 ACATCGCAAAGTACCTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGT 1441
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Qy  1442 TAAAGTGCTGCCAAGGAAGTGCAATAGCATTGTCAATAGCATTAGTCTGAAGAAGGAGGAGGACG 1501
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Db  1665 TAAAGTGCTGCCAAGGAAGTGCAATAGCATTGTCAATAGCATTAGTCTGAAGAAGGAGGAGGACG 1724

Qy  1502 ACTTCTTGGAGAAGGCCAGGAGAGATTAAAAAGTATGAGGCTGCTATGGTGGTCATGGCTT 1561
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Db  1725 ACTTCTTGGAGAAGGCCAGGAGAGATTAAAAAGTATGAGGCTGCTATGGTGGTCATGGCTT 1784

Qy  1562 TTGATGAAGAAGGACAGGCAACAGAAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCT 1621
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Db  1785 TTGATGAAGAAGGACAGGCAACAGAAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCT 1844

Qy  1622 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1681
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Db  1845 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1904

Qy  1682 TCCTAACCATTGGGACTGGAATGGACATGGGACTGTGATGCCATTAATTTTATCCATG 1741
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Db  1905 TCCTAACCATTGGGACTGGAATGGACATGGGACTGTGATGCCATTAATTTTATCCATG 1964

Qy  1742 CAACAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGTCTTTCCAACT 1801
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Db  1965 CAACAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGTCTTTCCAACT 2024

Qy  1802 TGTCCTTCTCCCTTCCGGAAGCAATGGAAGCAATTCAGAAGCAATGCATGGGGTTTTCCTTT 1861
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Db  2025 TGTCCTTCTCCCTTCCGGAAGCAATGGAAGCAATTCAGAAGCAATGCATGGGGTTTTCCTTT 2084

Qy  1862 ACCATGCAATCAAGTCTGCCATGCTGACATGAGATAGTGAATGCTGGAAACCTCCCTGTGT 1921
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Db  2085 ACCATGCAATCAAGTCTGCCATGCTGACATGAGATAGTGAATGCTGGAAACCTCCCTGTGT 2144

Qy  1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 1981
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Db  2145 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 2204

Qy  1982 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAAGACTCAAGGCACAGAGGAAGAAAG 2041
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Db  2205 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAAGACTCAAGGCACAGAGGAAGAAAG 2264

Qy  2042 TCATTCAGACTGATGAGTGGAGAAATGGAGAAATGGCCCTGTCGAAGAAATGCGCCCTTGAGTATGCCCCTG 2101
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Db  2265 TCATTCAGACTGATGAGTGGAGAAATGGAGAAATGGCCCTGTCGAAGAAATGCGCCCTTGAGTATGCCCCTG 2324

Qy  2102 TGAAGGGCATTGAAAACATATTATTGAGGATACTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA 2161
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Db  2325 TGAAGGGCATTGAAAACATATTATTGAGGATACTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA 2384

Qy  2162 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAATGAAAATTGTTG 2221
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Db  2385 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAATGAAAATTGTTG 2444

Qy  2222 GTGATCTTTTTGGAGCTCGGAAAAATGTGTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
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Qy  2282 TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAGAAAACCAGAG 2341
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Db  2505 TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAGAAAACCAGAG 2564

Qy  2342 TGCTTAACCGGCACAGTAGAAGAGGAGACCCTTACCAGGGCACCATCCGTGCTGGCCACTG 2401
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2565 TGCTTAACCGGCACAGTAGAAGAGGAGACCCTTACCAGGGCACCATCCGTGCTGGCCACTG 2624
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Db   405                                                              464
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Qy   242 CCAGGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC 301
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Db   465 CCAGGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC 524

Qy   302 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAACAAATACTTTTAGCA 361
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAACAAATACTTTTAGCA 584

Qy   362 GCACTAGTATTGCCCAAGCTGCTATGGCCTTGAACACTTGGCTTCGGATGAACATGT 421
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Db   585 GCACTAGTATTGCCCAAGCTGCTATGGCCTTGAACACTTGGCTTCGGATGAACATGT 644

Qy   422 GCTCTGCGAGGAGTGGCCAGAAAAGTCGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA 481
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Db   645 GCTCTGCGAGGAGTGGCCAGAAAAGTCGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA 704

Qy   482 GGTTTGTGTGCAGGGGGCTCTGGGTCCGACTAATAAGCACACTCTCTGTGTCCCATCTGTGG 541
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 GGTTTGTGTGCAGGGGGCTCTGGGTCCGACTAATAAGCACACTCTCTGTGTCCCATCTGTGG 764

Qy   542 AAAGGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGACAGG 601
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Db   765 AAAGGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGACAGG 824

Qy   602 CCAAAGGACTTCTGGATGTGGCGGGGTTGATATCTTACTCACTATTTTGATACTG 661
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Db   825 CCAAAGGACTTCTGGATGTGGCGGGGTTGATATCTTACTCACTATTTTGATACTG 884

Qy   662 CCAATGCCAAGGCAGCCTGTTGTTGCACTCAAAAATCTTTTTGAGGAGAAAATGCTCCCC 721
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Db   885 CCAATGCCAAGGCAGCCTGTTGTTGCACTCAAAAATCTTTTTGAGGAGAAAATGCTCCCC 944

Qy   722 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTTCCGGACAGA 781
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Db   945 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTTCCGGACAGA 1004

Qy   782 CAGGAGAGGATTGTCATCAGCGTGTCTCATGGGAACCACTCCACTACACTTGGATTAAATT 841
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Db  1005 CAGGAGAGGATTGTCATCAGCGTGTCTCATGGGAACCACTCCACTACACTTGGATTAAATT 1064

Qy   842 GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAGAATAATTGGAAATAATGTACAACAG 901
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Db  1065 GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAGAATAATTGGAAATAATGTACAACAG 1124

Qy   902 CCTATGTCCTCGTATCCCAATGCAGTCAGTGCCTTGGTGACTACTTTGGTGACTGATGATGAAA 961
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1125 CCTATGTCCTCGTATCCCAATGCAGTCAGTGCCTTGGTGACTACTTTGGTGACTGATGATGAAA 1184

Qy   962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG 1021
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1185 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG 1244

Qy  1022 TTGGAGATGCGTGTGGCAGCTGAGATGGCTGAAATTGCTGGAAGGTGTGAAAA 1081
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1245 TTGGAGATGCGTGTGGCAGCTGAGATGGCTGAAATTGCTGGAAGGTGTGAAAA 1304

Qy  1082 ATTGTAAGCCTAGAGTTCCACCTGCTCCTTTGAAGGACATATATGTTACTGTCTGCTC 1141
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1305 ATTGTAAGCCTAGAGTTCCACCTGCTCCTTTGAAGGACATATATGTTACTGTCTGCTC 1364

Qy  1142 TAGAGCCCCTTCAGGATTGACCGTACACCAACTTGTTAACATTGAAGGCGGCTGTAATG 1201
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1365 TAGAGCCCCTTCAGGATTGACCGTACACCAACTTGTTAACATTGAAGGCGGCTGTAATG 1424

Qy  1202 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGGCCAGGAAACTATGGAAGAGGCCTTGT 1261
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1425 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGGCCAGGAAACTATGGAAGAGGCCTTGT 1484

Qy  1262 GTGTTGCCAAAGTGCAGGTGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATG 1321
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321
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Qy  3482  AGCTCCATGAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGCCAGTGAGCAGCAGCTGGACG  3541
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Db  3705  AGCTCCATGAAAGAGTTCGCCGAGAACTGTGGCGCCTACTGTGCCAGTGAGCAGCAGCTGGACG  3764

Qy  3542  TCGCAGACCTGCGAAGGTGCGCTACAAGGGCATCCGCCCGGCTCCTGCTACCCCAGCC  3601
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3765  TCGCAGACCTGCGCGCAGGCTGCGCTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGCC  3824

Qy  3602  AGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGACAGTCTACAG  3661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3825  AGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGACAGTCTACAG  3884

Qy  3662  GCATTAGGTTAACAGAATCATTAGCAATGGCAACCTGCTTCAGCAGTCTCAGGCCTCTACT  3721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3885  GCATTAGGTTAACAGAATCATTAGCAATGGCAACCTGCTTCAGCAGTCTCAGGCCTCTACT  3944

Qy  3722  TCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGAAGATTCCAAGGATCAGGTTGAGG  3781
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3945  TCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG  4004

Qy  3782  ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGCTTGGACCCATTT  3841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4005  ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGCTTGGACCCATTT  4064

Qy  3842  TGGGATATGATACAGACTAACTTTTTTTTTTTTTTGCCTTTTTATTCTTGATGATCCT  3901
          |||||||||||||||||||||                 |||||||||||||||||||||
Db  4065  TGGGATATGATACAGACTAAC--TTTTTTTTTTTTTTTGCCTTTTTATTCTTGATGATCCT  4122

Qy  3902  CAAGGAAATACAACCTAG  3919
          ||||||||||||||||||
Db  4123  CAAGGAAATACAACCTAG  4140
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RESULT 3
US-09-347-878-4
; Sequence 4, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
;   APPLICANT: Yuan, Chong
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
;   FILE REFERENCE: 25885-1651
;   CURRENT APPLICATION NUMBER: US/09/347,878C
;   CURRENT FILING DATE: 1999-07-06
;   NUMBER OF SEQ ID NOS: 75
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 4
;   LENGTH: 7122
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (287)..(4084)
;   OTHER INFORMATION: Human methionine synthase cDNA
; PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: U75743/GenBank
US-09-347-878-4

Query Match   99.1%; Score 3884.8; DB 3; Length 7122;
Best Local Similarity   99.6%; Pred. No. 0;
Matches 3904; Conservative   0; Mismatches 12; Indels 2; Gaps 1;

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Qy    2  GTCACCTGTGGAGGAGCACGTCTTCTGCCGCGGCCCTCTGCGCAAGGAGGAGACTCGACA  61
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Db  225  GTCACCTGTGAGGAGCACGTCTTCTGCCGCGGCCCTCTGCGCAAGGAGGAGACTCGACA  284

Qy   62  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCAGGTCGAAGAAAACCCTGCGCGGG  121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  285  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCAGGTCGAAGAAAACCCTGCGCGGG  344

Qy  122  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTTGCTGATGAGTGATGGGGGACCA  181
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  345  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTTGCTGATGAGTGATGGGGGACCA  404
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Qy  2402  TTAAAGGCGACGTGCACGACATAGGCAAGAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA  2461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2625  TTAAAGGCGACGTGCACGACATAGGCAAGAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA  2684

Qy  2462  ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAGATACTGAAAGCTGCTC  2521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2685  ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAGATACTGAAAGCTGCTC  2744

Qy  2522  TTGACCACAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA  2581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2745  TTGACCACAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA  2804

Qy  2582  TGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG  2641
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2805  TGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG  2864

Qy  2642  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  2701
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Db  2865  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  2924

Qy  2702  TAATCCATGTCCTGGACGGTCCAAGAGTGTCGTGTGTGTTCCCAGCTGTTAGATGAAA  2761
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2925  TAATCCATGTCCTGGACGGTCCAAGAGTGTCGTGTGTGTTCCCAGCTGTTAGATGAAA  2984

Qy  2762  ATCTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAAGATATTAGACAGGACC  2821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2985  ATCTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAAGATATTAGACAGGACC  3044

Qy  2822  ATTATGAGTCTCTCAAGGAGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTCGTT  2881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3045  ATTATGAGTCTCTCAAGGAGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTCGTT  3104

Qy  2882  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAGCCCACGTTTATTGGGACCCAGG  2941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3105  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAGCCCACGTTTATTGGGACCCAGG  3164

Qy  2942  TCTTTGAAGACTATGACCATGACCTGCAGAAGCTGGTGACTACATTGACTGGAAGCCTTTCTTTG  3001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3165  TCTTTGAAGACTATGACCATGACCTGCAGAAGCTGGTGACTACATTGACTGGAAGCCTTTCTTTG  3224

Qy  3002  ATGTCTCTGCAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACA  3061
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3225  ATGTCTCTGCAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACA  3284

Qy  3062  AAACAGTAGGTGGAGAGGCCAGGAAGGTTCTACGATGATGCCCACAATATGCTGAACACAC  3121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3285  AAACAGTAGGTGGAGAGGCCAGGAAGGTTCTACGATGATGCCCACAATATGCTGAACACAC  3344

Qy  3122  TGATTAGTCAAAAGAAACTCCGGGGTGTGGTTCTGGTTCTGGCCAGCACAGAGTA  3181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3345  TGATTAGTCAAAAGAAACTCCGGGGTGTGGTTCTGGTTCTGGCCAGCACAGAGTA  3404

Qy  3182  TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGTGCCCAGAGCCCATAG  3241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3405  TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGTGCCCCAGAGCGCCATAG  3464

Qy  3242  CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGAACTGAGAAGGTCTGCCAGCACGGAGCCATACT  3301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3465  CCACCTTCTATGGGTTAAGGCAACAGGCTGAGAAGGAACTGAGAAGGTCTGCCAGCACGGAGCCATACT  3524

Qy  3302  ACTGCCTCTCAGACTTCATCGCTCCCTGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3525  ACTGCCTCTCAGACTTCATCGCTCCCTGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3584

Qy  3362  TTGCCGGTTGCACCCGCTGCTTGGGGTTAGAAGAGCTGAGCAAGGCCTATGAGGATGGTGACG  3421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3585  TTGCCGGTTGCTTGCTTTGGGGTTAGAAGAGCTGAGCAAGGCCTATGAGGATGGTGACG  3644

Qy  3422  ACTACAGCAGCATCATGGTCAAGGGCTGCTGGGGACCGGCCTTTGCAGAAG  3481
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3645  ACTACAGCAGCATCATGGTCAAGGGCTGCTGGGGACCGGCCTTTGCAGAAG  3704
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Column 1

```
Qy    182  TGATCCAGCGGGAGAAGCTAAACGAAGACACTTCCGAGGTCAGGAATTTAAAGATCATG   241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405  TGATCCAGCGGGAGAAGCTAAACGAAGACACTTCCGAGGTCAGGAATTTAAAGATCATG   464

Qy    242  CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC   301
           |||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465  CCAGGCCCCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC   524

Qy    302  AAATCCATAAGGAATACTTCGCTGGCTGGGCCAGATATCATTGAAACAAATACTTTAGCA  361
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    525  AAATCCATAAGGAATACTTAAGCTGGCTGGGCCAGATATCATTGAAACAAATACTTTAGCA  584

Qy    362  GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT  421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585  GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT  644

Qy    422  GCTCTGCAGGAGTGGCCAGAAAGCTGGCCGAGGAGTAACTCTCCAGACAGCAGAATTAAGA  481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645  GCTCTGCAGGAGTGGCCAGAAAGCTGGCCGAGGAGTAACTCTCCAGACAGCAGAATTAAGA  704

Qy    482  GGTTTGTGGCAGGGGCTCGGGTCCGACTAATAGAACTCTCTGTGTCCCCATCTGTGG     541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705  GGTTTGTGGCAGGGGCTCGGGTCCGACTAATAGAACTCTCTGTGTCCCCATCTGTGG     764

Qy    542  AAAGGCCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG  601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765  AAAGGCCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG  824

Qy    602  CCAAAGACTTCTGGATGCGGGGTTGATATCTTACTCACTCATTTTTGATACTG         661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825  CCAAAGACTTCTGGATGCGGGGTTGATATCTTACTCACTCATTTTTGATACTG         884

Qy    662  CCAATGCCAAGGCCAGCCTTGTTGCACTCTTTTTGAGGAGAAAAATGCTCCCC         721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885  CCAATGCCAAGGCCAGCCTTGTTGCACTCTTTTTGAGGAGAAAAATGCTCCCC         944

Qy    722  GGCCTATCTTTATTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTTCCGGACAGA    781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945  GGCCTATCTTTATTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTTCCGGACAGA   1004

Qy    782  CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGGACCACTCTGCATTGCATTGATTAATT  841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005  CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGGACCACTCTGCATTGCATTGATTAATT 1064

Qy    842  GTGCTTTGGGTGCAGCTGAGATGAGACACCTTTATTGAAATAATTGGAAAATGTACAACAG  901
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065  GTGCTTTGGGTGCAGCTGAGATGAGACACCTTTATTGAAATAATTGGAAAATGTACAACAG 1124

Qy    902  CCTATGTCCTGTTATCCCAATGCAGTTGCTTCCCAACACCTTTGGTGACTATGATGAAA    961
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125  CCTATGTCCTGTTATCCCAATGCAGTTGCTTCCCAACACCTTTGGTGACTATGATGAAA   1184

Qy    962  CGCCTTCTATGATGGCCAAGCACTCACCTAAAGGATTTTGCTATGGAAGGATGGCCTATAG 1021
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185  CGCCTTCTATGATGGCCAAGCACTCACCTAAAGGATTTTGCTATGGAAGGATGGCCTATAG 1244

Qy   1022  TTGGAGGATGCTGGGTCAACATCAGGTCTTCCCAACACCTTTGGTGAAGCTGTGAAAA   1081
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1245  TTGGAGGATGCTGGGTCAACATCAGGTCTTCCCAACACCTTTGGTGAAGCTGTGAAAA   1304

Qy   1082  ATTGTAAGCCTAGAGTTCCACCTGCTTTTGAAGGACATATGTTTACTGTCTGTGTC    1141
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1305  ATTGTAAGCCTAGAGTTCCACCTGCTTTTGAAGGACATATGTTTACTGTCTGTGTC    1364

Qy   1142  TAGAGCCCTTCAGGATTCAACGTGGATTGGACCGTACACCAACCTTTGTGTTAACATTGGA 1201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365  TAGAGCCCTTCAGGATTCAACGTGGATTGGACCGTACACCAACCTTTGTGTTAACATTGGA 1424

Qy   1202  TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATCGGCTAAACTGCAGAAACTATGGAAGA 1261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1425  TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATCGGCTAAACTGCAGAAACTATGGAAGA 1484

Qy   1262  GTGTTGCCAAGTGCAGTGGAAATGGGAGCCCAGTGTTGTTGACGTGTCAACATGGATGATG 1321
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Column 2

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Db   1485  GTGTTGCCAAGTGCAGTGGAAATGGGAGCCCAGTGTTGTTGACGTGTCAACATGGATGATG 1544
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1322  GCATGCTAGATGGTCCAAGTGCAATGACATGGATTTGCAACTTAATTGCTTCCGAGCCAG  1381

Db   1545  GCATGCTAGATGGTCCAAGTGCAATGACATGGATTTGCAACTTAATTGCTTCCGAGCCAG  1604
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1382  ACATCGCAAAGGTACCTTGTGTCGATCGACTCCTCCAATTTGTGTGATTGAAGCTGGGT   1441

Db   1605  ACATCGCAAAGGTACCTTGTGTCGATCGACTCCTCCAATTTGTGTGATTGAAGCTGGGT   1664
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1442  TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCATAGTGTGAAGAAGGAGACG 1501

Db   1665  TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCATAGTGTGAAGAAGGAGACG 1724
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1502  ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT  1561

Db   1725  ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT  1784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1562  TTGATGAAGAAGCACGCAACAGAAATCAGAGTGTGCACCCGGGCCT               1621

Db   1785  TTGATGAAGAAGCACGCAACAGAAATCAGAGTGTGCACCCGGGCCT               1844
           ||||||||||||||||||||||||||||||||||||||||||||||
Qy   1622  ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGAACATTATTATTTTGACCCTAATA 1681

Db   1845  ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGAACATTATTATTTTGACCCTAATA 1904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1682  TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTTATCCATG  1741

Db   1905  TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTTATCCATG  1964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1742  CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGTCTTTCCAACT   1801

Db   1965  CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGTCTTTCCAACT   2024
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1802  TGTCCTTCTCCTTCCGGAATGGAAGCAATGCATTGCGAGAGCAATGCATGGGGTTTTCCTTT 1861

Db   2025  TGTCCTTCTCCTTCCGGAATGGAAGCAATGCATTGCGAGAGCAATGCATGGGGTTTTCCTTT 2084
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1862  ACCATGCAATCAAGTCTGCACTGACATGGGGATAGTAGTGGAAACCTCCCTGTGT      1921

Db   2085  ACCATGCAATCAAGTCTGCACTGACATGGGGATAGTAGTGGAAACCTCCCTGTGT      2144
           |||||||||||||||||   |||||||||||||||||||||||||||||||||||
Qy   1922  ATGATGATATCCATCAGACTTCTGCAGCTCTGTGTGAAGATCTCATCTGGAATAAAGACC  1981

Db   2145  ATGATGATATCCATCAGACTTCTGCAGCTCTGTGTGAAGATCTCATCTGGAATAAAGACC  2204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1982  CTGAGGCCACTGACTGAGTGGAGAAGCTTCTTACGTTACGTATGCCCAAGGCACAGGAAGAAAG 2041

Db   2205  CTGAGGCCACTGACTGAGTGGAGAAGCTTCTTACGTTACGTATGCCCAAGGCACAGGAAGAAAG 2264
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2042  TCATTCAGACTGATGAGTGGAGAAATGGCCCTGTGAAGAACCGCCTGATGAATGGAATGCCCTTG 2101

Db   2265  TCATTCAGACTGATGAGTGGAGAAATGGCCCTGTGAAGAACCGCCTGATGAATGGAATGCCCTTG 2324
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2102  GTGATCTCTTTTGGAGCTGAAAAACATATTATTATTGAGGATATATTGAAAACAACCAAAAAA  2161

Db   2325  GTGATCTCTTTTGGAGCTGAAAAACATATTATTATTGAGGATATATTGAAAACAACCAAAAAA  2384
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2162  AATATCCCGACCTCTCAATATAATTGAAGGACACCCCTGATGAATGGATGAAAATTGTTG   2221

Db   2385  AATATCCCGACCTCTCAATATAATTGAAGGACACCCCTGATGAATGGATGAAAATTGTTG   2444
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2222  GTGATCTTTTTGGAGCTGGAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA   2281

Db   2445  GTGATCTTTTTGGAGCTGGAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA   2504
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2282  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAGAGAACCAGAG    2341

Db   2505  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAGAGAACCAGAG    2564
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2342  TGCTTAACGCACAGTAGAAGAGAGGACCCCTTACCAGGCACCATCGTGCTGCCACTGT    2401
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Db 2565 TGCTTAACGGGCACAGTAGAAGAAGAGAGACCCTTACCAGGGCACCCATCGTCGTGGCCACTG 2624
Qy 2402 TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA 2461
Db 2625 TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA 2684
Qy 2462 ATTTCCGAGTTATTGATTTAGGAGTCATGATCCATGTGATTAAGATACTGAAAGCTGCTC 2521
Db 2685 ATTTCCGAGTTATTGATTTAGGAGTCATGATCCATGTGATTAAGATACTGAAAGCTGCTC 2744
Qy 2522 TTGACCCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGGATGAAA 2581
Db 2745 TTGACCCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGGATGAAA 2804
Qy 2582 TGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCATTGTTGATTGGAG 2641
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Db 2865 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATACAGTGCACCTG 2924
Qy 2702 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTGTTCCCAGCTGTTAGATGAAA 2761
Db 2925 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTGTTCCCAGCTGTTAGATGAAA 2984
Qy 2762 ATCTAAAGGATGAATACTTTGAGGAAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT 2821
Db 2985 ATCTAAAGGATGAATACTTTGAGGAAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT 3044
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Db 3045 ATTATGAGTCTCTCAAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT 3104
Qy 2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG 2941
Db 3105 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG 3164
Qy 2942 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGAAGCCTTTCTTTG 3001
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Qy 3002 ATGTCTGGCAGCTCCGGGGCAAGTACCGGAATCGAGGCTTCCCCAAGATATTAACGACA 3061
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Qy 3062 AAACAGTAGGTGGAGAGGCCAGGAAGTCCAGGAAGTCCACCACCACCACAGACACAC 3121
Db 3285 AAACAGTAGGTGGAGAGGCCAGGAAGTCCAGGAAGTCCACCACCACCACAGACACAC 3344
Qy 3122 TGATTAGTCAAAAGAAACTCCCGGGCGTGTGGTTGGGGTTCTGCCAGCACAGAGTA 3181
Db 3345 TGATTAGTCAAAAGAAACTCCCGGGCGTGTGGTTGGGGTTCTGCCAGCACAGAGTA 3404
Qy 3182 TCCAAGACGACATTCACCCTGTACGCAGGAGGCTGCGTGCCCAGGGCTGCAGAGCCCATAG 3241
Db 3405 TCCAAGACGACATTCACCCTGTACGCAGGAGGCTGCGTGCCCAGGGCTGCAGAGCCCATAG 3464
Qy 3242 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAGGACTCTGCCAGCACGCAGGACTCGACA 3301
Db 3465 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAGGACTCTGCCAGCACGCAGGACTCGACA 3524
Qy 3302 ACTGCCTCTCCAGACTTCATCGCTTCCCTTGCATTCTGCATCCGTGACTACCGTGGGCTGT 3361
Db 3525 ACTGCCTCTCCAGACTTCATCGCTTCCCTTGCATTCTGCATCCGTGACTACCGTGGGCTGT 3584
Qy 3362 TTGCCGTTGCCTGCTGCTTTGGGTAGAGAGCTGAGCAGGCCTATGAGGATGATGGTGACG 3421
Db 3585 TTGCCGTTGCCTGCTGCTTTGGGTAGAGAGCTGAGCAGGCCTATGAGGATGATGGTGACG 3644
Qy 3422 ACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCCTTGCAGAAG 3481
Db 3645 ACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCCTTGCAGAAG 3704
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Qy 3602 AGCCCGACCACACCGAGAAGTCACCATGTGAGAGACTCGCAGACATCGAGCAGTCTACAG 3661
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Db 4123 CAAGGAAATACAACCTAG 4140
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RESULT 4
US-09-577-266-2
; Sequence 2, Application US/09577266
; Patent No. 6912492.
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057N
; CURRENT APPLICATION NUMBER: US/09/577,266
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/136,198
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 7122
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-577-266-2

Query Match   99.1%;   Score 3884.8;   DB 3;   Length 7122;
Best Local Similarity 99.6%;   Pred. No. 0;
Matches 3904;   Conservative   0;   Mismatches 12;   Indels 2;   Gaps 1;

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Qy    2 GTCACCTGTGAGAGCACGTCTTCCTGCGCCGCCCTCTGCGCAGGAGGAGACTCGACA 61
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Qy   62 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCGTGCCGAAGGTCGCAACCCTGCGGG 121
Db  285 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCGTGCCGAAGGTCGCAACCCTGCGGG 344
Qy  122 ATGAGATCAATGCCATTCTGCGAGAAGAGGATTATGTGCTCGATGAGGGATGGGGACCA 181
Db  345 ATGAGATCAATGCCATTCTGCGAGAAGAGGATTATGTGCTCGATGAGGGATGGGGACCA 404
Qy  182 TGATCCAGCGGGAGAAGCTAAACGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 241
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Db   465 CCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC 524

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Qy   662 CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC 721
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Db   885 CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC 944

Qy   722 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA 781
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Qy   842 GTGCTTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAG 901
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Db 1065 GTGCTTTGGGTGCAGCTGAAATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAG 1124

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Db 1125 CCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA 1184

Qy   962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG 1021
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Db 1185 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG 1244

Qy 1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1081
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Db 1365 TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCTGTAATG 1424

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Db 1485 GTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATG 1544

Qy 1322 GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCAG 1381
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Qy 1502 ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1561
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Qy 1562 TTGATGAAGAAGGACAGGCAACAGAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCT 1621
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Db 1785 TTGATGAAGAAGGACAGGCAACAGAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCT 1844

Qy 1622 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1681
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Db 1845 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1904

Qy 1682 TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTTATCCATG 1741
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Qy 1742 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 1801
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Qy 1802 TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTT 1861
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Qy 1862 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGGAAACCTCCCTGTGT 1921
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Db 2085 ACCATGCAATCAAGTCTGGCATGGACATGGGGATAGTGAATGCTGGAAACCTCCCTGTGT 2144

Qy 1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 1981
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2145 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACC 2204

Qy 1982 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAG 2041
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Db 2205 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAG 2264

Qy 2042 TCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTTG 2101
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2265 TCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTTG 2324

Qy 2102 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAA 2161
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Qy 2222 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
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Db 2445 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2504

Qy 2282 TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAGAGAAGAAACCAGAG 2341
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Qy   2402 TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA 2461
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Db   2745 TTGACCACAAGCAGAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA 2804

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Qy   2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGACCCAGG 2941
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Db   3165 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATACATTGACTGGAAGCCTTTCTTG 3224

Qy   3002 ATGTCTGGCAGTCCGGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACA 3061
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Db   3525 ACTGCCCTCTCAGACTTCATCGTCCCTTGCATTCTGGCATCCTGGACTACCTGGGGCCTGT 3584

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Db   3645 ACTACAGCAGCATCATGGTCAAGGCCTGTCAAGGGGCCGGACCCGCTGGCGCTGCAGAAAG 3704
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Db   3825 AGCCCGACCACACCGAGAAGTCACCCATGTGAGACTCGGAGACATCGAGACGAGTCTACAG 3884

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGCAATGCACCTGCTTCAGCAGTCTCAGGCCTCTACT 3721
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3885 GCATTAGGTTAACAGAATCATTAGCAATGCAATGCACCTGCTTCAGCAGTCTCAGGCCTCTACT 3944

Qy   3722 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGAATTCCAAGGATCAGGTTGAGG 3781
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3945 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGAATTCCAAGGATCAGGTTGAGG 4004

Qy   3782 ATTATGCATTGAGGAAGAACATATCTGCGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT 3841
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4005 ATTATGCATTGAGGAAGAACATATCTGCGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT 4064

Qy   3842 TGGGATATGATCAGACTAACTTTTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCCT 3901
          ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db   4065 TGGGATATGATCAGACTAAC--TTTTTTTTTTTTTTATTCTTGATGATCCT 4122

Qy   3902 CAAGGAAATACAACCTAG 3919
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Db   4123 CAAGGAAATACAACCTAG 4140
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RESULT 5
US-09-347-878-6
; Sequence 6, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
;   APPLICANT: Yuan, Chong
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
;   FILE REFERENCE: 25885-1651
;   CURRENT APPLICATION NUMBER: US/09/347,878C
;   CURRENT FILING DATE: 1999-07-06
;   NUMBER OF SEQ ID NOS: 75
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 7224
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (395)..(4192)
;   FEATURE:
;   OTHER INFORMATION: Human methionine synthase
;   PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: U73338/GenBank
US-09-347-878-6

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Query Match             99.1%;  Score 3883.2;  DB 3;  Length 7224;
Best Local Similarity   99.6%;  Pred. No. 0;
Matches 3903;  Conservative    0;  Mismatches   13;  Indels   2;  Gaps   1;

Qy      2 GTCACCTGTGGAGGAGCACGTCTTCTCTGCCGCGCCCTCTGCCAAGGAGGAGGAGGACTCGACA 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    333 GTCACCTGTGGAGGAGCACGTCTTCTCTGCCGCGCCCTCTGCCAAGGAGGAGGAGGACTCGACA 392

Qy     62 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTTCGAAGAAACCCTGCGGG 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTTCGAAGAAACCCTGCGGG 452

Qy    122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGATGGGGATGGGGACCA 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGATGGGGATGGGGACCA 512
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Qy    182 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG  241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG  572

Qy    242 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTAGTATAACTCAGCCTGATGTCATTACC  301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    573 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTAGTATAACTCAGCCTGATGTCATTACC  632

Qy    302 AAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA  361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    633 AAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA  692

Qy    362 GCACTAGTATTGCCCAAGCTGACTATGCCTTGAACACTTGGCCTACCGGATGAACATGT  421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693 GCACTAGTATTGCCCAAGCTGACTATGCCTTGAACACTTGGCCTACCGGATGAACATGT  752

Qy    422 GCTCTGCGAGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA  481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753 GCTCTGCGAGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA  812

Qy    482 GGTTTGTGTGCAGGGGCTCTGGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG  541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813 GGTTTGTGTGCAGGGGCTCTGGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG  872

Qy    542 AAAGGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG  601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    873 AAAGGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG  932

Qy    602 CCAAAAGACTTCTGGATGGCGGGGTTGATATCTCTTGTTTGCACTCCAAAATCTTTTGATACTG  661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    933 CCAAAAGACTTCTGGATGGCGGGGTTGATATCTCTTGTTTGCACTCCAAAATCTTTTGATACTG  992

Qy    662 CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC  721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    993 CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC  1052

Qy    722 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA  781
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Db   1053 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA  1112

Qy    782 CAGGAGAGGAGATTTGTCATCAGCGTGTCGTCATGGAGAACCACTCTGCATTGGATTAAATT  841
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Db   1113 CAGGAGAGGGATTTGTCATCAGCGTGTCGTCATGGAGAACCACTCTGCATTGGATTAAATT  1172

Qy    842 GTGCTTTGGGTGCAGCTGAGATGAGACCCTTTATTGAAATAATTGGAAAATGTACAACAG  901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1173 GTGCTTTGGGTGCAGCTGAAATGAGACCCTTTATTGAAATAATTGGAAAATGTACAACAG  1232

Qy    902 CCTATGTCCTCTGTTATCCCAATGCAGGTCTCCCAACACCTTTGGTGACTATGATGAAA  961
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Db   1233 CCTATGTCCTGTCTGTTATCCCAATGCAGGTCTCCCAACACCTTTGGTGACTATGATGAAA  1292

Qy    962 CGCCTTCTATGATGGCCAAGCACCACCTAAAGGATTTTGCTATGGCTTGGTCTAATATAG  1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1293 CGCCTTCTATGATGGCCAAGCACCACCTAAAGGATTTTGCTATGGCTTGGTCTAATATAG  1352

Qy   1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAAGTGCTGAAAGCTGTGAAAA  1081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1353 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAAGTGCTGAAAGCTGTGAAAA  1412

Qy   1082 ATTGTAAGGCTGAGTTCTCAGGTTGCACATTGTAACATTGGAGGACATATGTTACTGTCTGTC  1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1413 ATTGTAAGGCTAGAGTTCTCAGGTTGCACATTGTAACATTGGAGGACATATGTTACTGTCTGTC  1472

Qy   1142 TAGAGCCCTTCAGGATTGGACCGGACCTGCCACTGACCACCCGCCACTGACGGAGCCGCTGTAATG  1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1473 TAGAGCCCTTCAGGATTGGACCGGACCTGCCACTGACCACCCGCCACTGACGGAGCCGCTGTAATG  1532

Qy   1202 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGGCGAGGAAACTATGAAGAAGCCTTGT  1261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1533 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGGCGAGGAAACTATGAAGAAGCCTTGT  1592

Qy   1262 GTGTTGCCAAAGTGCAGGTGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATG  1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1593 GTGTTGCCAAAGTGCAGGTGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATG  1652

Qy   1322 GCATGCTAGATGGTCCAAGTGCAATGACAACCAGATTTGCAACTTAATTGCTTCCGAGCCAG  1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1653 GCATGCTAGATGGTCCAAGTGCAATGACAACCAGATTTGCAACTTAATTGCTTCCGAGCCAG  1712

Qy   1382 ACATCGCAAAGTACTTTGTCGATCGACTCCTCCAATTTGTGTGATTGAAGCTGGGT  1441
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Db   1713 ACATCGCAAAGTACTTTGTCGATCGACTCCTCCAATTTGTGTGATTGAAGCTGGGT  1772

Qy   1442 TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGACG  1501
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Db   1773 TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGACG  1832

Qy   1502 ACTTCTTGGAGAAGAAGGCCAGGAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT  1561
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Db   1833 ACTTCTTGGAGAAGAAGGCCAGGAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT  1892

Qy   1562 TTGATGAAGAAGACAGGCAACAGCAAAATCAGACACCAAAAAATCAGACTTATTTTGACCCTAATA  1621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1893 TTGATGAAGAAGACAGGCAACAGCAAAACAGACACCAAAAAATCAGACTTATTTTGACCCTAATA  1952

Qy   1622 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTATCCATG  1681
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Db   1953 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCATG  2012

Qy   1682 TCCTAACCATTGGGACTGGAATTAAAGAAACATTGTATGCCATTAATTTTATCCATG  1741
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Db   2013 TCCTAACCATTGGGACTGGAATTAAAGAAACATTGTATGCCATTAATTTTATCCATG  2072

Qy   1742 CAACAAAAGTCATTAAAGAACATTACCTGGAGCCAGAATAAGTGAGTCTTCCAACT  1801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2073 CAACAAAAGTCATTAAAGAACATTACCTGGAGCCAGAATAAGTGAGTCTTCCAACT  2132

Qy   1802 TGTCCTTCTCCTTCCTTTCCTCGAGGAATGGAAGCCATTCGAGAGCAATGGGGTTTTCCTTT  1861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2133 TGTCCTTCTCCTTCCTTTCCTCGAGGAATGGAAGCCATTCGAGAGCAATGGGGTTTTCCTTT  2192

Qy   1862 ACCATGCAATCAAGTCTCGGCATGGAGATAGTAGTGAAATGCTGGAAACCTCCCTGTGT  1921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2193 ACCATGCAATCAAGTCTCGGCATGGAGATAGTAGTGAAATGCTGGAAACCTCCCTGTGT  2252

Qy   1922 ATGATGATATCCATAAGAACTTCTGCAGCTCTGTGAGATCTCATCTGAATAAAGACC  1981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2253 ATGATGATATCCATAAGAACTTCTGCAGCTCTGTGAGATCTCATCTGAATAAAGACC  2312

Qy   1982 CTGAGGCCACTGAGAAGCTTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAAG  2041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2313 CTGAGGCCACTGAGAAGCTTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAAG  2372

Qy   2042 TCATTCAGACTGATGAGTGGAGAAATGGGAGAAATGGCCCTTGAGTATGCCCCTTG  2101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2373 TCATTCAGACTGATGAGTGGAGAAATGGGAGAAATGGCCCTTGAGTATGCCCCTTG  2432

Qy   2102 TGAAGGGCATTGAAGAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAA  2161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2433 TGAAGGGCATTGAAGAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAA  2492

Qy   2162 AATATCCCGACCTTCAATATAATAATTGAAGGAATGGAATGGAAGAATTGTTG  2221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2493 AATATCCCGACCTTCAATATAATAATTGAAGGAATGGAATGGAAGAATTGTTG  2552

Qy   2222 GTGATCTTTTGGAGCTGTTGGCACCTTATCCCTTTCATGGTGAAAAAGAAGAAGTAAAGGG TTA  2281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2553 GTGATCTTTTGGAGCTGTTGGCACCTTATCCCTTTCATGGTGAAAAAATGTTTTACTTCACCGGGTTA  2612

Qy   2282 TGAAGAAGGCTGTTGGCCACCTTACCCTTTCATGGAAAAAGAAGAAGAAACCAGAG  2341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2613 TGAAGAAGGCTGTTGGCCACCTTACCCTTTCATGGAAAAAGAAGAAGAAACCAGAG  2672

Qy   2342 TGCTTAACCGGACACAGTAGAAGAGACCCTTACCAGGGCACCATCGTGCTGCCACTG  2401
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RESULT 6
US-09-962-665-1
; Sequence 1, Application US/09962665
; Patent No. 6537759
GENERAL INFORMATION:
  APPLICANT: Stanton, Jr., Vincent P.
  TITLE OF INVENTION: FOLYLPOLYGLUTAMATE SYNTHETASE GENE SEQUENCE
  TITLE OF INVENTION: VARIANCES HAVING UTILITY IN DETERMINING THE
  TITLE OF INVENTION: TREATMENT OF DISEASE
  FILE REFERENCE: 11926-015004
  CURRENT APPLICATION NUMBER: US/09/962,665
  CURRENT FILING DATE: 2001-09-24
  PRIOR APPLICATION NUMBER: 09/658,659
  PRIOR FILING DATE: 2000-09-08
  PRIOR APPLICATION NUMBER: 09/596,033
  PRIOR FILING DATE: 2000-06-15
  PRIOR APPLICATION NUMBER: 09/357,743
  PRIOR FILING DATE: 1999-07-20
  PRIOR APPLICATION NUMBER: 09/357,024
  PRIOR FILING DATE: 1999-07-19
  PRIOR APPLICATION NUMBER: 60/093,484
  PRIOR FILING DATE: 1998-07-20
  NUMBER OF SEQ ID NOS: 16
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 1
  LENGTH: 7224
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 194_3209
  OTHER INFORMATION: n = c or g
  NAME/KEY: misc_feature
  LOCATION: 1136, 1334, 3150, 5551, 5934
  OTHER INFORMATION: n = a or g
  NAME/KEY: misc_feature
  LOCATION: 284, 1252, 1699, 5573, 5659, 5678, 5874
  OTHER INFORMATION: n = c or t

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;  NAME/KEY: misc_feature
;  LOCATION: 3207
;  OTHER INFORMATION: n = g or t
;  NAME/KEY: misc_feature
;  LOCATION: 5444
;  OTHER INFORMATION: n = c or a
US-09-962-665-1

Query Match    98.9%;  Score 3876.2;  DB 3;  Length 7224;
Best Local Similarity  99.4%;  Pred. No. 0;
Matches 3896;  Conservative 0;  Mismatches 20;  Indels 2;  Gaps 1;
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Qy      2  GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCTGCGCAAGGAGGAGACTCGACA    61
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Db    333  GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCTGCGCAAGGAGGAGACTCGACA   392

Qy     62  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG   121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG   452

Qy    122  ATGAGATCAAATGCCATTCTGCAGAAGAGGATTATGTGCTGGATGGGGGACCA   181
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453  ATGAGATCAAATGCCATTCTGCAGAAGAGGATTATGTGCTGGATGGGGGACCA   512

Qy    182  TGATCCAGCGGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTAAAGATCATG   241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513  TGATCCAGCGGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTAAAGATCATG   572

Qy    242  CCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC   301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    573  CCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC   632

Qy    302  AAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA   361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    633  AAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA   692

Qy    362  GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTTCAATAGCACATGT   421
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693  GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTTCAATAGCACATGT   752

Qy    422  GCTCCTGCGAGGAGTGGCCAGAAAAAGTCTGCCGCCGAGGAGTAACTCTCCAGACAGGA   481
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753  GCTCCTGCGAGGAGTGGCCAGAAAAAGTCTGCCGCCGAGGAGTAACTCTCCAGACAGGA   812

Qy    482  GGTTTGTGCGAGGCGGCTTCGGGTCCGACTAATAAGAACACTCTCTGTCCCCATCTGTGG   541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813  GGTTTGTGCGAGGCGGCTTCGGGTCCGACTAATAAGAACACTCTCTGTCCCCATCTGTGG   872

Qy    542  AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGACAGG   601
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    873  AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGACAGG   932

Qy    602  CCAAAAGACTTCTGGATGCGGGGGTTGATATCTTACTCAATTTTTGATACTG   661
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Db    933  CCAAAAGACTTCTGGATGCGGGGGTTGATATCTTACTCAATTTTTGATACTG   992

Qy    662  CCAATGCCAAGGCAGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC   721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    993  CCAATGCCAAGGCAGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC  1052

Qy    722  GGCCTATCTTATTTCAGGGACGATCGTTGCATCAGCGTGTCTCATGGAGAACCACTCTCGGATTAAATT   781
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1053  GGCCTATCTTATTTCAGGGACGATCGTTGCATCAGCGTGTCTCATGGAGAACCACTCTCGGATTAAATT  1112

Qy    782  CAGGAGAGGGATTTGTCATCAGCNTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT   841
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1113  CAGGAGAGGGATTTGTCATCAGCNTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT  1172

Qy    842  GTGCTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTGGAAAATGTACAACAG   901
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1173  GTGCTTGGGTGCAGCTGAAATGAGACCTTTTATTGAAATAATTGGAAAATGTGGAAAATGTACAACAG  1232

Qy    902  CCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA   961
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Db   1233  CCTATGTCCTCTGTTATCCNAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA  1292

Qy    962  CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGATGGCTTGGTCAATATAG   1021
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1293  CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGNATGGCTTGGTCAATATAG  1352

Qy   1022  TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGTGTGAAAA  1081
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Db   1353  TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGTGTGAAAA  1412

Qy   1082  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCGTTTGAAGGACATATGTTACTGTCTCGTC  1141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1413  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCGTTTGAAGGACATATGTTACTGTCTCGTC  1472

Qy   1142  TAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGGCTGTAATG  1201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1473  TAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGGCTGTAATG  1532

Qy   1202  TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGT  1261
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Db   1533  TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGT  1592

Qy   1262  GTGTTGCCAAAGTGCAGGTGGAAATGGGAGTGTTGATGATGCAACATGCAACATGGATGATG   1321
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Db   1593  GTGTTGCCAAAGTGCAGGTGGAAATGGGAGTGTTGATGATGCAACATGCAACATGGATGATG  1652

Qy   1322  GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAG   1381
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1653  GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATNGCTTCCGAGCCAG  1712

Qy   1382  ACATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGT  1441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1713  ACATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGT  1772

Qy   1442  TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTGAAGAAGAGAGGACG   1501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1773  TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTGAAGAAGAGAGGACG  1832

Qy   1502  ACTTCTTGGAGAAGCCAGGAGGTAACTCTCCAGACAGGAATTAAGA   1561
           |||||||||||||||||||||||||||||||||||||||||||||
Db   1833  ACTTCTTGGAGAAGCCAGGAGGTAACTCTCCAGACAGGAATTAAGA  1892

Qy   1562  TTGATGAAGAAGACAGGCAACAGACAACAAAAATCAGAGTGTGCACCCGGGCCT   1621
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1893  TTGATGAAGAAGACAGGCAACAGACAACAAAAATCAGAGTGTGCACCCGGGCCT  1952

Qy   1622  ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA   1681
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1953  ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA  2012

Qy   1682  TCCTAACCATTGGGACTGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATG   1741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2013  TCCTAACCATTGGGACTGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATG  2072

Qy   1742  CAACAAAGTCATTAAAGAGAAACATTACCTGGAGCCAGAGAATAAGTGGAGTCTTTCCAACT   1801
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2073  CAACAAAGTCATTAAAGAGAAACATTACCTGGAGCCAGAGAATAAGTGGAGTCTTTCCAACT  2132

Qy   1802  TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAGACGAAGCAATCGAGAGATGAAC   1861
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2133  TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAGACGAAGCAATCGAGAGATGAAC  2192

Qy   1862  ACCATGCAATCAAGTCTGCGCATGGACATGGGGATAGTGAAACCTCCCTGTGT   1921
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2193  ACCATGCAATCAAGTCTGCGCATGGACATGGGGATAGTGAAACCTCCCTGTGT  2252

Qy   1922  ATGATGATATCCATAAGAACTCTTCGCAGCTCGTGTGAAGATCTCATCTGGAATAAAGACC   1981
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2253  ATGATGATATCCATAAGAACTCTTCGCAGCTCGTGTGAAGATCTCATCTGGAATAAAGACC  2312

Qy   1982  CTGGAGGCCACTGAGAAGCTCTTACGTTACGTATGCCCAGACTCAAGGCACCAGCAGGAGGAAGAAG   2041
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Left column (continued alignment):

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Db   2313  CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAGAAGAAAG  2372
Qy   2042  TCATTCAGACTGAGTGAGGAAAATGCCCTGTCTGCGAAGAACGCCTTGAGTATGCCCTTG   2101
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2373  TCATTCAGACTGAGTGAGGAAAATGCCCTGTCTGCGAAGAACGCCTTGAGTATGCCCTTG   2432
Qy   2102  TGAAGGGCATTGAAAAACATATTATTGAGGAGGAACAGTTAAACCAAAAA            2161
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   2433  TGAAGGGCATTGAAAAACATATTATTGAGGAGGAACAGTTAAACCAAAAA            2492
Qy   2162  AATATCCCGACCTCTCAATATAATTGAAGAGACCCCTGATGAATGAAAATGTTTG        2221
           ||||||||||||||||-|||||||||||||||||||||||||||||||||||
Db   2493  AATATCCCGACCTCTCAATATAATTGAAGAGACCCCTGATGAATGAAAATGTTTG        2552
Qy   2222  GTGATCTTTTGGAGCTGGAAAAATGTTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTTA   2281
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2553  GTGATCTTTTGGAGCTGGAAAAATGTTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTTA   2612
Qy   2282  TGAAGAAGGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAGAAGAAACCAGAG      2341
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2613  TGAAGAAGGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAGAAGAAACCAGAG      2672
Qy   2342  TGCTTAAACGGCACAGTAGAAGAAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTG   2401
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2673  TGCTTAAACGGCACAGTAGAAGAAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTG   2732
Qy   2402  TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA   2461
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2733  TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA   2792
Qy   2462  ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGAACTGAAAAGCTGCTC   2521
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2793  ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGAACTGAAAAGCTGCTC   2852
Qy   2522  TTGACCACACAAAGCAGATAATAATTGGCCTGTCTCAGGACTCATCACTCCTTCCCTGATGAAA  2581
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2853  TTGACCACACAAAGCAGATAATAATTGGCCTGTCTCAGGACTCATCACTCCTTCCCTGATGAAA  2912
Qy   2582  TGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTGATTGGAG   2641
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2913  TGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTGATTGGAG   2972
Qy   2642  GAGCAACCACTTCAAAAACCCACACAGTTAAAATAGCTCCGAGATACAGTGCCACCTG    2701
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2973  GAGCAACCACTTCAAAAACCCACACAGTTAAAATAGCTCCGAGATACAGTGCCACCTG    3032
Qy   2702  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGTTCCCAGCTGTTAGATGAAA         2761
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   3033  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGTTCCCAGCTGTTAGATGAAA         3092
Qy   2762  ATCTAAAGGATGAATACTTTGAGGAAAATCATGAAGAATATTAGACAGAGACC        2821
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   3093  ATCTAAAGGATGAATACTTTGAGGAAAATCATGAAGAATATTAGACAGAGAGNCC       3152
Qy   2822  ATTATGAGTCTTCAAGGAGGAGAGAGTACTTACCCTTAAGTCAAGCCCAGAAAAAGTGGTT  2881
           |||||||||||||||||||||||||||||||||||||||||| ||||
Db   3153  ATTATGAGTCTTCAAGGAGGAGAGAGTACTTACCCTTAAGTCAAGCCCAGAAAAANTNGTT  3212
Qy   2882  TCCAAATGGATTGGCTGTCTGAACCTGCAGAAGCTGGTCAGCATTGGAGGACCCCAGG     2941
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3213  TCCAAATGGATTGGCTGTCTGAACCTGCAGAAGCTGGTCAGCATTGGGAGGACCCCAGG    3272
Qy   2942  TCTTTGAAGACTATGACCTGCAGAAGCTGGTCGGACTACATTGACTGGAAGCCTTTCTTTG  3001
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3273  TCTTTGAAGACTATGACCTGCAGAAGCTGGTCGGACTACATTGACTGGAAGCCTTTCTTTG  3332
Qy   3002  ATGTCTGGCAGCTCCGGGGCAAGTACCCCGAATCGAGGCTTCCCCAAGATATTTAACCACA  3061
           ||||||||||||||||||||||||||||||||||||||||||||
Db   3333  ATGTCTGGCAGCTCCGGGGCAAGTACCCCGAATCGAGGCTTTCCCAAGATATTTAACGACA  3392
Qy   3062  AAACAGTAGGTCGAGAGGCCAGGAAGGTTCTACGATGATGCCCACAATATGTGAACACAC   3121
           ||||||||||||||||||||||||||||||||||||||||||||
Db   3393  AAACAGTAGGTCGAGAGGCCAGGAAGGTTCTACGATGATGCCCACAATATGTGAACACAC   3452
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Right column (continued alignment):

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Qy   3122  TGATTAGTTCAAAAGAAACTCCGGGCCCCGGGGTGGGTGGTTCTCGCCAGCACAGAGTA   3181
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3453  TGATTAGTTCAAAAGAAACTCCGGGCCCCGGGGTGGGTGGTTCTCGCCAGCACAGAGTA   3512
Qy   3182  TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCAGGCTGCAGAGCCCCATAG   3241
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Db   3513  TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCAGGCTGCAGAGCCCCATAG   3572
Qy   3242  CCACTTTCTATGGTTAAGGCAACAGCTGAGAAGGACTCTGCCAGCACGGAGCCATACT   3301
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3573  CCACTTTCTATGGTTAAGGCAACAGCTGAGAAGGACTCTGCCAGCACGGAGCCATACT   3632
Qy   3302  ACTGCCTCTCAGACTTCATCGTCCTGCATTCTGGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3361
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3633  ACTGCCTCTCAGACTTCATCGTCCTGCATTCTGGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3692
Qy   3362  TTGCCGTTGCCTGCTTTGGGTAGAGAGCTGAGCAAGGCTCATGAGGATGATGGTGACG   3421
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3693  TTGCCGTTGCCTGCTTTGGGTAGAGAGCTGAGCAAGGCTCATGAGGATGATGGTGACG   3752
Qy   3422  ACTACAGCAGCATCATGTCAAGGCGCTGGGGGACCGGCTGCGCAGACCGGCCCTTTGCAGAAG  3481
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3753  ACTACAGCAGCATCATGTCAAGGCGCTGGGGGACCGGCTGGGCAGACCGGCCCTTTGCAGAAG  3812
Qy   3482  AGCTCCATGAAAGAGTTCGCCGAGAACTGTGCCCTACTGTCTGCAGTGAGCAGCTGGACG   3541
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3813  AGCTCCATGAAAGAGTTCGCCGAGAACTGTGCGGCCTACTGTGTGGCAGTGAGCAGCTGGACG   3872
Qy   3542  TCGCAGACCTGCGAGGTTGCGTACAAGGGCATCCGCCGGTCTCGGCTACACCCCAGCC    3601
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Db   3873  TCGCAGACCTGCGAGGTTGCGTACAAGGGCATCCGCCGGTCTCGGCTACACCCCAGCC    3932
Qy   3602  AGCCCGACCACCACCGAGAAGTCACCGAGACTGCGCAGACATCGAGCAGTCTCACAG   3661
           ||||||||||||||||||||||||||||||||||||||||||||
Db   3933  AGCCCGACCACCACCGAGAAGTCACCGAGACTGCGCAGACATCGAGCAGTCTCACAG   3992
Qy   3662  GCATTAGGTTAACAGAATCATTAGCAATGGCCACCTGCTTCAGCGGCCTCTACT       3721
           |||||||||||||||||||||||||||||||||||||||||||||
Db   3993  GCATTAGGTTAACAGAATCATTAGCAATGGCCACCTGCTTCAGCGGCCTCTACT       4052
Qy   3722  TCTCCAATTGAAGTCCAAATATTTTGCGTGTGGGAAGATTTCCAAGGATCAGGTTGAGG    3781
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   4053  TCTCCAATTGAAGTCCAAATATTTTGCGTGTGGGAAGATTTCCAAGGATCAGGTTGAGG    4112
Qy   3782  ATTATGCATTGAGGAAGAACATATCTGGCTGAGGTTGAGAAATGCCTTGAGACCCATTT   3841
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   4113  ATTATGCATTGAGGAAGAACATATCTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT    4172
Qy   3842  TGGGATATGATGATACAGACTAACTTTTTTTTTTTTTTTTTATCTTGATGATCCT      3901
           ||||||||||||||||||||||||||||||| |||
Db   4173  TGGGATATGATGATACAGACTAAC--TTTTTTTTTTTTTTTTTTATTCTTGATGATCCT   4230
Qy   3902  CAAGGAAATACAACCTAG                                            3919
           ||||||||||||||||||
Db   4231  CAAGGAAATACAACCTAG                                            4248
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;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 09/357,743
;  PRIOR FILING DATE: 1999-07-20
;  PRIOR APPLICATION NUMBER: 09/357,024
;  PRIOR FILING DATE: 1999-07-19
;  PRIOR APPLICATION NUMBER: 60/093,484
;  PRIOR FILING DATE: 1998-07-20
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn for Windows Version 4.0

SEQ ID NO 1
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  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: misc_feature
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  OTHER INFORMATION: n = c or g
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  OTHER INFORMATION: n = c or a
US-09-963-333-1

Query Match       98.9%;  Score 3876.2;  DB 3;  Length 7224;
Best Local Similarity  99.4%;  Pred. No. 0;
Matches 3896;  Conservative  0;  Mismatches  20;  Indels  2;  Gaps  1;
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Right column:

Qy 2762 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAATATTAGACAGACC 2821
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Db 3093 ATCTAAAGGATGAATACTTTGAGGAGAAATCATGGAAGAATATGAAGAATATTAGACAGGNCC 3152

Qy 2822 ATTATGAGTCTCTCAAGGAGGAGGAGAGATACTTACCCTTAAGTCAAGCCCAGTTGTT 2881
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Db 3153 ATTATGAGTCTCTCAAGGAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAANTNGTT 3212

Qy 2882 TCCAAATGGATTGGCTCTGTCGAACCTGAACCTCACCCAGTGAAGCCCACGTTATTGGACCCAGG 2941
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3213 TCCAAATGGATTGGCTCTGTCGAACCTGAACCTCACCCAGTGAAGCCCACGTTATTGGGACCCAGG 3272

Qy 2942 TCTTTGAAGACTATGACCTGGTGGTGACTACATTGACTGGAAGCCTTTCTTTG 3001
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Db 3273 TCTTTGAAGACTATGACCTGCGACAGAAGCTGGTGGGTGACTACATTGACTGGGAAGCCTTTCTTTG 3332

Qy 3002 ATGTCTGCAGCTCCGGGCAAGTGACCTCCCAAGAATCGGAGGCTTCCCCAAGATATTTAACGACA 3061
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Db 3333 ATGTCTGCAGCTCCGGGCAAGTGACCCCGGGCAAGTACCCGAAGATCGGAGCGCTTCCCAAGATATTTAACGACA 3392

Qy 3062 AAACAGTAGGTGAGAGCCAGGAAGTCTACGATGGCCACACAC 3121
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Db 3393 AAACAGTAGGTGAGAGCCAGGAAGTCTACGATGATGCCCACAAATGCTGAACACAC 3452

Qy 3122 TGATTAGTCAAAAGAAACTCCCGGGCCCGGGTGTGGTTGGGTTCTGCCAGCACAGAGTA 3181
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Db 3453 TGATTAGTCAAAAGAAACTCCCGGGCCCGGGTGTGGTTGGGTTCTGGCCAGCACAGAGTA 3512

Qy 3182 TCCAAGACGACATTCACCTGTACGCGGAGGCTGCGTGTGCCCCAGGCTGCCAGAGGCCCCATAG 3241
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Db 3513 TCCAAGACGACATTCACCTGTACGCGGAGGCTGCGTGTGCCCCAGGCTGCCAGAGGCCCCATAG 3572

Qy 3242 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGCTGAGAAGACTCTGCCAGCAGAGCCATACT 3301
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Db 3573 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGCTGAGAAGACTCTGCCAGCAGAGCCATACT 3632

Qy 3302 ACTGCCTCTCAGACTTCATCGCTCCCCTTGCATTCTCGGCATCCGCTCGGCATCCTCGGCGTCTGT 3361
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Db 3633 ACTGCCTCTCAGACTTCATCGCTCCCCTTGCATTCTCGGCATCCGCTCGGCATCCGCTCGGCGTCTGT 3692

Qy 3362 TTGCCGTTGCGCTGCTTTGGGGTAGAAGCTGAGAGCTGCAAGGCCTATGAGGATGATGGTGACG 3421
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Db 3693 TTGCCGTTGCGCTGCTTTGGGGTAGAAGCTGAGAGCTGCAAGGCCTATGAGGATGATGGTGACG 3752

Qy 3422 ACTACAGACAGCATCATGTCAAGGCGCGTCGGGGGCGCGGCTGGCGCTGGCCGGCACCGCGGCTTTGCGAGAG 3481
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Db 3753 ACTACAGACAGCATCATGTCAAGGCGCGTCGGGGGCGCGGCTGGCGCTGGCCGGCACCGCGGCTTTGCGAGAG 3812

Qy 3482 AGCTCCATGAAAAGAGTTCGCCGAGAACTGTGGGCCGCTACTGTGCAGTGAGCAGCTGGACG 3541
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Qy 3542 TCGCAGAGCCTGCGGAGGTTGCGGTACACAGGGCATCCCGCCTCCTGGCTCACCCCAGCC 3601
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Qy 3602 AGCCCGACCACCACCGAGAGCTCGAGACTCGAGACTCACCATGTGGATGAACATCGACAGTCTCAGG 3661
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Db 3933 AGCCCGACCACCACCGAGAGCTCGAGACTCGAGAACTGCGATCGGAACATCGACAGTCTCAGG 3992

Qy 3662 GCATTAGGTTAACAGAATCATTAGACAATATTTTCGTCGTGGGGAAGAGAATTCCAAGGATCAGGTTGAGG 3721
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Db 3993 GCATTAGGTTAACAGAATCATTAGACAATATTTTCGTCGTGGGGAAGAGAATTCCAAGGATCAGGTTGAGG 4052

Qy 3722 TCTCCAATTGAAGTCCAAAATATTTGCGTGGGGGAAGTTCCAAGGATCAGGTTGAGG 3781
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Db 4053 TCTCCAATTGAAGTCCAAAATATTTTGCGTGGGGGAAGTTCCAAGGATCAGGTTGAGG 4112

Qy 3782 ATTATGCATTGAGGAAGAACATATCTGTGGCTTGGAGGTTGAGAAATGGCTTGAGACCCATTT 3841
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Db 4113 ATTATGCATTGAGGAAGAACATATCTGTGGCTTGGAGGTTGAGAAATGGCTTGGAGACCCATTT 4172

Qy 3842 TGGGATATGATACAGACTAACTTTTTTTTTTTTTGCCTTTTTATCTTGATGATCCT 3901

Left column:

Qy 1682 TCCTAACCATTGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATG 1741
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2013 TCCTAACCATTGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATG 2072

Qy 1742 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 1801
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Db 2073 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 2132

Qy 1802 TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCGTGGGGTTTCCTTT 1861
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2133 TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCGTGGGGTTTCCTTT 2192

Qy 1862 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAAGTCTGAAACGTGCCCCTGTGT 1921
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Db 2193 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAAGTCTGAAACCTCCCTGTGT 2252

Qy 1922 ATGATGATATCCATAAGAACTTCTGCAGCTTGTGAAGATCTCATCTGGAATAAAGACC 1981
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Db 2253 ATGATGATATCCATAAGAACTTCTGCAGCTTGTGAAGATCTCATCTGGAATAAAGACC 2312

Qy 1982 CTGAGGCCACTGAGAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGGAGGAAGAAAG 2041
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Db 2313 CTGAGGCCACTGAGAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGGAGGAAGAAAG 2372

Qy 2042 TCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCGTTGAGTATGCCCCTTG 2101
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Db 2373 TCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCGTTGAGTATGCCCCTTG 2432

Qy 2102 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAA 2161
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Db 2433 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAA 2492

Qy 2162 AATATCCCCGACCTCTCAATAATTGAAGGACCCCTGATGAATGAAAATTGTTG 2221
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Db 2493 AATATCCCCGACCTCTCAATAATTGAAGGACCCCTGATGAATGAAAATTGTTG 2552

Qy 2222 GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
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Db 2553 GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2612

Qy 2282 TGAAGAAGGCTGTTGCCACCTTATCCCTTTCATGGAAAAAGAAGAAACCAGAG 2341
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Db 2613 TGAAGAAGGCTGTTGCCACCTTATCCCTTTCATGGAAAAAGAAGAAACCAGAG 2672

Qy 2342 TGCTTAACGGCACAGTAGAAGAGAGAGACCCTTACCAGGGCACCATCGTCGTGGCCACTG 2401
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Db 2673 TGCTTAACGGCACAGTAGAAGAGAGAGACCCTTACCAGGGCACCATCGTCGTGGCCACTG 2732

Qy 2402 TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTCCTTGGCTGCAATA 2461
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Db 2733 TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTCCTTGGCTGCAATA 2792

Qy 2462 ATTTCCGAGTTATTGATTTAGGAGTCATGAGCTCCATGTGAATAAGATACTGAAAGCTGCTC 2521
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Db 2793 ATTTCCGAGTTATTGATTTAGGAGTCATGAGCTCCATGTGAATAAGATACTGAAAGCTGCTC 2852

Qy 2522 TTGACCACAAAGCAGATATAATTGGGCCTGTCAGGACTCATCATCCCTGGATGAAA 2581
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Db 2853 TTGACCACAAAGCAGATATAATTGGGCCTGTCAGGACTCATCATCCCTGGATGAAA 2912

Qy 2582 TGATTTTGTTGCCAAGGAAATGGCCAAGAAATGGCCAAGTATTAGGAGAGATTAGTATAAGGATTGATTGGAG 2641
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2913 TGATTTTGTTGCCAAGGAAATGGCCAAGGAAATGGCCAAGTATTAGGAGAGATTAGTATAAGGATTGATTGGAG 2972

Qy 2642 GAGCAACCACTTCAAAAACCCCAAGACGCGTCCAAGAGTGTTGGTGGTGTGTTCCGAGATACAGTGCACCTG 2701
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Db 2973 GAGCAACCACTTCAAAAACCCCAAGACGCGTCCAAGAGTGTTGGTGGTGTGTTCCGAGATACAGTGCACCTG 3032

Qy 2702 TAATCCATGTCCTGGACGCGGTTCCCAAGAGTGTTCCCAAGCTTGTTAGATGAAA 2761
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3033 TAATCCATGTCCTGGACGCGGTTCCCAAGAGTGTTCCCAAGCTTGTTAGATGAAA 3092

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Db  4173 TGGGATGATGATACAGACTAAC--TTTTTTTTTTTTGCCTTTTTTATTCTTGATGATCCT 4230
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Qy  3902 CAAGGAAATACAACCTAG 3919
              |||||||||||||||||
Db  4231 CAAGGAAATACAACCTAG 4248
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RESULT 8
US-09-962-677-1
; Sequence 1, Application US/09962677
; Patent No. 6759200
; GENERAL INFORMATION:
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: THYMIDINE PHOSPHORYLASE GENE SEQUENCE
; TITLE OF INVENTION: VARIANCES HAVING UTILITY IN DETERMINING
; TITLE OF INVENTION: THE TREATMENT OF DISEASE
; FILE REFERENCE: 11926-015003
; CURRENT APPLICATION NUMBER: US/09/962,677
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/658,659
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/596,033
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/357,743
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/357,024
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 60/093,484
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 194, 3209
; OTHER INFORMATION: n = c or g
; NAME/KEY: misc_feature
; LOCATION: 1136, 1334, 3150, 5551, 5934
; OTHER INFORMATION: n = a or g
; NAME/KEY: misc_feature
; LOCATION: 284, 1252, 1699, 5573, 5659, 5678, 5874
; OTHER INFORMATION: n = c or t
; NAME/KEY: misc_feature
; LOCATION: 3207
; OTHER INFORMATION: n = g or t
; NAME/KEY: misc_feature
; LOCATION: 5444
; OTHER INFORMATION: n = c or a
US-09-962-677-1

Query Match   98.9%; Score 3876.2; DB 3; Length 7224;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 3896; Conservative 0; Mismatches 20; Indels 2; Gaps 1;

Qy   2 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCTCTGCCGCAAGGAGGAGACTCGACA 61
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   333 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCTCTGCCGCAAGGAGGAGACTCGACA 392

Qy   62 ACATGTCACCCGGCCTCCAAGACCTGTCGCAACCTGTGCTGGAGGTCTGAAGAAAACCTGGGG 121
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Db   393 ACATGTCACCCGGCCTCCAAGACCTGTCGCAACCTGTGCTGGAGGTCTGAAGAAAACCCTGCGGG 452

Qy   122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGAATTAAAGATCATG 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   453 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGAATTAAAGATCATG 512

Qy   182 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTCCGAGGTCAGGAATTTAAAGATCATG 241
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Qy   242 CCAGGCGCGCTGAAAGGCAACAATGACATTTAAGTATAAACTCAGCCTGATGTCATTACC 301
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Db   573 CCAGGCGCCCTGAAAGGCAACAATGACATTTAAGTATAAACTCAGCCTGATGTCATTACC 632

Qy   302 AAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA 361
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Db   633 AAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA 692

Qy   362 GCACTAGTATTGCCCAAGCTGACTATGGCCTGAACACTTGGCCTACCGGATGAACATGT 421
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Db   693 GCACTAGTATTGCCCAAGCTGACTATGGCCTGAACACTTGGCCTACCGGATGAACATGT 752

Qy   422 GCTCTGCGAGGAGTGGCCAGAAAAGCTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGA 481
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Db   753 GCTCTGCGAGGAGTGGCCAGAAAAGCTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGA 812

Qy   482 GGTTGTTGCGAGGGGCTCTGGGGTTCGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGG 541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   813 GGTTGTTGCGAGGGGCTCTGGGGTTCGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGG 872

Qy   542 AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGGAAGCATACCAAGAGACAGG 601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   873 AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGGAAGCATACCAAGAGACAGG 932

Qy   602 CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG 661
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Qy   662 CCAATGCCAAGGCAGCCGCCTGTTGCACTCCAAAATCTTTTGATAAAAGTGGGGCGGACTCTTCCGGACAGA 721
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Db   993 CCAATGCCAAGGCAGCCGCCTGTTGCACTCCAAAATCTTTTGATAAAAGTGGGGCGGACTCTTCCGGACAGA 1052

Qy   722 GGCCTATCTTATTTCAGGAGGACGATCGTTGATAAAGTGGGGCGGACTCTTCCGGACAGA 781
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Db  1053 GGCCTATCTTATTTCAGGAGGACGATCGTTGATAAAGTGGGGCGGACTCTTCCGGACAGA 1112

Qy   782 CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGGAGACCACTCTGCATTGATTAAATT 841
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Db  1113 CAGGAGAGGGATTTGTCATCAGCNTGTCATCAGNTGTCATGGGAGACCACTCTGCATTGGATTAAATT 1172

Qy   842 GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG 901
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Db  1173 GTGCTTTGGGTGCAGCTGAAATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG 1232

Qy   902 CCTATGTCCTCGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA 961
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Db  1233 CCTATGTCCTCGTTATCCNAATGCAGGTCTTCCNAACACCTTTGGTGACTATGATGAAA 1292

Qy   962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCATATAG 1021
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1293 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGNATGGCTATGNATGGCTTGGTCAATATAG 1352

Qy  1022 TTGGAGGATGCGTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1081
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Db  1353 TTGGAGGATGCGTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1412

Qy  1082 ATTGTAAGCCTAGAGTTCCACCTGCTTTGAAGGACATATGTTACTGTCTGGTC 1141
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Db  1413 ATTGTAAGCCTAGAGTTCCACCTGCTTTGAAGGACATATGTTACTGTCTGGTC 1472

Qy  1142 TAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTAATG 1201
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Qy  1202 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGT 1261
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Db  1533 TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGT 1592

Qy  1262 GTGTTGCCAAAGTGCAGGTGGAAATGGGAGGCCCAGGTGTTGGATGTGTCAACATGGATGATG 1321
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Qy 2733 TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCGCAATA 2792
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Qy 2462 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTC 2521
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Db 2793 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTC 2852

Qy 2522 TTGACCACAAAGCAGATATAATTGGCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA 2581
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Db 2853 TTGACCACAAAGCAGATATAATTGGCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA 2912

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Qy 2642 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 2701
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Qy 2702 TAATCCATGTCTCTGGACGCGTCCAAGAGTGTTGGTGTGTTCCCAGCTGTTGTAGATGAAA 2761
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Db 3033 TAATCCATGTCTCTGGACGCGTCCAAGAGTGTTGGTGTGTTCCCAGCTGTTGTAGATGAAA 3092

Qy 2762 ATCTAAAGGATGAATACTTGAGGAGAGGAAATCATGGAGAGATATGAAGATATTAGACAGGACC 2821
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Db 3093 ATCTAAAGGATGAATACTTGAGGAGAGGAAATCATGGAGAGATATGAAGATATTAGACAGGNCC 3152

Qy 2822 ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGTT 2881
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Qy 2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGGTGCTACATTGACTGGAGCCTTCCTTG 2941
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Db 3213 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGGTGCTACATTGACTGGAGCCTTCCTTG 3272

Qy 2942 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGCTACATTGACTGGAAGCCTTTCTTTG 3001
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Db 3273 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGCTACATTGACTGGAAGCCTTTCTTTG 3332

Qy 3002 ATGTCTGCAGCTCCGGGCAAGTCACCCGAGCTGGGCTTTCCCAAGATATTTAACGACA 3061
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Db 3333 ATGTCTGCAGCTCCGGGCAAGTCACCCGAGCTGGGCTTTCCCAAGATATTTAACGACA 3392

Qy 3062 AAACAGTAGGTGGAGAGCCAGGAAGTCTACGAGGAAGTGCCACATGATGCCAACACAC 3121
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Db 3393 AAACAGTAGGTGGAGAGCCAGGAAGTCTACGAGGAAGTGCCACATGATGCCAACACAC 3452

Qy 3122 TGATTAGTCAAAAGAAAACTCCGGGTGTGGTTGGGTGTCTGGCCAGCACAGAGTA 3181
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Db 3453 TGATTAGTCAAAAGAAAACTCCGGGTGTGGTTGGGTGTCTGGCCAGCACAGAGTA 3512

Qy 3182 TCCAAGACGACATTCACCTGTACGGAGGAGGCTGCTGTGCCCAGGCTGCGAAGGCCCATAG 3241
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3513 TCCAAGACGACATTCACCTGTACGGAGGAGGCTGCTGTGCCCAGGCTGCGAAGGCCCATAG 3572

Qy 3242 CCACTTTCTATGGGTTAAGGCAACAGGCGCTGAGGAAGGAAGGAGACTCTGCCAGCACGGAGCCATACT 3301
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Db 3573 CCACTTTCTATGGGTTAAGGCAACAGGCGCTGAGGAAGGAAGGAGACTCTGCCAGCACGGAGCCATACT 3632

Qy 3302 ACTGCCCTCCAGACTTCATCGCTTCAGATTCTCGGCATCGGACTACCTGGGCCTGT 3361
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Db 3633 ACTGCCCTCCAGACTTCATCGCTTCAGATTCTCGGCATCGGACTACCTGGGCCTGT 3692

Qy 3362 TTGCCGGTTGCCTGCCTGCTTTGGGGTTAGAAGAGCTGAGCAAGGCCTATGAGGAGGTGACG 3421
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3693 TTGCCGGTTGCCTGCCTGCTTTGGGGTTAGAAGAGCTGAGCAAGGCCTATGAGGAGGTGACG 3752

Qy 3422 ACTACAGCAGCATCATGGTCAAGGCGCTCGGGGGACCCGCTCGGGGGACCGGGCCTTTGCAGAAG 3481
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Db 3753 ACTACAGCAGCATCATGGTCAAGGCGCTCGGGGGACCCGCTCGGGGGACCGGGCCTTTGCAGAAG 3812

Qy 3482 AGCTCCATGAAAGAGTTCGCCAGAACGTGTGGCCTACTGTGCGAGCACGTGACG 3541
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Qy 1322 GCATGCTAGATGGTCCAAGTGCAACTTAATTGCTTCCGAGCCAG 1381
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Qy 1382 ACATCCGAAAGTACCTTGTGCATGCATCCTCTCCAATTTGCTGTGATTGAAGCTGGGT 1441
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Db 1713 ACATCCGAAAGTACCTTGTGCATGCATCCTCTCCAATTTGCTGTGATTGAAGCTGGGT 1772

Qy 1442 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGGACG 1501
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Db 1773 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGGACG 1832

Qy 1502 ACTTCTTGGAGAAGGGCCAGGAAGATTAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1561
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Db 1833 ACTTCTTGGAGAAGGGCCAGGAAGATTAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1892

Qy 1562 TTGATGAAGAGGACAGGCAACAGAACAGGCAACAGAAAATCAGAGTGTGCACCCCGGGCCT 1621
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Db 1893 TTGATGAAGAGGACAGGCAACAGAACAGGCAACAGAAAATCAGAGTGTGCACCCCGGGCCT 1952

Qy 1622 ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATA 1681
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Db 1953 ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATA 2012

Qy 1682 TCCTAACCATTGGGACTGGAATGGAGGAACAACAACTGTATGCCATTAATTTTATCCATG 1741
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Db 2013 TCCTAACCATTGGGACTGGAATGGAGGAACAACAACTGTATGCCATTAATTTTATCCATG 2072

Qy 1742 CAACAAAAGTCATTAAAGAAGAAACATTACCTGGAGCCAGAATAAGTCAATGCAATGCAATG 1801
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Qy 1802 TGTCCTTCTCCTTCCGAGGAATGGAAGCAATGCAATGCAATGTGGGTTTTCTTT 1861
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2133 TGTCCTTCTCCTTCCGAGGAATGGAAGCAATGCAATGCAATGTGGGTTTTCTTT 2192

Qy 1862 ACCATGCAATCAAGTCTGGCATGACATGGAGAGTAGTGAATGCTGGAAACCTCCCTGTGT 1921
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Db 2193 ACCATGCAATCAAGTCTGGCATGACATGGAGAGTAGTGAATGCTGGAAACCTCCCTGTGT 2252

Qy 1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGAAGTAAAGACC 1981
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Db 2253 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGAAGTAAAGACC 2312

Qy 1982 CTGAGGCCACTGAGAGAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAAG 2041
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2313 CTGAGGCCACTGAGAGAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAAG 2372

Qy 2042 TCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCCAAGAACGCCTTGAGTATGCCCTTG 2101
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Qy 2102 TGAAGGGCATTGAAAAACATATTATTATGAGGATGAGGAGCCAGTTAAACCAAAAAA 2161
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Db 2433 TGAAGGGCATTGAAAAACATATTATTATGAGGATGAGGAGCCAGTTAAACCAAAAAA 2492

Qy 2162 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAAATGTTG 2221
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Db 2493 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAAATGTTG 2552

Qy 2222 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTGTTATAAAGTTCAGCCCGGGTTA 2281
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Db 2553 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTGTTATAAAGTTCAGCCCGGGGTTA 2612

Qy 2282 TGAAGGAGGCTGTTGGCCACCTTCATCCCTTTCATGGAAAAAGAAGAGAAGAACCAGAG 2341
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Db 2613 TGAAGGAGGCTGTTGGCCACCTTCATCCCTTTCATGGAAAAAGAAGAGAAGAACCAGAG 2672

Qy 2342 TGCTTAACGGCACCAGTAGAAGAGGACACCGTACCAGGGACCACCATCGTGCTGGCCACTG 2401
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Db 2673 TGCTTAACGGCACCAGTAGAAGAGGACACCGTACCAGGGACCACCATCGTGCTGGCCACTG 2732

Qy 2402 TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCGCAATA 2461

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Db 3813 AGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGCAGTGAGCAGCTGGACG 3872
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Qy  124 GAGATCAATGCCATTCTGCAGAGAGAGGATTATGGTGTCGGATGGAGGGATGGGACCATG 183
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Db   61 GAGATCAATGCCATTCTGCAGAGAGAGGATTATGGTGTCGGATGGAGGGATGGGACCATG 120

Qy 3542 TCGCAGACCTGCGGAAGGTTGCGGTACAAGGGCATCCGCCGGCTCCTGGCGTACCCCAGCC 3601
        ||||||||||||||  |||| |||||||||||||||||||||||||||| |||||||||||
Db 3873 TCGCAGACCTGCGCGCAGCGCGGGTACAAGGGCATCCGCCGGCTCCTGGCTACCCCAGCC 3932
Qy  184 ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATGCC 243
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATGCC 180

Qy 3602 AGCCGACCACCACCACGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACAG 3661
        |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db 3933 AGCCCGACCACCACCACGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACAG 3992
Qy  244 AGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACCAA 303
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Db  181 AGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACCAA 240

Qy 3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCCGTCTCAGGCCCTCTACT 3721
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3993 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCCGTCTCAGGCCCTCTACT 4052
Qy  304 ATCCATAAGGAATACTTGCTGGCTGGGGCAGATCATTGAAACAAATACTTTTAGCAGC 363
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATCCATAAGGAATACTTGCTGGCTGGGGCAGATCATTGAAACAAATACTTTTAGCAGC 300

Qy 3722 TCTCCAATTTGAAGTCCAAAATATTTTGCTGTGTGGGGAGATTTCCAAGGATCAGGTTGAGG 3781
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4053 TCTCCAATTTGAAGTCCAAAATATTTTGCTGTGTGGGGAGATTTCCAAGGATCAGGTTGAGG 4112
Qy  364 ACTAGTATTGCCCAAGCTGACTATGGCCTTGACACTTGGCCTACCGGATGAACATGTGC 423
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Db  301 ACTAGTATTGCCCAAGCTGACTATGGCCTTGACACTTGGCCTACCGGATGAACATGTGC 360

Qy 3782 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAAATGGCTTGACCCATTT 3841
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4113 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAAATGGCTTGACCCATTT 4172
Qy  424 TCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGTAACTCTCCAGGACAGGAATTAAGAGG 483
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGTAACTCTCCAGGACAGGAATTAAGAGG 420

Qy 3842 TGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTTGCCTTTTATTCTTGATGATCCT 3901
        ||||||||||||||||||||  |||||||||||  |||||||||||||||||||||||||
Db 4173 TGGGATATGATACAGACTAAC--TTTTTTTTTTATTCTTGATGATCCT 4230
Qy  484 TTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGGAA 543
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 TTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGGAA 480

Qy 3902 CAAGGAAATACAACCTAG 3919
        ||||||||||||||||||
Db 4231 CAAGGAAATACAACCTAG 4248
Qy  544 AGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCC 603
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCC 540

Qy  604 AAAGGACTTCGGATGGCGGGGTTGATATCTTCACTCATTGAAATCTATTTTTGATACTGCC 663
        ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AAAGGACTTCTGGATGGCGGGGTTGATATCTTCACTCATTGAAATCTATTTTTGATACTGCC 600

Qy  664 AATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTTGAGGAGAAAATATGCTCCCCGG 723
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 AATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTTGAGGAGAAAATATGCTCCCCGG 660

Qy  724 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGACA 783
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGACA 720

Qy  784 GGAGAGGATTTGTCATCAGCGTGTCTCATGAGAACCACTCTGCATTGGATTAAATTGT 843
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 GGAGAGGATTTGTCATCAGCGTGTCTCATGAGAACCACTCTGCATTGGATTAAATTGT 780

Qy  844 GCTTTGGGTGCAGTGAGATGAGACCTTTATTGAAATAATTGAAAATGTACAACAGCC 903
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GCTTTGGGTGCAGTGAGATGAGACCTTTATTGAAATAATTGAAAATGTACAACAGCC 840

Qy  904 TATGTCCTGTTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAACG 963
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 TATGTCCTGTTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAACG 900

Qy  964 CCTTCTATGATGGCCAAGCACCTGAAAGGATTTGCTATGGATGGCTTGTGAAGCTGTCAATATAGTT 1023
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 CCTTCTATGATGGCCAAGCACCTGAAAGGATTTGCTATGGATGGCTTGTGAAGCTGTCAATATAGTT 960

Qy 1024 GGAGGATGCGTGTGGTCAACACGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1083
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 GGAGGATGCGTGTGGTCAACACGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1020

Qy 1084 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACACATATGTTACTGCTGGTCTA 1143
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACACATATGTTACTGCTGGTCTA 1080

Qy 1144 GAGCCCTTCAGGATTGGACCGTACCAACTTGTTAACATTGGAGAGCGCCTGTAATGTT 1203
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 GAGCCCTTCAGGATTGGACCGTACCAACTTGTTAACATTGGAGAGCGCCTGTAATGTT 1140

Qy 1204 GCAGGATCAAGGAAGTTTGCTAAACTCATCATGCGAGAAACTATGAAGAAGCCTTGTGT 1263
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GCAGGATCAAGGAAGTTTGCTAAACTCATCATGCGAGAAACTATGAAGAAGCCTTGTGT
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RESULT 9
US-08-980-326-75
; Sequence 75, Application US/08980326
; Patent No. 6703197
GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 75
; LENGTH: 3856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(1265)
; OTHER INFORMATION: Coding sequence for mutant methionine synthases:
; OTHER INFORMATION: 2640-2642 can be AAT or deleted;2756 can be A or
; OTHER INFORMATION: G;2758 can be C or G.
US-08-980-326-75

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Query Match     98.3%;  Score 3851;  DB 3;  Length 3856;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 3851;  Conservative  0;  Mismatches  5;  Indels  0;  Gaps  0;

Qy  64 ATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGGAT 123
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGGAT  60
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Db  1141 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1200
Qy  1264 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATGGC 1323
Db  1201 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATGGC 1260

Qy  1324 ATGCTAGAATGGTCCAAGTGCAATGCAACCAGAGATTTGCAACTTAATTGCTTCCGAGCCAGAC 1383
Db  1261 ATGCTAGAATGGTCCAAGTGCAATGCAACCAGAGATTTGCAACTTAATTGCTTCCGAGCCAGAC 1320

Qy  1384 ATCCGCAAAGGTACCTTTGTGCATCGCAACTCCTCCAATTTGCTGTGATTGAAGCTGCTCTT 1443
Db  1321 ATCCGCAAAGGTACCTTTGTGCATCGCAACTCCTCCAATTTGCTGTGATTGAAGCTGCTCTT 1380

Qy  1444 AAGTGCTGCCAAGGGAGTGCATTGTCAATAGCATTAGTGCTGAAGGAAGAGAGAGACGAC 1503
Db  1381 AAGTGCTGCCAAGGGAGTGCATTGTCAATAGCATTAGTGCTGAAGGAAGAGAGAGACGAC 1440

Qy  1504 TTCTTGGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGTGGTCATGGCTTTT 1563
Db  1441 TTCTTGGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGTGGTCATGGCTTTT 1500

Qy  1564 GATGAAGAGGACAGGCCAACACAGAACAGAAAATCAGAGTGTGCACCCGGCCTAC 1623
Db  1501 GATGAAGAGGACAGGCCAACACAGAACAGAAAATCAGAGTGTGCACCCGGCCTAC 1560

Qy  1624 CATCTGCTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATATC 1683
Db  1561 CATCTGCTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATATC 1620

Qy  1684 CTAACCATTGGGACTGGAATGAGGAGGAACAACTTGTATGCCATTAATTTTATCCATGCA 1743
Db  1621 CTAACCATTGGGACTGGAATGAGGAGGAACAACTTGTATGCCATTAATTTTATCCATGCA 1680

Qy  1744 ACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGTCTTTCCAACTTG 1803
Db  1681 ACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGTCTTTCCAACTTG 1740

Qy  1804 TCCTTCTCCTTCCGGAGAATGGAAGCCATTCGAGAAGCAATGCATGGGTTTTCCTTTAC 1863
Db  1741 TCCTTCTCCTTCCGGAGAATGGAAGCCATTCGAGAAGCAATGCATGGGTTTTCCTTTAC 1800

Qy  1864 CATGCAATCAAGTCTGAGAAGTCTCTGGACGACATGGAGAGTAGTGAAACCTCCCTGTGTAT 1923
Db  1801 CATGCAATCAAGTCTGAGAAGTCTCTGGACGACATGGAGAGTAGTGAAACCTCCCTGTGTAT 1860

Qy  1924 GATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCT 1983
Db  1861 GATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCT 1920

Qy  1984 GAGGGCCACTGAGAGAAGCTCTTACGTTACGTTATGCCCAGAACTCAAGGCACACAGGAAGTC 2043
Db  1921 GAGGGCCACTGAGAGAAGCTCTTACGTTACGTTATGCCCAGAACTCAAGGCACACAGGAAGTC 1980

Qy  2044 ATTCAGACTGATGAGTGGAAATGGGCCCTGTCGAGAACGCCTTGAGTGAGTGCCCTTGTG 2103
Db  1981 ATTCAGACTGATGAGTGGAAATGGGCCCTGTCGAGAACGCCTTGAGTGAGTGCCCTTGTG 2040

Qy  2104 AAGGGCCATTGAAAAACATATTATTGAGGATACTGAAGGACCCCTGTAAACCAAAATTGTTGGT 2163
Db  2041 AAGGGCCATTGAAAAACATATTATTGAGGATACTGAAGGACCCCTGTAAACCAAAATTGTTGGT 2100

Qy  2164 TATCCCCGACCTCTCAATATAATTGAAGGAATATTGAGGACCCCTGATGAATGAAAATGAAAATGAAAAT 2223
Db  2101 TATCCCCGACCTCTCAATATAATTGAAGGAATATTGAGGACCCCTGATGAATGAAAATGAAAATGAAAAT 2160

Qy  2224 GATCTTTTTGGAGCTGGAAAAAATGTTTCTACCTTGACGTTATAAAGTCAGCCCCGGGGTTATG 2283
Db  2161 GATCTTTTTGGAGCTGGAAAAAATGTTTCTACCTTGACGTTATAAAGTCAGCCCCGGGGTTATG 2220

Qy  2284 AAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAGAAGAAACCAGAGTG 2343
Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2221 AAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAGAAGAAACCAGAGTG 2280
Qy  2344 CTTAACGGCACAGTAGAGAAGAGAGAAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTT 2403
Db  2281 CTTAACGGCACAGTAGAGAAGAGAGAAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTT 2340

Qy  2404 AAAGGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAAT 2463
Db  2341 AAAGGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAAT 2400

Qy  2464 TTCCGAGTTATTGATTTAGGAGTCATGATCCATGTGATAAGATACTGAAAGTGCTCTT 2523
Db  2401 TTCCGAGTTATTGATTTAGGAGTCATGATCCATGTGATAAGATACTGAAAGTGCTCTT 2460

Qy  2524 GACCACAAAGCAGATATAATTGCCTGTCAGGACTCATCACTCCTTCCCTGATGAAATG 2583
Db  2461 GACCACAAAGCAGATATAATTGCCTGTCAGGACTCATCACTCCTTCCCTGATGAAATG 2520

Qy  2584 ATTTTTGTTGCCAAGGAAATGAGAGATTAGCTATAAAATAGCTCCGAGATACAGTGCACCTGTA 2643
Db  2521 ATTTTTGTTGCCAAGGAAATGAGAGATTAGCTATAAAATAGCTCCGAGATACAGTGCACCTGTN 2580

Qy  2644 GCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCCGAGATACAGTGCACCTGTGTN 2703
Db  2581 GCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCCGAGATACAGTGCACCTGTN 2640

Qy  2704 ATCCATGTCCTGACGCGGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTAGATGAAAAT 2763
Db  2641 NNCCATGTCCTGACGCGGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTAGATGAAAAT 2700

Qy  2764 CTAAAGATGAATACTTTGAGAAATCATGAGAAGAATATGAAGATATTAGACAGGACCAT 2823
Db  2701 CTAAAGATGAATACTTTGAGAAATCATGAGAAGAATATGAAGATATTAGACAGGNCNAT 2760

Qy  2824 TATGAGTCTCTCAAGGAGGAGGAGATACTACCCTTAAGTCAAGCCAGAAAAAGTGGTTC 2883
Db  2761 TATGAGTCTCTCAAGGAGGAGGAGATACTACCCTTAAGTCAAGCCAGAAAAAGTGGTTC 2820

Qy  2884 CAAATGATTGGCTGTGTCGAACCTCACCCAGTGAAGCCCAGTTTATTGGGACCCAGTC 2943
Db  2821 CAAATGATTGGCTGTGTCGAACCTCACCCAGTGAAGCCCAGTTTATTGGGACCCAGTC 2880

Qy  2944 TTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGGAGCCTTTCTTTGAT 3003
Db  2881 TTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGGAGCCTTTCTTTGAT 2940

Qy  3004 GTCTGGCAGCTCCGGGCAGCTCCGGGGCCCGGGGTGTGTTGCGCCCGTGTGCCCCAGGCT 3063
Db  2941 GTCTGGCAGCTCCGGGCAGCTCCGGGGCCCGGGGTGTGTTGCGCCCGTGTGCCCCAGGCT 3000

Qy  3064 ACAGTAGTGGAGAGGCCAGGAAGGTCTACGATGCCACAATATGCTGAACACACTG 3123
Db  3001 ACAGTAGTGGAGAGGCCAGGAAGGTCTACGATGCCACAATATGCTGAACACACTG 3060

Qy  3124 ATTAGTCAAAAGAAACTCCGGGACCTTCGGGGTGTTCGGCCAGCACAGAGTATC 3183
Db  3061 ATTAGTCAAAAGAAACTCCGGGACCTTCGGGGTGTTCGGCCAGCACAGAGTATC 3120

Qy  3184 CAAGACGACATTCACCTGTACGGCTGCTGAGAGGACTCTGCCAGCACGGAGCCCATAGCC 3243
Db  3121 CAAGACGACATTCACCTGTACGGCTGCTGAGAGGACTCTGCCAGCACGGAGCCCATAGCC 3180

Qy  3244 ACTTTCTATGGGTTAAGCAACAGGTTAAGCAACAGGTTAAGCAACAGGTTAAGCAACAGGTTAAGGCCATACTAC 3303
Db  3181 ACTTTCTATGGGTTAAGCAACAGGTTAAGCAACAGGTTAAGCAACAGGTTAAGGCCATACTAC 3240

Qy  3304 TGCCTCTCAGACTTCATCGCTTCATTCTGCATCCGTGACTACCTGGGCCTGTTT 3363
Db  3241 TGCCTCTCAGACTTCATCGCTTCATTCTGCATCCGTGACTACCTGGGCCTGTTT 3300

Qy  3364 GCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCTATGAGATGGTGACGAC 3423
Db  3301 GCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCTATGAGATGGTGACGAC 3360
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Qy   3424 TACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCAGAGGCCTTTGCAGAGAG 3483
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCAGAGGCCTTTGCAGAGAG 3420

Qy   3484 CTCCATGAAAGAGTTCGGCGAGAACTGTGGCGAGACTGTGGCAGTGGACGTC 3543
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 CTCCATGAAAGAGTTCGGCGAGAACTGTGGCGAGACTGTGGCAGTGGACGTC 3480

Qy   3544 GCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCCGGCTCCCCAGCTACCCCAGCCAG 3603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCCGGCTCCCCAGCTACCCCAGCCAG 3540

Qy   3604 CCCGACCACCGAGAAGCTCACCATGTGGACTCGCAGCACTCGAGCAGTCTACAGGC 3663
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CCCGACCACCGAGAAGCTCACCATGTGGACTCGCAGCACTCGAGCAGTCTACAGGC 3600

Qy   3664 ATTAGGTTAACAGAATCATTAGCAATGCCACCTGCTTCAGCAGTCTCAGGCCTCTACTTC 3723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 ATTAGGTTAACAGAATCATTAGCAATGCCACCTGCTTCAGCAGTCTCAGGCCTCTACTTC 3660

Qy   3724 TCCAATTTGAAGTCCAAATATTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT 3783
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TCCAATTTGAAGTCCAAATATTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT 3720

Qy   3784 TATGCATTGAGGAAGAAGAACATATCTGTGCGCTGAGGTTGAGAAATGGCTTGGACCCATTTG 3843
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATGCATTGAGGAAGAAGAACATATCTGTGCGCTGAGGTTGAGAAATGGCTTGGACCCATTTG 3780

Qy   3844 GGATGATGATACAGACTAACTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCCTCA 3903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGATGATGATACAGACTAACTTTTTTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCCTCA 3840

Qy   3904 AGGAAATACAACCTAG 3919
          ||||||||||||||||
Db   3841 AGGAAATACAACCTAG 3856
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RESULT 10

US-09-252-991A-13448/c
; Sequence 13448, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13448
; LENGTH: 3762
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13448

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  Query Match             23.0%;  Score 903;  DB 3;  Length 3762;
  Best Local Similarity   55.2%;  Pred. No. 1.9e-265;
  Matches 2074;  Conservative 0;  Mismatches 1580;  Indels 103;  Gaps 12;
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Qy    113 CCCTGCGGGATGAGATGAATCAATGCCATTCTGCAGAAGAGAGAGATTATGGTGCTGGATGGAGGGA 172
          ||||      |||   ||||||||  |  |||  | |||    |||||||||||||||
Db   3701 CCCGCCTGCAAGCCCTCCAGCAGCCCCTTCCAGCGGAACGTATCCTGATCCTCGATGGCGGCA 3642

Qy    173 TGGGGACCATGATCCAGCCGGAGAAGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTA 232
          |||   |||    ||  ||||| |||||| || ||  |  |  |||||||| |||||
Db   3641 TGGGCACCCATGATCCAGCCGGAGGAGAAGCCGGCCCGACTACCGCGAGCGCTTCG 3582

Qy    233 AAGATCATGCCCAGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATG 292
          |||||  |  |||| || |  |||||||  |  |||| ||||||| || |||
Db   3581 CCGACTGCCGAGCCGACGTGAAAGGCAACACAGCACCGACCTTCTGCTGCTGCCGCCGACG 3522
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Db   3581 CCGACTGCCGAGCCGACGTGAAAGGCAACACAGCACCGACCTTCTGCTGCTGCCGCCGACG 3522

Qy    293 TCATTTACCAAATCATTAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATA 352
          |     ||| |   ||  |||||| || ||||   |||  | ||||  |   |||
Db   3521 TGATCCAGGCCATCGAACGGCTACCTCGGCCGGCGGCCGGACCACAACA 3462

Qy    353 CTTTTAGCAGCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTCACCGGA 412
          |||||||||||||||    ||||||||  ||| |||||||||||||||||
Db   3461 CCTTCAAGCGACGTGTCCCAGGCGACTGAGAGTCGGGCCGATGGCCGAGGCGAGTGGGCCACGAAC 3402

Qy    413 TGAACATGTGCTTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGA 469
          |||| | |||| || |  ||| |  |||| | |||||||| ||| || ||   |||
Db   3401 TCAACCTTCGAAGAGGGGCCGCCTGGCCGCGGCACTCGGAGACTGGCGGAAGACCGCCGAGACCC 3342

Qy    470 CAGGAATTAAGAGGTTTGTTGCAGGGGGCTTGGCAGGGGGGTCCGACTAATAAGACACTCTGT 529
          ||||||  || |  |||| ||  ||| ||| |||| |  |||||||||   |||| |  ||
Db   3341 CGGACAAGCGGCGCGGCTTCGGTGCTCGGCTCGGCCAGCAGCCGGCCTCACCTGCTCGATTT 3282

Qy    530 CCCCATCTGTGAAAAGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCAT 589
          |||  ||| ||  |||  | |||   ||  |||  |||   ||||| |  |||||
Db   3281 CCCCGGACGTGAACAACCCGCTACCGGCACGTCACCTTCGACGAACTGGTGGAGAACT 3222

Qy    590 ACCAAGAGCAGGCCAAAGGACTTCTGGAGTTGTGATATCTTACTACTTCATTGAAAACTA 649
          ||||| |  |||  |||   |  |||||   ||| |  |   ||  |  |  | | ||||
Db   3221 ACGTCGAGGGCGACCCGGCCTGTGATCGAAGGCGGCGGCGACCTGATCGAGACGACCA 3162

Qy    650 TTTTGATACTGGCAATGCCAAGGCAGCAGCCTCTGTTGCACTCCAAAATCTTTTGAGGAGA 709
          |||||  ||  |  |  ||||| |||| | ||||    ||||  || ||  || |||||
Db   3161 TCTTCGACACCCTCAAGCCCAAGGCGGCGGATCTTCCGCGTCCCAGGGTCGTGTTGAGGAAC 3102

Qy    710 AATATGCTCCCCGGCCTCATCTTATTTCAGGACGATCGTTGATAAAAGTGGCGGCGCTC 769
          ||||| ||    || | |  |   | | |||| |  ||| || |||  ||  |  | ||
Db   3101 TCGGCGTGGAGCTGCCGATCGATCCTCCGGAACATCACCGACCGGAACCACTCTGCA 3042

Qy    770 TTTCCGGACAGACAGGAGAGGAGGGGATTTGTCATCAGCGTGTCTCATGAGAACCACTCTCGG 829
          |||| |  | | | |  | ||   ||| | ||| | |   || | |  |||  | |  |||||
Db   3041 TGTCGGGGCCGCAGACCACCGAGGCCTTCGGTGGAACTCGGTCCCGATCTCGG 2982

Qy    830 TTGGATTAAATTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAA 889
          ||  | ||| || |||  |||| | || ||  | ||| |  |||| ||| || |||
Db   2981 TAGGCCTGAACTGCGCCCTCCGGGAATTGCGGCCGTACAGTGCGGAACTGTCGA 2922

Qy    890 AATGTACAACAGCCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTG 949
          |||| |  |   |   |||    |   || ||    | |||| |  |||   |  |||||
Db   2921 CCAAGGCCGACACTCATGTCTCGGCCACCCACCCAACGCCCTTCGGGG 2862

Qy    950 ACTATGATGAAAACGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCT 1009
          |||| | |  |   |||   ||||| |||   | |    | |||| ||  | ||| ||  |
Db   2861 AATACGACGAATCGCCGGGAAATGCGGCTGGGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTG 2802

Qy   1010 TGGTCAATATAGTTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTG 1069
          ||    | || | || | | || | || | || |||| ||  |   ||| |||| |||
Db   2801 TCCTCAATATCGTCGGCGGCTGGGAAGTGGCCCCACGTGATCGGCGCGCCCAGGTGACATCA 2742

Qy   1070 AAGCTGTGAAAAATTGTAAGCTAGAGTTCATGAGACATACCGGTTTGAAGACACATATGT 1129
          |||| |||  |   | ||   || |  |||| | ||||   |  |  |||| ||||| |
Db   2741 AGGGCAGTGCCAAGTGCCAAGTACCCGGCGGCATCCCGGAGATTCCCGGGCCGTGTC------ 2688

Qy   1130 TACTGTCTCGGTCTAGAGCCCTTCAGGATTGGACCGTACCACCAACTTTGTTAACATTGGAG 1189
          || |||||||||  |||||||  |  |||||| |||| |||||  ||||| | |  |||| |
Db   2687 GCCTGTCCGGCTGGAGCCGTTCACCATCGACCGCAGCTCGTTGTTCGTCACGGCGGAACTATG 2628

Qy   1190 AGCCCTGTAATGTTGCAGGATCAAGGAAGTTTGTAAACTCATCATGGCGAGGAAAACTACG 1249
          |||| |  |  |  |  ||   |  ||| | |  |  | || |  ||||  | ||  | ||
Db   2627 AGCCGCACCAACATCACCGGTTCGCCCGCCCAAGTTCGCCGGCGGCTGATCCGCGATGGCGCA 2568

Qy   1250 AAGAAGCCTTGTGTTGTTGCCAAAGTGCAGCAGCCGGCCCAGGTGTTGGATGTCA 1309
          ||||| || | |   || ||||| ||  ||||||  ||||||| | |  |  |||
Db   2567 CGGAAGCTCGCGAGGTCGCCGCAGCAGGTGGAAGCCCGGCGCCCAGGTGATCGACATCA 2508

Qy   1310 ACATGGATGATGCCATGCAATGACAATTTAAGTATAACTCAGCCTGATG 1369
          | |||||| |||||| |  |||    ||||  || ||   |||| |||
Db   2567 TGGGCACCCATGATCCAGCCGGAGAAGAGGCAACATTTCCAAGTGCAATGACCAGATTTTCGAACTTAATTG 1369
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Qy   2447 TCCTTGGCTGCAATAATAATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGA 2506
          || |||  || || |  ||| ||       |  ||  || || |||||| ||  | ||  |||
Db   1406 TGCTTCGGCTGCAACGGCTATGACGTGGTCGACCTCGGCGTCGACATGGTGCCGGCGGAGAGA 1347

Qy   2507 TACTGAAAGCTGCTCTTGCACCACAAAGCAGATATAATTGGCTCGTGCAGGACTCATCACTC 2566
          | ||| |||| || ||| | || | |||  |  | | ||| || |||  ||| || ||||| |
Db   1346 TCCTGCAGACGCCCATGCGCCGGAGAATGCACATCATCGGCCTCTCGGCCTGCCTGATCACGC 1287

Qy   2567 CTTCCCTGATGAAATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGAGATTC 2626
          | ||| ||| || || |   |||  || |||  | || ||| || |||  | || || | |
Db   1286 CGTCGCTCGACGAGATGGTCCACGTCGCCAAGGAAATCAGCCGCAGCAGTTAAAATAGCTGC 1227

Qy   2627 CATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCAGCAAAAATCAGAGTGT 2686
          | ||| |||||||| |||| ||| |  |||| ||| || || || | ||   |
Db   1226 CGCTGATGATCGGCGGCGGCCCACTACCTCGAGGCGCATACCGCGTGAAGATCGATCCGC 1167

Qy   2687 GATACAG---TGCACCTGTAATCCATGTCCTCTGCAGACGCGCCTCTGCAGAGTGTGGTGTGTT 2743
          |||||||   |  ||  |  ||||||  | | || |  || || || | |||| | || || | |
Db   1166 AGTACAGCAACGACCGGTGGTCTACGTGGTCAACGACCGCCAGCGCCCGCGGCGGTAGGCGTGGCCA 1107

Qy   2744 CCCAGCTGTTAGATGAAAATTTAAAGGAATGAATACTTTGAGGAAATCATGAAGAAAATG 2803
          ||||| || | |||  || |||  |  | || ||  | |  ||| |||  | || ||| ||
Db   1106 CCAGCCTGTGTCAAGGAGCTGAAGGCCGACGTGGCCCCGCGCCGCACCCGCCGACTACG 1047

Qy   2804 AAGATAT----TAGACAGGACCATTATGAGTCTCTCAAGAGAGGAGGATACTTACCCTT 2858
          |||| ||    | | |||||| |  || |||  |||||| |  |  ||| ||   | |
Db   1046 CGGTGGTCCGGAACGGCCACGGCCCAACCGCCAGCGCCCGCGCCGAGCGGCTGAGCTACGAAC 987

Qy   2859 AAGTCAAGCAGAAAAGTGGTTCCAAATGGTTCTGACTGGCGAGAAGCAATGCATG 2918
          || || ||  |  | |  |   ||| | |  || ||  |||| |||  || || |
Db    986 AGGCGATCGCCAACAGCCGGGCGTTCCGACTGGGCGCGGAGGCGATCCACT 935

Qy   2919 GCCCACGTTTATTGGACACCCAGTCTTGAGACTATGACTGCGAGAAGCTGCGGACTA 2978
          || || |||  | || || |||  | ||| || || || || ||||||| |  ||||
Db    934 GCCTTCCTCACCGGCGCTCAGGCGTCGCAGGTGCTCGACGAGCTCGGCCTCGCCGAGTA 875

Qy   2979 CATTGACTGGAAGCCTTTCTTTGATGTCTGTGGCAGCTCCGGGCCAAGTACCACCGAATCGAGG 3038
          || ||||  | || || ||  ||  | |  ||  |  |  |||| |||| || |||| | ||
Db    874 CATCGACTGGACGCCGTTCTCCATTTCTGGGACCTCGGCGACCTCGGCGACCAGTACCCG 823

Qy   3039 CTTCCCAAGATATTTAACGACAAAACAGTAGTGGAGACCGGCCAGGAGGTCTACGATGA 3098
          || ||| ||| | |  |||  |||  | ||  || || ||| | ||| | || ||  |
Db    822 --------CGCATCCTCACCGACGAAGTGGTCGCGACGAGCAAGTGGTGCTCACCGTGTTCAACGA 770

Qy   3099 TGCCCACAATATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGCGTCGTCGT 3158
          || || ||| |||| || || || || |  | || |||  |  |||| | |  |||
Db    769 CGCCCAGGCAGGTGCCGATGTCGAAGAGCTGATGACGAGAGCTGATTCGTCGCCGCGTGTT 710

Qy   3159 TGGGTTCGGCGAAGCCTTGTGGGTACGGCAGGAGGCTGCTGT 3218
          ||||  |||| |||| |   | ||  |||| |||||   |||
Db    709 CGGCTTCTCGGCCGGCATCGGGCCACCTGTACGCGGCCGCGATGG 650

Qy   3219 GCCCCAGGCTCGAGGCCTGAGACGCTGTAAGGCTGAGAAGGA 3278
          || ||| | || |||  | || ||| ||  ||||| || | |
Db    649 C--------GAGACCTCCACCCGACCACCTGCGCAGCAGGATCAAGCC 602

Qy   3279 CTCTGCCAGCACGAGGAGCCCATACTACTGCCTCCAGACTTCATCCTCG 3338
          || | || | || | ||||||     | || || ||  |   ||  |||
Db    601 GGACGGCA------AGCCGAACCTGTCGCTCGTGGGCCGGGTGTT 548

Qy   3339 CATCCGTTGACTACCTGGCCTCGTTTG---CCGTTGCCTGCTTTTGGGGTAGAGAGCTGAG 3395
          || || || ||||  ||  |   | |    |||  | | | | ||  || | |||  | ||
Db    547 CGTGCGGCTACTACATCGGCGGCTTCATCCACCACCGCGGATCGGCCGAGAGGAAGTGGC 488

Qy   3396 CAAGGCCTATGAGGATGATGTGACAGCTACCACGTCAAGGCGCCACCA 3455
          ||||||  | || |  | ||||| | || ||  |||  || | |||  |
Db    487 CAAGGCGTACGAAGCCAAGGGCGACTACAACAGCATCAGCATGAAGAGTGC 428

Qy   3456 CCGGCTGCGAGAGCCTTTGCAGGACATAGGCAAGAACATAGTTGGAGTAG 3515
          || |  | || || || || || || || || ||||  |  | ||| |
Db    427 CCGCCTTCGCCGGAGGCTGCCGAGTAGTGGCTGCGCAAGGAGGTACTGGGG 368

Qy   1370 CTTCCGAGCCAGACATCGCAAAGTACCTTTGTCATCGACTCCTCCAATTTTGCTGTGA 1429
          || ||||||| | ||| ||  |||||| | | ||||||||| || || || |||| |
Db   2447 CCTCCGAGCCGACATCTCGCGCGTGCCGTCGATCATGATCGACTCGACTCCAAGTGGGAAGTGA 2388

Qy   1430 TTGAAGCTGTGGGTTAAAGTGCTGCCAAGGAAGTGCATTGCATTGTCAATAGCATTAGTCTGAAGG 1489
          |||||||||| || ||||||| || ||||||  ||| ||| | | ||||   | |   |  ||||
Db   2387 TCGAGGCCGGCGGCCTGAAGTGCATCAGGGCAAGGGCAACATCGATCCGATCTCGATGAAGG 2328

Qy   1490 AAGGAGGACGACTTCTTGAGAGGAAGAGGCCAGAAGATTAAAAAGTAATGATGAGCTGCTATGG 1549
          ||||| ||||  ||   |  || |||| ||||  || |||  |   |  ||||| || | ||||
Db   2327 AAGGCGTCGAGGCCTTCAAGCACACCGCCCGTGCCAGCACCCAGCCGCCGTCGCTCCGGTGG 2268

Qy   1550 TGGTCATGGCTTTTGATGAAGAAGGACAGGCAACAGCAGAAACAGACACAAAAATCAGAGTGT 1609
          |||| ||||| || |||| || || ||||  ||  || ||| |||||   |  |||||||  |
Db   2267 TGGTGATGGCCTTCGACGAGACGGCGCGGCGCCACACCGCGGCATACCGCGTGAAGGAAGAAATCT 2208

Qy   1610 GCACCCGGCCTACCATCTGCTTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTT 1669
          ||||| |||| ||||| |||  | || || |||||  |  ||  || | || |  | |||
Db   2207 GCAAGCGCTCCTACGACATCTCGGTCTTCGCGCAGAGTCGGCCTTCCCACCCGAAGACATCATCT 2148

Qy   1670 TTGACCCTAATATCCTAACCATTGGGACTGGAATGAGGACCACACAACTTGTATGCCATTA 1729
          | || || || || | | ||| ||||  |  |  ||||| ||||| || | ||| |||||
Db   2147 TCGATGCGAACATCTTCGCCCGGCATCGCCGAGGCGACCACGGCCTCGCCGTCACTACGCGTCG 2088

Qy   1730 ATTTTATCCATGCAACAAAAGTCATTAAAGAACATTACCTGGAGCCAGAGATAAGTGGAG 1789
          || | ||||| |||  |  || || |  ||||||||| ||  |||| || ||  | ||  |
Db   2087 ATTTCATCAACGCGCCTACAGTCGCGCCCTACATCCGCGGGCTCGGAGCCCTACGCTCGGGGCG 2028

Qy   1790 GTCTTTCCAACTTGTCCTTCTCCTTCCGAGGAATGCCATTCGAGAAGCCATTGACATTGCATG 1849
          |  | ||| | || || |  | |  | ||  |  || ||  || || || || ||  ||| |
Db   2027 GGGTGTCCAACGTCCTCCTTCTCGTTCCGGCGGGCAACACCCGTGGTGGCGGAGGCGATCCACT 1968

Qy   1850 GGGTTTTCCTTTACCATGCAATCAATCAAGTCTGCATGGAATGGAATGTGAATGCTGGAA 1909
          ||||  ||| | |||| | ||  ||  || || || ||| | |  ||||| | || ||||
Db   1967 CGGTGTTCCTCACGGGCGATCGCCGATCCGCAACGGCCATGGGCATCGTCAACGGGCGGCC 1908

Qy   1910 ACCTCCCTGTGTATGATGATCCATAAGGAACTTCTGCAGTCTGTGAAGATCTCATCT 1969
          || || | || || ||||| | || || || |  | |||  |  | |  || |||
Db   1907 AGCTGGAAATCTACGACGAGATTCCATAGGAAGGCGTGCCGGGTCGAGGACGTGGTGC 1848

Qy   1970 GGAATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAA---GGCA 2026
          || || ||  ||| | || ||| ||||| ||  | || |  ||  || ||||   |||
Db   1847 TCAACCGCACGCCGCCGGAGCCCATCGCCGATCGCTGGCATCGGCGACTACAAGGGCG 1788

Qy   2027 CAGGAGGGAAGAAAGTCATTCAGAGTGAAGGGCCTTGTGTCTGAAGAACGCC 2086
          ||||| ||||||| || || ||| || ||| | | |||||  |||| ||| |
Db   1787 GCGGCGCGGTCAAGGAGGCCGAGGACAGTGAAGGTCGCAGCTACAGTGTCGAGAAGCGCGCC 1728

Qy   2087 TTTGAGTATGCCCTTGTGAAGGCTGCATTGAAAACATATATTATTGAGGATACTGAGGAGCCA 2146
          ||||| ||  |||  || |||| || |   || ||||| | | || || || |||| || | |
Db   1727 TCGAGCATGCCGGCTGGCATCGTCGAGGACGTGGTCGAGGGGCCAGGAGGGGCCAAGA 1673

Qy   2147 GGTTAAACCAAAAAAATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATG 2206
          || | |||| ||   | |||| | |  | || ||  ||||||| | ||  || | | |
Db   1672 ---ATGCCGCCAGTGTGCGGTGCCATCGAAGGCGTGCCGGCGATGTCCG 1617

Qy   2207 GAATGAAAATTGTTGGTGATCTTTTTGGAGCTGGAAAAAATGTTTCTACCTCAGGTTATAA 2266
          ||||| || |  | || || |  |||  || ||||  | ||  | |||| |||  || | |
Db   1616 GGATGAACGTGTCGCGGGACCTGTTCGGCGCCGGCAAGAATGTGTCCTCCCGCAGGTGTCA 1557

Qy   2267 AGTCAGCCCGGGTTATGAAGAGAGGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAA 2326
          || || | |||| ||||||||| ||  || | ||||||  | || || ||| |||  | |
Db   1556 AGTCCGCGCAGTATGATGAAAACAGGCTCATCGGCCCCACCTTACCAGGCGCCACCA 1497

Qy   2327 GAGAAGCATGGGCGATGAAACCAGAGTGCTTAACGGCCACAGTAGAAGAGAGGACCTTA 2386
          ||||| | |||||| | |||||||  ||| |||   |||||||| || || ||||  |
Db   1496 AAGGCCGGATA--------------AGCCGGAAGCCAAGGGCCACCA 1467

Qy   2387 TCGTGCTGGCCACTGTTAAAGGCGACGTGCACGAACATAGGTTGGAGTAG 2446
          ||||| |||||| | | ||| ||||||||||| | || ||  | || |  |
Db   1466 TCCTGATGCGGTCGAAGGCGACGACACTCGGCGAAGAACATCGTCGCGGTGG 1407
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Qy 419 TCAACCTCGAAGGGCGGCGCCCTCGCCCCCAGCTGGCGCCGACGGCGAAGACCGCCGAGACCC 478

Db 470 CAGGAATTAAGAGGTTTGTGGCAGGGGCCTTCGGGTTCGACTAATAAGACACTCTCTGTGT 529

Qy 479 CGGACAAGCCGGCTTCGTCGTGCCCTCGGCGCTGCCCGACCAGCCGCACCTGCTCGATTT 538

Db 530 CCCCATCTGTGGAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCAT 589

Qy 539 CCCCGGACGTGAACAACCCCGGCTACCGGCAAGCTCACCTTCGACGAACTGGTGGAGAACT 598

Db 590 ACCAAGAGCAGGCCAAAGGACTTCTGATGGCGGGGGTTGATATCTTACTCATTGAAACTA 649

Qy 599 ACGTCGAGGCGACACCGGCCGGCCCTCGATCGAAGGGCGGCGCCGACCTGATCGAGACCA 658

Db 650 TTTTTGATACTGCCAATGCCAAGGCAGCCTGTTGCACTCCAAAATCTTTTGAGGAGA 709

Qy 659 TCTTCGACACCCTCAAGCGCCAAGGCGGCGATCTTCGCCGTCCAGGGCGTGTTCGAGGAAC 718

Db 710 AATATGTCCCCGGCCTATCTTATTTGCAGGACGATCGTGATAAAAGTGGGCGGACTC 769

Qy 719 TCGGCGGTGGAGCTGCCGATCATGATCTCCGGAACCATCACCGACGCCTCCGGCGCACCC 778

Db 770 TTTCCGGACAGACAGGAGAGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCA 829

Qy 779 TGTCGGGGCCAGACCACCCGGAGGGCCTTCTGGAACTCGGTGCGGCATGCCCGGCCGATCTCGG 838

Db 839 TTGGATTAAATTGTGCTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGAA 889

Qy 839 TAGGCCTGAACTGCGGCCCTCGGCGCGCCAAGGAATTGCGGCCGTACATCGAGGAACTGTCGA 898

Qy 890 AATGTACAACAGCCTATGTCCTCTGTATCCCAATGCAGGTCTTCCCAACACCTTTGGTG 949

Db 899 CCAAGGCCGACACTCATGTCTCGGGCCACCCAAGCCGCTGCCGAACGCCTTCGGCGCG 958

Qy 950 ACTATGATGAAACGGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCT 1009

Db 959 AATACGACGAATCGCCCGGCGAAATGGCCGTGGTGGTCGAGGAATTCCGCGCCCGGCT 1018

Qy 1010 TGGTCAATATAGTTGGAGGATGCTGGGGTCAACACCAGATCATCATCAGGGAAATTGCTG 1069

Db 1019 TCCTCAATATCGTCGGGCGGCTGCTGCGACGAGTTCCACCTGCCCACTGCTTTGAAGGACATATGT 1078

Qy 1070 AAGCTGTGAAAAATTGTAAGCCTAGAGTTCCCGCGGGCCATCCGCGAGATTCCGAAGGACATATGT 1129

Db 1079 AGGCAGTGCCAGTGACCACCCGCGCGGGCCATCCGCGAGATTCCCGGGGCCTGTC------ 1132

Qy 1130 TACTGTCTGGTCTGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAG 1189

Db 1133 GCCTGTCCGGCCTCGGCCTCGGACCGTTCCACCTGACCCCAGGTCGGCTGTTCGTTCGTCAACGCTCGCG 1192

Qy 1190 AGCGGCTGTAATGTGCAGGATCAAGAGAGTTGCTAAACTCATCATGCGAGGAAACTATG 1249

Db 1193 AGCGCACCAACATCACCGGTTCGGCCCAGTTCGCCCGGCTGATCGGCGAGGAAAACTACG 1252

Qy 1250 AAGAGCCTTGTCGTGTTGCGCAAGTGCAGGTGAAATGGGAGCCCCAGGTGTTGGATGTCA 1309

Db 1253 CGGAAGCTCTCGAGGTCGCCGAGCAGCAGGTGGAAGCCGGCGGCCCAGTGAGCGCTTCG 1312

Qy 1310 ACATGGATGATGGCATGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTG 1369

Db 1313 ACATGGACGAAGGCATGCTGGACTGGAACGGCGGCATGGTCACCTTCCTCAACCTGATCG 1372

Qy 1370 CTTCGGAGCGCCAGACATGCGCAAAGTACCTGCTGGGCGCAGATATCATTGAAACAAATA 1429

Db 1373 CCTCCGAGCCGGACATCTCCGCGTGCGGATCATGATCGACTCCTCCAAGTGGGGAAGTGA 1432

Qy 1430 TTGAAGCTCGGTTAAAGTGCTGCCAAGTGCGCTATGGCCTTGGCCTACCGGA 1489

Db 1433 TCGAGGCCGGCGCCTTCTCGAGGTCATCCTCGAAGTCATCTCAACTCGATCTCGATGAAGG 1492

Qy 1490 AAGGAGAGGACGACTTCTTGGAGAGGCCAGAGATTAAAAAGTATGGAGCTGCTATGG 1549

Db 1493 AAGGCGTCTCGAGGCCTTCAAGCACCCATGCCGCCCTGTGCAAGCCGCTACGGCGGGTGG 1552

Qy 3516 CTACTGTGGCAGTGAGCAGTCGGACGTCGCAGACCTTGCGCAGACGTTGCGGTACAAGGGGCAT 3575

Db 367 CTACGCCCGGCCGCTCCTGGCTACCCCGCCTGCCCGACCAGCCGCCCGACTACCCCGCTGGCAT 308

Qy 3576 CCGCCGGCCGTCCTGGCTACCCCGGCTACCCGGCTCGCCGTCAACATTGGCAT 3635

Db 307 CCGCCCCGGCACCGGCGGGGGCTACCCGGCTACCCGGCGCCCTCGCCCTGTTCGA 248

Qy 3636 ACTCCGCAGACATCGAGCAGTCGACGAGTCTACAGGCATTAGGTTAACAGAATCATTAGCACTGGCACC 3695

Db 247 ACTGCTCGATCCGATCCGCAGGGCCTGTCCGCGTCAGCCTGCCCAATTGAAGTCCAAATATTTGTCCC 188

Qy 3696 TGCTTCAGCAGTCTCAGGCCTCTCACTTCTCCAATTTGAGTCCAAATATTTCGTGTGGG 3755

Db 187 CGCCCGGCGGGTGGTGTGGTGTATTTCGCCCCACCCGGGCCAGTACTTCGCCGGTCGG 128

Qy 3756 GAAGATTTCCAAGGATCAGGTTGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGA 3815

Db 127 CAAGATCGACACAAGGACCAGGTGAACGCTACAGCCCAGGGCGACAGGGCCAGGAAGCCAGCGT 68

Qy 3816 GGTTGAGAAATGCTTGGACCCATTTTGGGATATGAT 3852

Db   67 CAGCGAGCGCTGCTGCGCGCCGCCGAACCTTGGCTACGAT 31

RESULT 11
US-09-252-991A-13693
; Sequence 13693, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13693
; LENGTH: 3795
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13693

Query Match   23.0%; Score 903; DB 3; Length 3795;
Best Local Similarity   55.2%; Pred. No. 1.9e-265;
Matches 2074; Conservative   0; Mismatches 1580; Indels 103; Gaps 12;

Qy 113 CCCTGCGGATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGAGGGA 172

Db 119 CCCGCCTGCAAGCCCTCCAGCAGCGGGAGAAGCTAAACGAGACACTTCCGAGGTCAGGAATTTA 178

Qy 173 TGGGGACCATGATCCAGCCGGCACAGCTCACAGAGTGGAACGCTACAGCGCTTCG 232

Db 179 TGGGCACCATGATCCAGATCGAGAAGAGTGGACAGGAGCGGCCGGCCGGCGCGCCGGCTACCG 238

Qy 233 AAGATCATGCCAGCCGCGCTGAAAGCCAACATTTAAGTAGTATAACTCAGCCTGATG 292

Db 239 CCGACTGGCCGAGCGACGGTGAAAGGCCGTGAAAGGCCAACAACGACCTCCTTGCTGCTGGGCGCAGCCGCGACG 298

Qy 293 TCATTTACCAAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATA 352

Db 299 TGATCCAGGCCATCGAGAGAGGCCATCGACGCTGCACCGCCGCCGCCGCCCGACCAACA 358

Qy 353 CTTTTAGCAGCACTAGTATTGCCCAAGTGACTATGGCCTTGGCCTTACCGGA 412

Db 359 CCTTCAAGCGCCCGGCTGTCCCAGGGCCGACTACGCAGTCGTGCGTCGGCCCTTACCGAAC 418

Qy 413 TGAACATGTGCTCTGCAAGTGCTGGCGAGTGAGTCGCCAGGAAAAGCTGCCAGGAGAGTAACTCTCCAGA--- 469

Db 419 AAGGCGTCTCGAGGCCTTCAAGCACCCATGCCGCCCTGTGCAAGCCGCTACGGCGGGTGG 469

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Qy    1550 TGGTCATGGCTTTGATGAAGAAGGACAGGCAACAGAAACAGACACAAAAATCAGAGTGT 1609
                |||||  ||||||||||||   ||||    ||||     |||      ||||
Db    1553 TGGTGATGGCCTTCGACGAGGACGGCCAGGCCGCACCCGGCCAAGGCGCAAGGAAGAAATCT 1612

Qy    1610 GCACCCGGGCCTACCATCTGCTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTT 1669
                ||||  ||||||| ||| ||||||  |||||||||  ||||||||||||||
Db    1613 GCAAGGCGCCTCCTACCTACGAGCAGTCCGCTTCCACCGGAGACAATCATCT 1672

Qy    1670 TTGACCCTAATATCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTA 1729
                |||||||   ||| |||||||||  |||||||    ||  ||||||||
Db    1673 TCGATGCGAACATCTTCGCCATCGCCGGCATCGAGGAGCACAACTACGCCGTCG 1732

Qy    1730 ATTTTATCCATGCAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAG 1789
                ||||| ||||| |||  ||  ||||    |||||||   ||||    |||    ||||
Db    1733 ATTTTCATCAACGACGCTGCGCGCCTACATCCGCCCTACGAGCTCGGGGCG 1792

Qy    1790 GTCTTTCCAACTTGTCCTTCTCCCTGGCTTCTTCTCGGTCGTCTCTGCGTGCGGCGAATGCATG 1849
                |||||  ||||| || ||||||| |||  |||||||
Db    1793 GGGTGTCCAACGTCGTCCTTCTCGTTCGTCTGCGGTGCGCGGAGGAGCTGCCACT 1852

Qy    1850 GGGTTTTCCTTTACCATGCAATCAGTCTGGCATGACATGGAGATAGTGAATGCTGGAA 1909
                ||| ||||| ||||| ||  |||||||||   ||  ||  ||| ||||
Db    1853 CGGTGTTCCTCTACTACGGCGATCCGCAACCGGCTGACCACGTGTCAACGCGCGGCC 1912

Qy    1910 ACCTCCCTGTGTATGATGAATATCCATCTGCAGCTTCTGCAGCTCTGTGAGATCTCATCT 1969
                ||||  ||| |||  ||  ||||  |||  |||||   |||    ||||   |||||||
Db    1913 AGCTGAAAATCACGACGAGATTCCGAAAGGCTCCGAAAGCGCTGCGGTCGGTGGTGC 1972

Qy    1970 GGAATAAGACCCTGAGGCCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAA--GGCA 2026
                |||| |  ||||   |||  ||  |||| |||| ||||||||  ||||||||  ||||
Db    1973 TCAACCGCACGCCCGGAGCCCTGCCTGGCGATCGCCGACACTACAAGGGGCG 2032

Qy    2027 CAGGAGGGAAGAAAGTCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGCC 2086
                |||||| || ||||||   |||||  | |||| ||||||||||  |||||||||||||
Db    2033 GCGGGCCGGTCAAGGAGCGCGGAGGAATGGGCGCAGTCAGTGTCGAGGAGAGGCC 2092

Qy    2087 TTGAGTATGCCCTTGTTGAAGGGCCATTGAAAAACATATTATTGAGGATAATTGAGGAAGCCA 2146
                |||| ||  |||||  |||||||| |||   |||  ||  ||   ||||  ||   ||||
Db    2093 CGGCTTCTTGGCCTGGTCGAAGGGCATCACCACCCTGATCGTCTCGAGGAC-----GAGGA 2147

Qy    2147 GGTTAAACCAAAAAAATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATG 2206
                ||  |||| ||| ||  ||||  |   |||| |||||||||||||  ||||||| |||
Db    2148 ----ATGCCGCCAGCAGTGTGCGCGTCCCATCGAGGTCATCGAGGGTCATCGAGGTCCG 2203

Qy    2207 GAATGAAAAATTGTTGTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTTCAGGTTTATAA 2266
                |||||||| ||  |  | ||   ||| ||  |||| ||| | ||    ||||| ||||
Db    2204 GGATGAACGTGTGTCGGCGACCTGTTCGGCGACCTCGGCGCAAGATGTTCCTCCCCCAGGTCGGTCA 2263

Qy    2267 AGTCAGCCCGGTTATGAAGAAGGCGTGTTGGCCACCTTATCCCTTTCATGAAAAAGAAA 2326
                ||||  |||||  |  |||||||||| || |||||   ||  ||| |||   |||||||
Db    2264 AGTCCGCTGCGACTGAAACAGGCGCGTGGCGCCCACCTGATCCCGATTCCCTTTCATGAAAAAGAAA 2323

Qy    2327 GAGAAGAACCAGAGTGCTTAACGGACCAGAGCACAGTAGAAGAAGAGAAGACACCTTACCAGGGCCACCA 2386
                             ||||||| ||||  |||
Db    2324 -------AGGGCGATA--------AGCCGGAAGCCAAGGGCCAAGA 2353

Qy    2387 TCGTGCTGGCCACTGTTAAAGGCGACCTGACGCACATAGGCAAGAACACAGTTGGAGTAG 2446
                ||||  |||||||  ||  |||||  | || | |||| ||||| |||||| |||| |||
Db    2354 TCCTGATGGCCACGCGTGAAGGCGTGACCGAGTGCTTGGGACTAGCTGATACTGGGG 2413

Qy    2447 TCCTTGCTGCAATAATTTCCGAGTTATTGATTAGGAGTCATGACTCCATGTGATAAGA 2506
                ||||| ||| ||| |||||| ||   ||| ||||||||| |||  |||||||||||||
Db    2414 TGCTCGGCTGTGACCATCTCGCGGTGGTGGTGCGTGATGGTTCCCGGCGTGATGTGGCCCGGCATAACGCTGCGCAGC 2473

Qy    2507 TACTGAAAGCTTCTCTTGACCACCAAAAGCAGCAGATATAATTGGCCTGTCGCAGGACTCATCACTC 2566
                || ||||||  |||| ||||||||  ||| |||||||    |||| ||||| ||||| |||||||
Db    2474 TGCTCTGCAGAAAATGATTTGTTGTCCAAGGGAAATGGCACATACTCGGGCCTGTCTGGTCGATCAAGC 2533

Qy    2567 CTTCCCTGATGAAATGATTTTGTTGCCAAGGACTATAAGGATTC 2626
                ||||| ||||| |||| |||| ||||| ||||||    ||||||
Db    2534 CTCTCGCCTGGACGATCGGTCGCCCAAGGAAATGCAGCGCGGCGAGAATTTCCAGTTGC 2593
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Qy    2627 CATTGTTGATTGGAGAGCACCACTTCAAAAACCCACAGCAGTTAAAAATAGCTCCGA 2686
                || |||| |||||||||  |||  ||  |||||  |||| |||   |||||||||||
Db    2594 CGCTGATGATCGGCGGCGGCGGCCCACTACCTCGAAGCGGGCGTATACCGGTGAAGATCGATCCGC 2653

Qy    2687 GATACAG---TGCACCTGTAATCATGTCCTGACGCGTCTCCAGAGTGTGGTCGTGTCTT 2743
                |||  ||   |||||| |  |||||   || ||| |||||| |||||  || |||||||
Db    2654 AGTACAGCAACGACGAGTGGTGGTGTGTGTCTTCCCCGCGCGGCGGTAGGCCGTGGCCA 2713

Qy    2744 CCCAGCTGTTAGATGAAAATCTAAAGGATGATGAATTGAGGAGGAGATACTTGGAAGAATATG 2803
                ||||||| || | |||| ||     |||||| || | |  ||||||| ||||  |||||||
Db    2714 CCAAGCCTGCTGTCGTCCAAGGAGTCGAAGCCGCGTCGGTCCGCGCCGCACCCGGCGACTACG 2773

Qy    2804 AAGATAT-----TAGACAGGACCATTATGAGTGTCTCAAGGAGGAGATACTTACCCTT 2858
                ||||||      ||  |||| | |||  |||||||||| |||||   ||||||||  ||
Db    2774 CGGTGGTTCCGCGAACGCACGGGCCAACCGGCCCCGAGGGCCGGCTGAGCTACGAAC 2833

Qy    2859 AAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGATTGGTCGTGTTCAGGCAATGCATG 2918
                ||| ||||||||||||| || |  |||||||  || | |||| ||||  |||||||
Db    2834 AGGCGATCGCCAACAGCCGCGTTCGACTGGGCCGGCTACCAGCCGCCGAC------- 2885

Qy    2919 GCCCACGTTCATTGGGACTACCAGTCTTCTTGAAGACTATGACCTGCAGAAGCTGCGGTGGACTA 2978
                || ||| ||  |||||||||  |||   | |||||| ||| ||||| |||||||||  ||||||
Db    2886 GCCTTCCTTCACCGGCCGTCGAGGGTGTGCTCGACGATCGGCATCGTCAACGCCGGCC 2945

Qy    2979 CATTGACTGGAAGCCTTTCTTTGATGTCGAGCTCTGCAGCTCCGGGGCAAGTACCCGAATCGAGG 3038
                |  |||| ||  |||| | || |||  | ||  | ||||  |||| | ||||||||||||||
Db    2946 CATCGACTGGACGCCGTTCTTCATTTCCTGGGACCTGGCGCGGGCCGGAAGTACCCG------ 2997

Qy    3039 CTTCCCAAGATATTTAACGACAAAACAGTAGTGGAGAGAGGGCCAGGAAGGTCACGATGA 3098
                || |  |||| ||||||||||||||||||| | || |||| |   || ||||| |||||
Db    2998 ------CGCATCCTCACCGACGAGTGGTCGCGGCGAGGTGGTCGGGAGGCGCCGCCACCTCGTTGTTCAACGA 3050

Qy    3099 TGCCCACAATATGCTGAACACACTGATTAGTAGTCAAAAGAAACTTCGGGGCCCGGGGTGTGT 3158
                |||| || ||  ||||||||  || ||||| |  |||| | |||  |||||||||||||||
Db    3051 CGCCCAGGCCGATGCGGATGGCCCAGAGAAGCTGATCGATCGAGAAGCTGATTTCGTCGCGGCGCCGGTGTT 3110

Qy    3159 TGGGTTCTGCGGCCAGCACAGAGTATCCAAGAGACACAATTCACCTGTACGGACGAGGCTGCTGT 3218
                || | ||||| ||||| |||| ||| ||  ||||| ||| | ||  | ||| |||||||||| ||
Db    3111 CGGCTTCTCGGGCCGCTGGAGGTTCTACGGCGACTGGAGGTCTACGGCGCCGCGGCCGGCGATGG 3170

Qy    3219 GCCCCAGGCTGCGAGAGCCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGA 3278
                |   || || || |||  |  ||| |||| |  || ||||||||||||||| |||
Db    3171 C------GAGACCCTGCCACCCCTGCCACCCTGCTACTGCGGCAGCGATCAAGCC 3218

Qy    3279 CTCTGCCACGACGGAGCCGATACTACTGCTCCTCTCAGACTTCATCGTCTTGGATT CTCTCG 3338
                |||  |||||  | ||| || |||| ||||  |||| ||| | || ||| | |  ||||| ||
Db    3219 -AGCCGAACCGTGCGCTGCCGATTTGTCGTCGCGGCCGATTTCGTCGCGCGCCCGATGTGGT 3272

Qy    3339 GAATGAAAAATTGTTGTGGCATTCCGAGTCATTTTAGGAGTCATGATTGGGACAGAAAGAAA 3395
                ||||||| |  || |  ||| | |||  |||| | |||| ||    |  | |||| |||||
Db    3273 GGATGAAGCTTCATCGGCGGCTTCATCATCGGCAGAAGTGGCGCTGGGATCATGTGGCGGGGA 3332

Qy    3396 CAAGGCCTATGAGATGGATGATGTGACAGACTACAGCAGCATCATGGTCAAGGCTGTGGGGGA 3455
                ||||| |||||||| | ||||| || |||| || |||  ||||| |||||||| | | |||||
Db    3333 CAAGGGCTACGAGGAGCCGATGCTGCGGGCTGCTCAAGGACCATCATCGTCAAGGCGCTCGCCGA 3392

Qy    3456 CCGGTGCTGGTGAGTTGGGAGACATAGTTGGAGTAGGTCTGCGGAGAACTGTGGGC 3515
                ||  | |  ||| || ||  | || |    |||  | || |  ||||||||||  ||
Db    3393 CCGGCCTTCGCCGAGGCTGGTGGGGTGCGCGGGTGCTCCGGAGGAGTACTGGGG 3452

Qy    3516 CTACTGTGGCAATAATTTCGCCAGTTATTGATTTCCGAGTGGGTTGCCTGCTTTGGGGTAGAAGAGCTGCGGCAT 3575
                || | |||| || |||||  |   | ||  || || ||||||  ||||||  ||| ||||||| ||  |  ||||
Db    3453 CTACGCCGGCGCCAACTACGGCGTGTGAGTCTCATCGGCGTGATGTTTCCCGGCGGAGTTCGGCCAATACGTCGGCAT 3512

Qy    3576 CCGCCCCGGCTCCTGGCTCACCCGCCTGTCACCCCAGCGCCCGCCCGCCCCTGTCAATGGCCATGTGGGGA 3635
                |||| || |||| ||||||||| |||| |||| ||  |||||||| ||||| ||| |  ||||| |||||
Db    3513 CCGCCCCGGCTCTCGGCTACCGCCTGCCACCGGCGTTAACGAATCATTAGGTTAACAGAATCAATGGCC 3572

Qy    3636 ACTCGCGAGAGCAGTCGAGCAGTTAGCTATAAGGATTC 3695
                ||| |||| || ||| | | ||||||| |||||||  |
Db    3573 ACTGCTCTGACCCGGCTGTCGCCGCGACTACGCGATGTTCCC 3632

Qy    3696 TGCTTCAGCAGTCTCAGCGTCCTCTACTTCTCCAATTTGAAGTCAAGTATTTGCTGTGGGG 3755
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RESULT 12
US-09-543-681A-3077
; Sequence 3077, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3077
; LENGTH: 3750
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3077

  Query Match   23.0%; Score 901; DB 3; Length 3750;
  Best Local Similarity   55.0%; Pred. No. 7.9e-265;
  Matches 2045; Conservative   0; Mismatches 1575; Indels   99; Gaps   10;

Qy   145 AAGAGGATTATGTGTCTGAGATGAGGGATGGGACCATGATCAGCGGAGAAGCTAAAC 204
           |||||| ||| | ||| || |||||||||| |||||| ||||||||| || ||
Db   112 AAACGTTTAATAAAGAGGTAATTACCAAGAGCCCTGATGTTGCTCGTCAGCAAGTT 171

Qy   205 GAAGAACACTTCCGAGGTCAGGAGTTTAAAGATCATGCCAGCCGCGTCGAAAGGCAACAAT 264
           ||||| |||| ||| ||||| ||| ||||| || ||||||||| || |||
Db   172 GAAGAAGATTACCGAGGTGAACGTTTTGCCCCATTGGCGTTTAAAGGGAATAAT 231

Qy   265 GACATTTAAGTATAACTCAGCCTGATGTCATTTACCAAATCATAAGGAATACTTGCTG 324
           || || |||| ||| ||||| |||||| ||| |||| | || |||||
Db   232 GACCTTTTAGTCTTGACGCAGCCGCAGATCATTGAAACAAATACTTTATGTTGAA 291

Qy   325 GCTGGGGCAGATATCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCCAAGCTGAC 384
           |||| | ||||||| || | ||||| ||| ||||||||| ||| ||||||||
Db   292 GCCGGTGCAGATATCGTTAGAAACAAACACCTCTATTGCCATGGCTGAT 351

Qy   385 TATGGCCCTTGAACACTTGGCTACCGGATGAACATGTGCTCTGCAGGAGTGGCCAGAAAA 444
           ||||| ||| ||||||||||| | |||| |||||| || ||||||||| | |||||
Db   352 TATCAGATGGAAGGGTTATGTGCAGAATTGAATGAGAAGAGGGCTGCTAAAC 411

Qy   445 GCTGCCGAGGA---GGTAACTTCCAGACAGCAAGGAATTAAGAGGTTTGGCAGGGGCTCTG 501
           || ||| ||||| |||| |||||||| ||||| |||| |||||||||| ||| |||
Db   412 TGTGCTGATAAATGGAGTGCATTAACGCGTTATGTTGCAGGGGTATTA 471

Qy   502 GGTCCGACTAATAAGAACACTCTCTGTGTCCCCATCGTTGGAAAGGCCGGATTATAGGAAC 561
           |||||||| || | |||| ||| | |||| ||||||| || ||||| |||| || |
Db   472 GGGCCAACCAATGAACAGACAGCATCAATCATTTGATGTTAACGAATCCCGCATTTCGTAAT 531

Qy   562 ATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCCAAAGACTTCTGGATGGC 621
           || || ||||| ||| || || ||||| ||| || |||| |||| ||||
Db   532 ATCTTCATTTGATACATTGATGGCTTCATCGATGTCGGTTGCGTGTAGCAACGGGT 591

Qy   622 GGGGTTGAATCTTACTCATTGAAACTATTTGATACTATTTGCCAAATGCCAAGGCAGCCTTG 681
           ||||| || || | |||| |||| || ||| ||| |||||| |||||||||| ||
Db   592 GGGGTGGATTTAATTATGGTGAAACCATTTTTGACACTCTTTGTGCGGATATTTAAATCT 651

Qy   682 TTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCCGGCCTATCTTTATTTCAGGG 741
           || || |||||||| || |||||||| ||||| |||||||| |||| |||| |||||
Db   652 TTTGCGATTAAATGTGAGTTTGATAAATCTTAATATTGAATTACCGGTGATGATCTCAGG 711

Db   3633 CGGCCGGCGGTCAGCGGTTGTATTTCGCCCACCCGCAGGCGCAGTACTTCGCGGTCGG 3692
            || |||| ||| |||| ||| |||| | ||||| |||||||| |||||| |||
Qy   742 ACGATCGGTTGATAAAGTGGGCGACTCTTCCGGACAGACAGCAGGAAGCAGGGCTCATC 801

Db   3756 GGAGATTTCCAAGGATCAGGTTGGAGGATTATGCCATTCGGGATTAATGTGGTGCTGA 3815
            || |||| || |||||| ||| |||||||| | ||||| ||| || ||| |||
Qy   712 ACTATCACTGATCGCGTCAGGTAGAACATTAACAGGGGCAAACCAGAGGCCAGAGCGT 771

Db   3693 CAAGATCGACAAGGACCAGTGAACGTCGTGCTGGCTACGCAGCCAGGGCCGAAGCCAGCGT 3752
            |||| ||| |||| |||||||| ||| |||||||| ||| |||| || |||||||||
Qy   802 AGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGTGCTTTGGGTGCAGCTGAG 861

Db   3816 GGTTGAGAAATGGCTTGGACCCATTTGGGATATGAT 3852
            |||||||||||| || ||| |||| |||||||||
Qy   862 ATGAGACCTTTATTGAAATAATTGACAACAGCTACAACAGGCTATGTCCTCTCTGTTATCCC 921

Db   3753 CAGCGAGCGCTGCTGGCGCCGAACCTTGGCTACGAT 3789
            |||| ||| ||||| ||| |||||||||||| |||
Qy   832 TTACGCCAATATATTCAAACTCTCTCCCAAAATATCAGAAAACTTATGTCAGTGCTCACCCT 891

Qy   922 AATGCAGGTCTTCCACACCTTTGGTGACTATGATGAAACGCCTTCTCATGATGGCCAAG 981
           ||| |||| || | ||| |||| ||| |||||||| | |||| |||||||| |||
Db   892 AATGCTGCTTACCTAATGCCTTTGGGCCGGATATGATGATTTAGATGATGGCGGAA 951

Qy   982 CACCTAAAGAGATTTGCTATGATGGCTTGGTCATTAATAGTTGGAGGATGCTGTGGGTCA 1041
           || || |||||| | | || |||||| ||| ||| ||| | ||| |||||| |||
Db   952 CAAATCAAGGAGGTGGGCCGAAGCTGGGTTTCTTAATATTGTCGGTGGTTGTGTGGCACA 1011

Qy   1042 ACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATTGTAAGCTACGAGTTCCA 1101
            | |||| || ||||||| |||||| ||| || ||||| |||| ||| ||||||| |
Db   1012 ACCCCTGCCCATTCAGGCTATTGCTCAAGCGGTTATGGCATAGCACCTAGAACATTA 1071

Qy   1102 CCTGCCACTGCTTTGAAGGACATATGTTACTGTCTGGTCTCAGACCCCTTCAGGATTGAA 1161
            | | | ||| || || | | || ||| ||| ||| || ||| |||| |||||||
Db   1072 CCTGTCA------TTAAAAAGCCTGTCGACTTCAGGTCTTGAGCCTTTGGTCATTGAT 1125

Qy   1162 CCGTACACCAACTTGTTAACATTGGAGAGCGCGTATAATGTGCAGGATCAAGGAAGTTT 1221
            || | ||| ||| |||| |||| ||| ||||| || |||| | |||| |||
Db   1126 GATAATTCGTCGTTCGTCAATGTGGGGGACGAATGTGACATTGGACAGGTTCGGCTAAATTT 1185

Qy   1222 GCTAAACTCATCATCAGGCAGGAAGGACCTGTGTGTTGCCAAAGTGCAGTG 1281
            ||| | || | | |||||| ||||| || ||| |||| ||||| |||
Db   1186 AAACGTTTAATAAAGAGGTAATTACCAAGAGCCCTGATGTTGCTCGTCAGCAAGTT 1245

Qy   1282 GAAATGGGAGCCAGGTGTTGGATGTCAACATGGATGGCTAGATGCTCCAAGT 1341
            |||||| || ||| || |||| ||| |||||| ||||| ||| ||||
Db   1246 GAAAAACGGTGCTCAAATCATCGATATCAATCAATATCATGAGAAGGCATGCTGAGATGAA 1305

Qy   1342 GCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGACATCGCAAAGGTACCTTTG 1401
            || || | ||| || | || |||| || ||| |||| || || |||| |||||
Db   1306 GCAATGACAACGTTTTCTTAATCTTATTGTCGGGTGAACCCGATATTGCCAAAGTCCCGATT 1365

Qy   1402 TGCATCGACTCCTCCAATTTGCTGTGATTGAGAAGTGCTGGGAAGGGAAG 1461
            || || |||| || ||| | | | |||| |||| || ||||||
Db   1366 ATGATTGACTCGTCAAAATGGCAAGTCATTGAGGAAGATTGAAATGTTTATTCAGGGTAAG 1425

Qy   1462 TGCATTGTCAATAGCATTAGCTTTGATGAAGGAGAGGGGAAGGTACCTGGCCAGG 1521
            |||| || | || |||||| ||||||||||| ||| ||||| |||| ||||
Db   1426 GGAATAGTGCAATTGCGATTTCGATTTGCGATTTTTATTGAGCATCATGCAAA 1485

Qy   1522 AAGATTAAAAAGTATGGACGTCTGCTATGGGTTCATGGGTGGTTATGTGGTGCCAGAGCC 1581
            |||| || |||| |||||||| |||| ||| || ||| ||| ||| |||||| |||||
Db   1486 TTAGTTCGTAAGTATGTGTCTGCAGTTGCTGTTGTGATGCATTTGATGAAAAATAGGGCAAGCA 1545

Qy   1582 ACAGAACAGACACCAAAATCAGAGTGTGCACCCGGGCTACCATCTGCTTGTGAAAAAA 1641
            || | ||| | || || ||| ||||||||| || ||| ||||||||| |||||||
Db   1546 GATACTGCAGAGGCAAAAATAGAAATTGTGCTATCCATCATCTAACCATTGGGACTGAAAAA 1605

Qy   1642 CTGGGCTTTAATCAAATGACATTATTTTGACCCTAATATCCTAAACCATTCGGTAAT 1701
            ||||| ||| |||| || | |||| | ||||| || || |||||| ||||||
Db   1606 GCTGGATTTCCACCAGAGAGATATTATTTTTTGATCCCAATAITTTTGTCGTGTAGCAACGGGT 1665

Qy   1702 ATGGAGGAACACAACTTGTATGCCATTAATTTTATCCATGCAACAAAAGTCATTAAGAA 1761
            ||||| || || | || | || ||||| ||| | || ||||| || || |||||||
Db   1666 ATTGCTGAACATAATAATATGCGGTTGATTTTTATAGAAGTTGTCGTGATATTAAATCT 1725

Qy   1762 ACATTACCTGGAGCCAGATAAGTAAGTGGAGTTCTTCCAACTTGCGTCCCTTCCTTCCGAGGG 1821
            |||| | | ||||||||||| | |||| | ||| | | || || |||| |||| |||||

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Db  1726 CAACTGCCTTATGCTTTAATTTCTGGCGGTGTTCTAATGTGTCATTCTCTTTTCGGGGC 1785
                  ||||||||| || ||||| ||||  ||||| |||| |||| |||
Qy  1822 ATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTCCTTTACCATGCAATCAAGTCTGGC 1881
Db  1786 AATGATCCCGTTCGGGAAGCGATCCACTCACTGTTTATTACCGTGTAAAAAATAGGT 1845

Qy  1882 ATGGACATGGAGATAGTGAAACCTCCCTGTGTATGATGATATCCATAAGGAA 1941
                  || |||| |||  || || |||| |||  | |||||| || |
Db  1846 ATGGATATGGGGATTGTCAATGCTCGGGCAACTCGCTATTTATGACTCATTAGCGGATGAA 1905

Qy  1942 CTTCTGCAGCTCGTGTGAAGAGATCTCATCTGGAATAAAAGACCCTGAGGCCACTGAGAAGCTC 2001
                  || ||| |  |  || |   |||| || || ||  |||| ||||| ||||
Db  1906 CTACGTAATGCGGGTAGGAGGATGTTATTTTAAATCGGCCATGCAGAGTACTGATAATTTA 1965

Qy  2002 TTACGTTATGCCCAGACTCAAGC------ACAGGAGGAAGAAAGTCATTCAGACTGAT 2055
                  |||| | ||||||||||||| ||      || |||| |||| | |||| || ||
Db  1966 CTGGCAGCTCGGCAGAGAGGCGTATCGTGTACTAAAAGTTGAGGAACAGCACTCTACGCTTGCG 2025

Qy  2056 GAGTGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTTGTGAAGGGCATTGAA 2115
                  | ||| |||| || |||| |  |  || || |||||| |||||| | ||| |||| ||
Db  2026 CAATGGCGACAATGGGGAGGTCGAAAAGCGCCTAGAGTAGTAGGGGATCACC 2085

Qy  2116 AAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAAAATCCCGACCT 2175
                  ||  || | || ||||||||| |||||||||||  |||  | |||| | |||||||
Db  2086 GAATTTATCATTGAAGATACAGAAG--------CGTGCCGCCAACAAGCTTCGAGTCCT 2136

Qy  2176 CTCAATATAATTGAAGACCCCTGATGAATGAAATTGTTGGTGATCTTTTTGGA 2235
                  || || | | ||||  |  | ||  |||||| ||||||||| ||| | ||||
Db  2137 ATCGAAGTGATAGAAGGGGCCATTAATGAATGCATGAACAGTGGGGCGATCTCGTTTTGGT 2196

Qy  2236 GCTGAAAAATGTTTCTACCTTCAGGTTATAAAGTCAGCGGGTATGAAGAAGGCTGTT 2295
                  ||||||||||| ||| |  || || |||||||| | |  || ||||| |||||| ||
Db  2197 GAAGGTAAAATGTTTTTTACCCCAAGTAGTAAAATCGGCACGGGTGATGAAAACAGGCCGTA 2256

Qy  2296 GGCCACCTTATCCCTTCATGGAAAAAAGAAGAGAGAAACCAGAGTGCTTAACGGCACA 2355
                  |||||| |||| ||| | |  |||| ||| || |   | |||| || | ||  ||
Db  2257 GCTTACCTTGAACCTTATATTCAAGCGGACAAAAAAAAAGCAGCAG------------ 2300

Qy  2356 GTAGAAGAGAGGACCCTGTGGCCACATGCTGCTGGCCACTGTTAAAGGCGACGTG 2415
                  || || |   ||  ||| ||||||| ||  |  |||  ||||||| |||||||||
Db  2301 ----------CTCCGGCAGGAAAAGTGTTACTGGCGGTAAAGGTAAAGGGGGAGATGTC 2343

Qy  2416 CACGACATAGGCAAGACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCCGAGTTATT 2475
                  ||||| || || |  | || ||||| || | | | ||||||||||| ||| ||||| |
Db  2344 CACGACATTGGCAAAAATATTGTCGGAGTGGTGTTCGGGTTGTTGCAAAATGAAAATATC 2403

Qy  2476 GATTTAGGAGTCATGACTCATGTGATAAGATCATAGAGAACTACTGAAAGTGCTCTTGACCACAAGCA 2535
                  ||||| ||||| ||  || |||||| ||  | || || |||| | ||||||| || |||||||||| |
Db  2404 GATCTCGGGGGTCATGTGCATGTGAATTTGCGGATAAATCTTGCAAACAGCCATTGGTTCAAACAGTT 2463

Qy  2536 GATATAATTGGCCTGTCGAGGACTCATCATCTCCCTGGATGAAATGATTTTTGTTGCC 2595
                  ||||| ||||| | |||| | |  || ||| |  |||| |||| ||| || || |||
Db  2464 GATATTATTGGATTGTCTGGATTGATCACTCACTGACTGATGAGAGTGGTTGAATGTTGCT 2523

Qy  2596 AAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCA 2655
                  ||||| ||| || || || | || | |  |||| |||| |||||| || || ||| | |
Db  2524 AAGGAGGATGGAAAAGACGCGGGTTTTCTCTTTTTAATGATGGTGGTGCGACAACATCG 2583

Qy  2656 AAAACCACACAGCAGTAAAATAGTCTGGAGAATAGCTAGCCTGTCACCTGTAATCCATGTCCTG 2715
                  |||| || || ||||| | |||  | |  |||| || || |  | ||| ||||  || || ||
Db  2584 AAAGCGCACACACGGCCAGTGAAAATTCTGAACCTAATTACAGCCACCCAACCGTTTATGTGCAG 2643

Qy  2716 GACGCGTCCAAGAGTGTGGTGGTCGTGTGTTCCCAGCTGTTAGATGAAAATCTAAGGATGAA 2775
                  ||||| |||| |  | ||| |||| ||| ||| ||||||| | ||||||||| |||||||||
Db  2644 AATGCGTCAAGAACCGGTCGGGGTGTCGCTGCATTATTCGGCTCGCCAATGCCTGCCAAAAGGCTGAT 2703

Qy  2776 TACTTTGAGGAAATCATGGAAGAAATAGCAGAGGACCATTATGAGTCTCTC 2835
                  || ||| | |  | |  | || || ||| | | ||| | ||||| | |||
Db  2704 TTTGTCGCTAAAACACGCGGTGAATATGGTACGTCAGCAGTATGCGGAGAAAAAA 2763

Qy  2836 AAGGAGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAGTGGTTCCAAATGGATTGG 2895
                  ||||| |  || || | || |||| | ||| | ||| |  | |||||||||  |||
Db  2764 CCGGTACGCGCTCCCGTTTCCTTAGCGACGCAGCTCGTCGCCAATGCCATTGCAGCTTGACTGG 2823
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Db  2896 CTGTCTGAACCTCACCCCAGTGAAGCCACGTTATTGGACCCAGGTCTTTGAAGACTAT 2955
                  |||| |||||| | ||||| |||||||||  || |  |||  || || |||  | |||
Db  2824 CAACACTATACGGCCACTAAGCCGACCAACCAATTAGGGTACACACAAGTTACAGCCAATATT 2883

Qy  2956 GACCTGCAGAAGCTGGTGGACTACATTCATTGGGATCTGGAAGCCTTCTTGATGTCTCGGCAGCTC 3015
                  |||       |||| | ||| | || ||| |||| ||| ||   |||  |||| ||||| ||
Db  2884 GAA-----ACTTACGTGAGTATATCGACTGGACTGGACGCGCTTTCTTTATGACTTGGTCATTG 2937

Qy  3016 CGGGGCAAGTACCCGAATCGAGCGTTCCCCAAGATATTTAACGACAAAACAGTAGGTGGA 3075
                  || || | ||| | |  |  |||  || |  |||||||||    |     ||||  | ||
Db  2938 GCGGGGAAATATCCACGT----------ATATTAGAGATGAGGCGTGTCGGGACAA 2982

Qy  3076 GAGGCCAGGAAGGTCTACGATGATGAGGTCCACAATATGCTGAACACACTGATTAGTCAAAAG 3135
                  || ||||| ||| ||| |  |||| |||| |  |||||| |||  |  | |||  || ||||
Db  2983 GAGGCAAGACCGCGTTTTTGCGAGATGCCATGTTGGATAAAACTCAGCCGTGAAAA 3042

Qy  3136 AAACTCCGGGCCCGGGGTGTGGTTGGGTTCTGCCAGCACAGAGTATCCAAGACGACATT 3195
                  |  |||||| |  |  | || | |||| |  || ||| || |||| ||| | ||||||
Db  3043 TTACTGACACCGAAAAGTATCGTTGGTTTATTCCGTCTAATCGCCTTGGTGTGATGACATT 3102

Qy  3196 CACCTGTACGGCAGAGGCTGCTGCTGCGCCCAGCGTCAGAGCCCATAGCCACTTCTATGTGG 3255
                  || || || | | ||   ||  |   ||| |||| |||||||||| ||   |  |||||||
Db  3103 ATTATTTTACCAAGGTGAAACGCGACAGCATG--------AGTTATTACGTTGTTGCCAT 3153

Qy  3256 TTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGGCCATACTACTACTGCCTCTCAGAC 3315
                  || || ||  |  ||||| | | || | || ||| || |  | |||  |  |||  ||  ||||
Db  3154 TTACGCCAACAACAGAGAAAAAAA--------GAGTACCCAACATATGCTTAGCAGAC 3204

Qy  3316 TTCATCGTCTCCCTTGCATTCTGCGATCCGTGACTACCGTGGGCGTCTTGTTGCGTTGCCTGC 3375
                  || || | | |||| | | |||| |||||||| | |||   |  || |||  |||  | ||||
Db  3205 TTTATTGCCCCTGTGGATAGTGTCTTGCTGCTACTAATTTTTGCGTTTCAGTTACCCGGC 3264

Qy  3376 TTTGGGTAGAAGA---GCTGAGCAAGGCCTATGGAGGATGGTTGACGACTACAGCAGC 3432
                  ||||| |  | ||   ||| ||| |  |  |  | |||| | |||| || |  |||||
Db  3265 GGTCTAGAAGAAGATGCACTCGCTAATGGGTATGATAATAATGCTCATGATGATTACAATAAA 3324

Qy  3433 ATCATGGTCAAGGCGCTGGGGGACCGGGCCTGTCAGAGAGAGTCCATGAA 3492
                  || |||  ||| | |||| ||||| || ||  ||| ||||| ||||||||
Db  3325 ATTATGTGGTAAAAGCGCTATCCGATCGGATCGGCGAAGCTTTTGCCATCAA 3384

Qy  3493 AGAGTTCGCCGAGAACTGTGGGGCCTACTGTGGCAGTGAGCGACGTCGGACCTG 3552
                  ||| || ||||| | | |||  ||| | || || || |  ||||| |||| ||
Db  3385 CAAGTGAACCAAAAATTTGGGTTACAGTCTCTGACGAAGCGCCTGAGAGTTG 3444

Qy  3553 CGAAGGTTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCCAGCCGACCACCAC 3612
                  ||||||| ||||| |  | ||| || || |  ||| | ||||||| ||||| |
Db  3445 ATTAGAGAAAAATATCAAGGAACAAGGACCTGCACCGGGATCAGTTGCCCAGAGCAC 3504

Qy  3613 ACCGAGAAGCTCACCATGTGGGACTGTGGAGGACTCGACAGTCTCACAGGCATTAGGTTA 3672
                  ||| |||| ||||| ||  |||| ||  |  ||| ||| | ||| ||||| |||||||||
Db  3505 ACAGAAAAAGCAAAAATTTGGCAACTGTTAAATGTAGAAAATCGCATTGGTATGAAGCTT 3564

Qy  3673 ACAGAATCATTAGCAATGGCCACCTGCTTCAGCAGTCTCCAGTTTTGTATCATCCTT 3732
                  |||  || || | | |||  ||| ||| | || || | ||| || |  |||||| |
Db  3565 ACTGATGCTTATGCGATGTGGCCGGGGGCTTCGGTTATCGGGTTGGTATTTAGTTAGTCATCATTG 3624

Qy  3733 AAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGATATGCATTG 3792
                  ||||| ||| | ||||| |  ||  | ||||| |  ||| | ||||  |||| | |  |||
Db  3625 GAAAGTAAAATATTTTTCGCGTGGCTGCTCAATTCAAAAAGATCAGGTAGAAGATTACGCCAAA 3684

Qy  3793 AGGAAGAACATATCTGTGGCTTGAGGTTGAGAAATGGCTTGAGAATGA 3851
                  || ||| || || |  || ||| ||| ||| | ||| | |||| |||
Db  3685 CGTGCGTGTATGAGTATGAGTATGAAGTTGAGCGTTGGTTAGCCCCTAATTTAGGTTATGA 3743
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; TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1578
; LENGTH: 3702
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1578

Query Match   22.9%;   Score 895.8; DB 3;   Length 3702;
Best Local Similarity 55.1%; Pred. No. 3.1e-263;
Matches 2060; Conservative   0; Mismatches 1567; Indels 114; Gaps   11;

Qy   128 TCAATGCCATTCTGCGAGAAGAGGATTATGGTGCTGGATGAGGAGGATGGGACCATGATCC   187
Db   35 TAAAAGCGCTTCTTGCTAAACCATTCTGATTATTGATGGTGCAATCGGAACCATGATCC   94

Qy   188 AGCGGGAGAAGCTAAACGAAGAACACTTCCAGAGTCAGGAATTTAAAGATCATGCCAGGC   247
Db   95 AGCGCCATAAAATTGGAAGAGCTGACTATCGTGTGGTGAGCGTTTGCTGATTGGGCACATG   154

Qy   248 CGCTGAAAGGCAACAATGACATTTTAAGTAATAAACTCAGCCTGATGTCATTTACCAAATCC   307
Db   155 ACTTAAAAGGTAACAATGACCTTTTGGTTTTAACACAGCCTCAAATCATTCAAGGTATTC   214

Qy   308 ATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCAGCACTA   367
Db   215 ATGAAGCCTACCTCGATGCTGGTGCAGACATTTGTTCCAGATTAACCAACGGCACAC   274

Qy   368 GTATTGCCCAAGCTGACTATGGCCTTGAACACTTGCCTACCCGGATGAACATGTGCTCTG   427
Db   275 GTGTTTCAATGTCTGCACTATCACATGGAAGATCTTGTTCCAGATTAACCGTGAAGCAG   334

Qy   428 CAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAAGAGGTTTG   487
Db   335 CACGTTTAGCCAAAGCAGCTTGCCGAAA---ATATTCGACTCCAGACAAACCCGGTTTTG   391

Qy   488 TGGCAGGGGCTCTGGGGTCCGACTAATAAGAACACTCTCTGTGTCCCATCTGTGGAAAGGC   547
Db   392 TGGCAGGTGTACTGGGGCCAACATCTCGTACATGTTCAAATCTCCAGATGTGAACAACC   451

Qy   548 CGGATTATAGGAACACATCACCATTTGATGAGCGTTGTTGAAGCATACCAAGAGAGCAGGCCAAAG   607
Db   452 CTGCTTTTCGTAACATTAGCTTTGATGAACTAAAAGAAAATTATATGAAGCAACTCATG   511

Qy   608 GACTTCTCGGATGGCGCGGGGTTGATATCTTCATTGCATTTTGATACTGCCAATG   667
Db   512 CACTAATTGAAGGTGGTGCAGACATTATCCTGATTGAAAACTGTATTGATACTTTAAACT   571

Qy   668 CCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATGTCTCCCCGGCCTA   727
Db   572 GTAAAGCAGCGGATTTTCTGCGCGCCCTCACGTAAAAATTGGTCGCCGGAATTACCAA   631

Qy   728 TCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGACTCCTTTCCGGACAGAGGAG   787
Db   632 TTATGATTTCAGGGACCATTACCGATGCATCAGGCCGTACTTTAACAGGTCAGCAGCGCG   691

Qy   788 AGGGATTGTCATCAGCGTGTCTCATGATGAGAACCACTTGCATTGGATTAAATTGTGCTT   847
Db   692 AAGCTTTCTGGAATTCGGTTCGTTCGTTCAATCGGTTTTCAATCGGTTTAACTGTGCCC   751

Qy   848 TGGGTGCACTGAGATGAAATGTATTATTGAAAATATGATGAAAATGTACACAGCCTATG   907
Db   752 TTGGTGCAGATGCCATGCGCCCTCACGTAAAAATACTATTTCCGATGTCGCAGATACCTTTG   811

Qy   908 TCCTCTGTTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAAACGCCTT   967
Db   812 TTTCAGCGCACCCCAAATGCAGGCTTACCAAACTGGTGAATATGACGAAACTCCAG   871

Qy   968 CTATGATGGCCAAGCACACTCAAAGGATTTTGCTATGGATGGCTTGGTCAATATAGTTGGAG   1027
Db   872 AGCAAACTGCAGCTTCTTCTAAAAGAGTTGCTGAAAGCGGTTTGATTAACATTACGGGTG   931

Qy   1028 GATGCTGGTGGTCAACACCAGTCATATATCAGGGAAATTGCTGAAGCTTGTGAAAAATTGTA 1087
Db   932 GCTGCTGGTGGTACGACACCAGCCATATTGCCAATGCTATTGCCAATGCGTAAAAGACATTG   991

Qy   1088 AGCCTAGAGTTCCACTGCCCACTGCTTTGAAGGACATATGTTACTGTCTCGGTCTAGAGC   1147
Db   992 CGCCTCGCCTGCCTGAAAACGTGCTGAAACAGTACCGCTGCTGCC------GCTTAAGTGGTTTAGAAC   1045

Qy   1148 CCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCGTGTAATGTTGCAG   1207
Db   1046 CATTTAATATTTATAAGTCATTGTTTGTAAACGTTGGTGGTGGACGTACTAACGTTACTG   1105

Qy   1208 GATCAAGGAAGTTGCTAAACTCATCATCGGCCAGGAAACTATGAAGAAGAGCCTTGTGTGTTG   1267
Db   1106 GTTCTAAAAAATTCTTACGTCCATTCCATTCGTGAAGAGAACTTTGCAGAAGCTTTAGAAGTTG   1165

Qy   1268 CCAAAGTGCAGGTGGAAATGGGAGCCCCAGGTGTTGGATGTCAACATGGATGGATGGCATGC   1327
Db   1166 CACAGCAACAAGTCGAAGCTGGCGGCACAGATTATTGACATTAACATGATGAAGGGATGC   1225

Qy   1328 TAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCAGACATCG   1387
Db   1226 TCGATTCGCAAAATGCGATGGGTGCATTTCTTAAACCTTGTGAGCATCCGAACCTGACATTT   1285

Qy   1388 CAAAGGTACCTTTGTGCATCGACTCCTCCCAATTTGCTGTGATTGAAGCTGGGTAAAGT   1447
Db   1286 CACGTGTACCGATCATGATTGACTCATCGAAAATGGGAAAATCATTGAAGCTGGCTTAAAAT   1345

Qy   1448 GCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGAGACGACTTCT   1507
Db   1346 GGCTACAAGGTAAACCGGTTGTTAACCTCAATTTCTTAAAAGAAGGAGGTTATGACGAGTTCG   1405

Qy   1508 TGGAGAAGGCCAGGAAGATTAAAAGTATGGAGCTGCTGTGTCTATGGCTTTGATG   1567
Db   1406 TCGAAAAAGCCCGCCTCTGCCGTCAATACGGTGCTGCAATTATTGTGATGGCATTTGACG   1465

Qy   1568 AAGAAGGACAGGCAACAGACAGAACAAAATCAGAGTGTGCACCCGGGCCTACCATC   1627
Db   1466 AAGTAGGTCAGGCCGACACTGCTGAACGTAAACGTGAAATCTGTAAGCGCTCTTACGACA   1525

Qy   1628 TGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATATCCTAA   1687
Db   1526 TTTTAGTAAACGAAGTAGGCTTCCCTGCTGCAAGTTTTTTGACCCGAACGTGTTTG   1585

Qy   1688 CCATTGGACTGAATGGAGAATGGAGAACACAACTTGTATGCCATTAATTTATCCATGCAACAA   1747
Db   1586 CAGTTGCAACTGGTTATTGAAGAACACACAACACACGCAGTCGATTTTATTGAAGCAACCG   1645

Qy   1748 AAGTCATTAAAGAAGAAACATTACCTGGAGGCGAGAATAAGTGGAGTCTTCTTCCAACTTGTCCT   1807
Db   1646 GCTGGATTAAACAGAACTTACCGCACTCCATGATTTCTCGGTGGTGTGTCTAACGTTTTCGT   1705

Qy   1808 TCTCCTTCCGCAAGTGAAGCAATGAAGCCATCATTCGAGAAGCACAGAGGAG   1867
Db   1706 TCTTCATTCCGTGGCCATGAGCAGCCATTCACTCGTATTCTTGTACCATG   1765

Qy   1868 CAATCAAGTCTGCCATGACATCGAGATAGTGAGATGCGGGAAACCTCCCTGTGTTATGATG   1927
Db   1766 CCATCAAACAAGGCATGACCATGGTATTGTGAACGCAGGTCAAGTTGCATGGCTATTTATGATG   1825

Qy   1928 ATATCCATAAGGACTTCGCAGCTCTGCAGCTCATCTCGAATCTCGAGAATAAAGACCCTGAGG   1987
Db   1826 ATATTCCTACCGAGCTAAAAGAAGCGGTTGAAGATGTCATTTTAAATCAGAATCAAGGTG   1885

Qy   1988 CCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACA------   2028
Db   1886 AGTTGGTCAGGCTGCACCGAATTACTTGAAGTTGCAGAAAATACCGTGACAAG   1945

Qy   2029 --GGAGGGAAGAAAGCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCGCC   2086
Db   1946 GTGGTGCAACAAAAGAAGCCGAGAACCTTGGTCAATGAATGAATCGTCAATATAGTTGGAG   2005

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Qy  2087 TTGAGTATGCCCTTGTGAAGGGCCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCA 2146
         ||||    |||||||||  ||  ||  |      | || |||| |     |||||| |||
Db  2006 TTGAATATGCCCTTGGTTAAAGGTATTACGACTTATATTGACCAAGACACCGAAGAGAGCTC 2065

Qy  2147 GGTTAAACCAAAAAAAAATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATG 2206
         | |||||  ||||    |          |||  ||| |||||| ||| ||| || |||| |
Db  2066 GCTTAAAATCAAAA--------CGTCCTTTAGATGTGATTGAAGGGCCACTAAATCGGACG 2116

Qy  2207 GAATGAAAATTGTTGGGTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAA 2266
         | ||||| | ||| ||||||    |  ||| | |||||||||||   | |||  ||| ||
Db  2117 GCATGAACGTCGTCGGTGACTTATTCGGTTCAGGCAAAATGTTCTTGCCACAAGTTGTAA 2176

Qy  2267 AGTCCAGCCCGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAA 2326
         | ||  ||| ||| ||||| ||| || | ||  ||  |||||  |||| | || |  |||
Db  2177 AATCTGCCCAGAGTCATGAAACAAGCAGTGGCATGGCTCAACCCGTACATCGAAGCTGAAA 2236

Qy  2327 GAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAGAGACCCTTACCAGGGCACCA 2386
                            |||  || ||| ||  |    | ||  ||||| |||| |||
Db  2237 -------------------AGACCGAAGGACAGTCTAAAGGTAAAG 2263

Qy  2387 TCGTGCTGGCCACTGTTAAAGGCGACGTGCACGACAAGAACATAGTTGGAGTAG 2446
         || | |||| |||||||||||| |||  | | ||  |    ||| || | | ||
Db  2264 TCCTAATGGCAACGGTTAAAGGTGACTACACGATATTGGTAAAAATATTGTAGGCGGTAG 2323

Qy  2447 TCCTTGGCTGCAATAATTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGA 2506
         | ||||||||  || | |  ||| ||||| || ||||| |||| | | ||  | |||||
Db  2324 TACTTGGCTGTAATGGCTATGTGACATTGTGACCTTGGCGTAAATGGTACCTTGCGAGAGA 2383

Qy  2507 TACTGAAAGTGCTCTTGACCACAAAGCAGATATATTGGCCTGTCAGGACTCATCACTC 2566
         |  | ||| ||| |||||   |||| ||| |||| ||  |  |||| || ||||| |
Db  2384 TCTTACAAACTGCAATTGATGAAAAATGTGACAATCATCGGATTATCTGGTCGATCACCC 2443

Qy  2567 CTTCCCTGGATGAAATGATTTTTGTTGTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTC 2626
          |||  | |||| ||||| |  || |  |||| |||| |  |  |||  |||| ||| ||||
Db  2444 CATCTTTTAGATGATGAAATGGTATTGTTTGCTAAAGAAATGCAGCGTAAAGGCTTTAACATTC 2503

Qy  2627 CATTGTTGATTGGAGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAG---CTC 2683
         | ||||||||||| | |    | |||| |||| |   | | ||| ||||||||   |
Db  2504 CTTTATTGATTGGTGGTGGCGACTACTTCTAAAGCACATACAGCAGTAAAAATTGACCCCTC 2563

Qy  2684 CGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGTGTGTGTT 2743
          |  || ||  | ||  |||||   || ||||| || | |  ||||| || | |||
Db  2564 AGTATCAAAACGATGCGGTAATTATGTTGCTGATGCTTCACGTGCTGTGTGGTGTGAGCGA 2623

Qy  2744 CCCAGCTGTTAGATGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATG 2803
         | | |||| | ||| |||||||   | |  ||| | | | |||| ||| |||| |||||||
Db  2624 CAACCTTGCTTTGCCAGAAAATGCCGTTGGCCCGCATTTATTGAAGAACATCGCTGCTGAATATG 2683

Qy  2804 AAGATATTAGACAGGACCATTATGAGTCTCTCAAGGAGAGAGGAGATACTTACCCCTTAAGTC 2863
         | |  || | || |  || ||| || || ||||| |||  | | ||| || || | |||
Db  2684 CCAAAATTCGTGAGCGTTTAGCCGTTTCCAACAAACACCAAAAGCGGCCAAACTGACTTATAAAG 2743

Qy  2864 AAGCCAGAAAAGTGGTTTCCAAATGATTGGCTGTCTGACCTCACCCAGTGAAGCCCA 2923
         |||| |||| |||||||   |||||| ||    |  |||| |||||| |||| |
Db  2744 AGTCCGGTTGAAAAATGGTTTAAAATTGATGAAAGCTACGTGCCAC------CAAAACCAA 2797

Qy  2924 CGTTTATTGGGACCCAGGTCTTGAAAGACTATGACCTGCAGAAGCTGGTGGACTACATTG 2983
         ||||||||||||  |||| ||| |||||| |||| || | | | |||||||| |  |||
Db  2798 ATCTTTTGGGAACACAAGTTTTAAGAAATTATCCGCTTGCTACACTCGTGGATTATTTTG 2857

Qy  2984 ACTGGAAGCCTTTCTTTGATGTCTGGCAGCTCCGGGGCAAGTAGCCCGAATCGAGGCTTCC 3043
         |||||| ||| ||||| |  ||| ||||| | |   | | |||      |  ||  ||||
Db  2858 ACTGGACGCGCCATTCTTTATTTCTTGGAGTTTAACTCGCAA-------ATTCC 2902

Qy  3044 CCAAGATATTTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCC 3103
          | || ||||| | ||| ||  ||| || | | |||  || |||| |  || ||||| |
Db  2903 CGAAAATTTTTAGAAGATGAAGTGGTCGGCGAAGCAGCAACTTGTACAACCAAGCAC 2962

Qy  3104 ACAATAATGCTGAACACACTGATTAGTCGACAACAATCGTTTTGATGCTGCTGTGTATTTGGTA 3163
         |  | | || | ||  ||| |||| | |||   ||||| ||||| || | |||| | |||||||
Db  2963 AAGGCGATGTTGAAAGATGTTGAAAGATATTATCGACACAGAAATATTCGTTTGATGCTGCTGTGTATTTGGTA 3022
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Qy  3164 TCTGGCCAGCACAGAGTATCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCC 3223
          | | ||| || || | ||      | || || |||  | || | | |  | ||||
Db  3023 TGTTCCCTGCTCAGCGTACAGACGCAGATACAGTCAGCGTATTGATGAAGCTGGTCAAA 3082

Qy  3224 AGGCTGCAGAGCCCATAGCCACTTTCTATGGGTTAAGCCAACAGGCTGAGAAGGACTCTG 3283
          | || || | || || | | || |  |  || ||| | | | |||  |||  | |
Db  3083 ATGTTACGCA--------TACTTTGAGCACTTACGCCAGCAATCTGACAAAGTGACAG 3133

Qy  3284 CCAGCACGGAGCCATACTACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCGGCATCC 3343
         | |        |  |   || |  |   || || || ||  ||||||  | || |
Db  3134 GCA------AACCAAACTTGTCTTTGGCAGATTACAT---TCGTGCTACCGCGAGCAGC 3184

Qy  3344 GTGACTACCTGGGCTGTTGCCGTTGCCTGCTTTGGGTAGAAGAGCTGAGCAAGGCCT 3403
          | ||||| ||||| |    |  | ||  | | ||||||| | |  ||| ||| || |
Db  3185 AAGACTACTTGGGCGGATTCACTGTATCGATTTTGGTGCAGAGAACTGGCAAATGAAT 3244

Qy  3404 ATGAGGATGATGGTGACGACTACAGCAGCATCATGGTCAAGGCGCTCGGGGGACCGGCTGG 3463
          | | | | || | |  | || | |  | |||  |||| |||||   ||| ||||| |||
Db  3245 ACAAAGCCAAAGTGATGACTACTCTGCAATCTTAGTTCAGTCAGTCGACCGTTTTG 3304

Qy  3464 CAGAGGGCCTTTGCAGAGAGAGCTCCATGAAAGAGTTCCGCCGAGAACTGTGGGCCTACTGTG 3523
         |||  | | ||||||||  || |  |||||| |||||| || | ||  ||||| ||| |||
Db  3305 CAGAAGCTTTTGCAGAACACTTACATGAAGTTCTGGGGTTATAAAG 3364

Qy  3524 GCAGTGAGCAGCTGGACGTCCGCAGACTGCGGTACAAGGTTGCGGTACAAGGGCATCCGCCCGG 3583
         |  | | ||| ||| |  |  | ||| || |  | || |||| |||  ||| ||| | || ||
Db  3365 CGGATGAACAGTTAGCAATGAAGAACTGATTAAAGAGAAATATGTCGGTATTCGTCCTG 3424

Qy  3584 CTTCCTGGCTACCCCGCCAGCCCGACCACCGAGAAGCTCACCATGTGGAGACTCGGCAG 3643
         |  | ||| ||||| || || || |||| ||  | || |||   |||||  | |||||
Db  3425 CACCGGGTTACCCTGCTTGCCCTGAGCACTCTGAAAAGGCAGTGTTATTTGACTGGTTAG 3484

Qy  3644 ACATCGACGAGCTACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAG 3703
         | |  | || | ||  |    | |  | || || | |  |||| |||| ||| |   |
Db  3485 GTTCTACCGACAAAAATCGGTACTAAACTCACTGAACACTTTGCAATGATGCCACCATCTT 3544

Qy  3704 CAGTCTCAGGCCTCTACTTCTCCAATTGAAGTCCAAATATTTTGCTGTGGGGGAAGATTT 3763
         | || |  | ||| ||| | |   |||  | || ||||||| | ||| | || ||||||
Db  3545 CGTAAGTGGTTTCTATTATTCTCAATCGGTGTTTCATCCTCAAAGTGAATACTTAACGTGGGTAAAATTT 3604

Qy  3764 CCAAGGATCAGTTGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGA 3823
         | ||| | ||| || | ||||||   | | ||  |    |  || ||  | || |||
Db  3605 CTCAAGACCAACTTGAAGATTATGCGAAACGTAAAGGTTGGACACTGGATGAAGCGAAGC 3664

Qy  3824 AATGGCTTGGACCCCATTTTGG 3844
         | ||| |||| || | |||| |
Db  3665 GTTGGTTAGCGCCGAATTTAG 3685
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Query Match        17.9%;  Score 701;  DB 3;  Length 3138;
Best Local Similarity  54.2%;  Pred. No. 1.6e-203;
Matches 1648;  Conservative  0;  Mismatches 1311;  Indels  81;  Gaps  8;
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;  CURRENT FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: US 60/074,788
;  PRIOR FILING DATE: 1998-02-18
;  PRIOR APPLICATION NUMBER: US 60/094,190
;  PRIOR FILING DATE: 1998-07-27
;  NUMBER OF SEQ ID NOS: 33142
   SEQ ID NO 13893
;  LENGTH: 2349
;  TYPE: DNA
;  ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13893

Query Match    15.7%;  Score 615.8;  DB 3;  Length 2349;
Best Local Similarity  56.1%;  Pred. No. 1.9e-177;
Matches  1251;  Conservative  0;  Mismatches  957;  Indels  21;  Gaps  4;
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Qy      113  CCCTGCCGGATGAGATCAATGCCATTCTGCAGAAGAAGATTATGGTGTCGATGGAGGA 172
                  |||||||||||||| || ||||| | ||  |||||||||  | |  || |||
Db      135  CCCGCCTGCAAGCCCTCCAGCACGCCCTCAGGGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTA 194

Qy      173  TGGGACCACCATGATCAGCGGGAGAAGCTACAAAGCTGGAAGAGGCCGAGCGGCTTCG 232
                  |||||||||||||||||||| ||| ||  ||||
Db      195  TGGGCCACCATGATCCAGGAGCTACCAAGCTGGAAGAGGCCGAGCGGCTTCG 254

Qy      233  AAGATCATGCCAGGCCGCTGAAAGCCAACAATGACATTTAAGTATAACTCAGCCTGATG 292
                  |||| ||||  |   |||| |||||||||||||
Db      255  CCGACTGGCCGAGCGACGTGAAAGCCAAGGCAACAACGACCTCTTGCTGCTGAGCCGCCGGACG 314

Qy      293  TCATTTACCAAATCCATAAGGAATACTTGCTGGCTGGGCTGGGCAGCCAGATATCATTGAAACAAATA 352
                  ||  |  ||| |||||| || |||| |||| |||||
Db      315  TGATCCAGGCCATCGAGAAGGCCTACCTCGACGGCCGCGGCCTTGAACACTTGACACTGGCCTACCGGA 374

Qy      353  CTTTTAGCAGCACTAGTATTGCCCAAGTCGACTATGGCCCAGCACATCGCAGCGCGACGAGT 412
                  |||||||
Db      375  CCTTCAACGCCACCACCAGGTGTCCCAGGCCGACTACCAGTCAGTCGGTCGGCTGGCCTACGAAC 434

Qy      413  TGAACATGTGCTCTGCGAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGA--- 469
                  |||  |   ||||||||| ||||
Db      435  TCAACCTCGAAGGGCCGCGCGCCTGCCCGCCGGGGGCTCCGGGGTCCGACTAATAAGACACCGCCGAGACCC 494

Qy      470  CAGGAATTAAGAGAGTTGTTGGTCAGCTGAGATTGGGGCTCTGTCGGCCGTTTGACTGGG 529
                  ||||| ||||||| |   |||
Db      495  CGGACAAGCCCGCGCTTCGTCGCGCGGTGCTCGGCCGCCCACCCGACCCCACCGCCTGCTCGATTT 554

Qy      530  CCCCATCTGTGGAAAGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAGCAT 589
                  |  ||||||||||||
Db      555  CCCCGGACGTGGACAACCCCGGTACCGCAACGTTACCGACCTCGACGAACTGAGGGAGGAGAACT 614

Qy      590  ACCAAGAGCAGGCCAAAGGACTTCTGATGGCGGGGTTGATATCTTACTCATTGAAAACTA 649
                  ||  |||  | ||||  | ||||
Db      615  ACGTGCAGGCCGGACGCCGCCTGATCGAAGGGCGGCCGGCCAGCATCACCGACGTGTCATCAGCGACCA 674

Qy      650  TTTTGATACTGCCAATGCCAAGGCAGCCTTGTTGCACTCGAAGGCAGCCTTTGAGGAGA 709
                  ||||||||||||||||
Db      675  TCTTCGCACCCCTCAACGCCAAGGCGGCGATCTTCGCCGTGCTCCAGGGCGTGTTCGAGGAAC 734

Qy      710  AATATGCTCCCCGGCCGCCATCTTTATTGCGGACGATCGTTGATAAAAGTGGGCGGACTC 769
                  ||||||
Db      735  TCGGCGTGGAGCTGCCGATCATGATCTCCGGACCATCACCGACGCGTCCATCCGGCCGCACCC 794

Qy      770  TTTCCGGACAGAGCAGGAGGATTTGTCATCGAGCGGCCCGGATCTCGG 829
                  |  |||||||| |
Db      795  TGTCGGGCCGGAGCCACCGAGGCCTTCGGTGCGGGCCATGGCCCGGATCTCGG 854

Qy      830  TTGGATTAAATTGGCTTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAA 889

Db      855  TAGGCCTGACCTGCGGCCCTCGCCCAAGAGGAATTGCGGCCGTACATCGAGAGAACTGTCGA 914

Qy      890  AATGTACAACAGACCTATGTCCTCTGTATCCCAATGCAGAGGTCTTCCCACACCTTTGGTG 949

Db      915  CCAAGGCCGACACTCATGTCTCGGCCCCAACGCCCACCCCAAGCGCGACCGCTTCGGCG 974

Qy      950  ACTATGATGAAACCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCT 1009
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Db     2231  AAGGCAAAATGTTCCTGCCGCAGGTGGTGAAATCCGCCCGTGTAATGAAACAGGCGGTGG 2290

Qy     2297  GCCACCTTATCCCTTTCATGGAAAAGAAGAAGAAGAAACCAGAGTGCTTAACGGCACAG 2356

Db     2291  CCTACCTTGAGCCGTTTATTGAAGCCAGTA--------------------------- 2320

Qy     2357  TAGAAGAGAGACCCTTACCAGGGCACCCATCGTGCTGGCCACTGTTAAAGGCGACTGC 2416

Db     2321  ---AAGACCAGGGCTCCAGTAACGGCAAAATGGTGAATTGCCACGGTAAAAGGCGACGTTC 2377

Qy     2417  ACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTCCCAGTTATTG 2476

Db     2378  ATGACATTGGCAAAAACATCGTCGGCGTGGTGCTCGCAGTGCAATAACTACGAAATCATCG 2437

Qy     2477  ATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGACCACAAAGCAG 2536

Db     2438  ATCTTGGCGTGATGGTCCCGCCGGGGATAAAATTCAAAACGGCCAAAGAGGTAAAACGCGG 2497

Qy     2537  ATATAATTGGCCTTGTCAGGACTCATCACTCCTGGCGCGATGAAATGATTTTTGTTGCCA 2596

Db     2498  ATCTAATTGGTCTTCTTCCGGGCTGATTACTCCATCGCTCGACGAGATCGTTAATGTGCGA 2557

Qy     2597  AGGAAATGGAGAGATTAGCTATAGAGGCCTTTACCATCGTTGTTGATTGGAGGAGCAACCACTTCAA 2656

Db     2558  AAGAGATGGAGCGGCCAGGGCTTTACCATCCCCGCTGCGTGATAGGCGGCGGGACCACCTCGA 2617

Qy     2657  AAACCCACACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCCATCCTGG 2716

Db     2618  AAGCGCATACGGCGGTGAAATCGAGCAGGCTACACCGGCCCGACCCGTTTACGTACCTACAGA 2677

Qy     2717  ACGCGTCCAAGAGTGTGGTGTGTGTTCCCAGCTGTTAGATGATGAAAATCTAAAGGGATGAAT 2776

Db     2678  ACGCCTCGCGCCACGTCGGGTGTGTCTGGCCTGTCTGGTGTGCTGTGTGTTCGTCGCAGAGT 2737

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; Sequence 13893, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
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GenCore version 5.1.7
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(without alignments)
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	3851	98.3	3856	7	US-10-607-712-75	Sequence 75, Appl
3	914.6	23.3	3786	7	US-10-282-122A-25522	Sequence 25522, A
4	911.8	23.3	3684	7	US-10-282-122A-8842	Sequence 8842, Ap
5	902.6	23.0	3669	7	US-10-282-122A-32592	Sequence 32592, A
6	901.4	23.0	3705	7	US-10-282-122A-30149	Sequence 30149, A
7	899	22.9	3681	7	US-10-282-122A-19987	Sequence 19987, A
8	894	22.8	3705	7	US-10-282-122A-32118	Sequence 32118, A
9	892.2	22.8	3717	7	US-10-282-122A-33284	Sequence 33284, A
10	883.8	22.6	3684	7	US-10-282-122A-20596	Sequence 20596, A
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ALIGNMENTS

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; Sequence 1, Application US/10607712
; Publication No. US2004007301BA1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
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; SEQ ID NO 1
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Other
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; OTHER INFORMATION: Entire cloned cDNA encoding wild type methionine
; OTHER INFORMATION: synthase.
US-10-607-712-1

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Db   2281  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  2340
           ATGAGAAGAGGCTGTTGGCCACCTTATCCCTTTCATGTCATGCCTTATCCCTTTCATGTCATGCCTTATCCCTTTCATGAAAAGAAGAGAGAAAACCAGA

Qy   2341  GTGCTTAACGGCACAGTAGAAGAAGAGGCACCCTTACCAGGGCACCATCGTGCTGGCCACT  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  GTGCTTAACGGCACAGTAGAAGAAGAGGCACCCTTACCAGGGCACCATCGTGCTGGCCACT  2400

Qy   2401  GTTAAAGGCGACGTGCACGACGACTAGGCAAGAACATAGTTGGAGTAGTTCCTTGGCTGCAAT  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  GTTAAAGGCGACGTGCACGACGACTAGGCAAGAACATAGTTGGAGTAGTTCCTTGGCTGCAAT  2460

Qy   2461  AATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCT  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  AATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCT  2520

Qy   2521  CTTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAA  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  CTTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAA  2580

Qy   2581  ATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGA  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  ATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGA  2640

Qy   2641  GGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATACAGTGCACCT  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  GGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATACAGTGCACCT  2700

Qy   2701  GTAATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTGTGTTCCCAGCTGTTAGATGAA  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  GTAATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTGTGTTCCCAGCTGTTAGATGAA  2760

Qy   2761  AATCTAAAGGATGAATACTTTGAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGT  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  AATCTAAAGGATGAATACTTTGAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGT  2820

Qy   2821  CATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGT  2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  CATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGT  2880

Qy   2881  TTCCAAATGATTGGCTGTCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAG  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  TTCCAAATGATTGGCTGTCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAG  2940

Qy   2941  GTCTTTGAAGACTATGACCTGCAGAAGCTGTGGTGGACTACATTGACTGGAAGCCTTTCTTT  3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  GTCTTTGAAGACTATGACCTGCAGAAGCTGTGGTGGACTACATTGACTGGAAGCCTTTCTTT  3000

Qy   3001  GATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGGCTTCCCCAAGATATTTAACGAC  3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  GATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGGCTTCCCCAAGATATTTAACGAC  3060

Qy   3061  AAAACAGTAGGTGGAGGAGGGCCAGGAAGGTCTACGATGATGCCCAATAATGCTGAACACA  3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  AAAACAGTAGGTGGAGGAGGGCCAGGAAGGTCTACGATGATGCCCAATAATGCTGAACACA  3120

Qy   3121  CTGATTAGTAGTCAAAAGAAACTCCGGGCCCGGGGGTGTGGTTCGGTTCTGGTCGCACAGAGT  3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  CTGATTAGTAGTCAAAAGAAACTCCGGGCCCGGGGGTGTGGTTCGGTTCTGGTCGCACAGAGT  3180

Qy   3181  ATCCAAGACGACATTCACCTGTACGGAGCTGTGTGCCCAGGCTGCAGAGCCCATA  3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  ATCCAAGACGACATTCACCTGTACGGAGCTGTGTGCCCAGGCTGCAGAGCCCATA  3240

Qy   3241  GCCACTTTCTATGGGTTAAGGCAACAGCTGAGAAGGACTCTGCCAGCACGGAGCCATAC  3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  GCCACTTTCTATGGGTTAAGGCAACAGCTGAGAAGGACTCTGCCAGCACGGAGCCATAC  3300

Qy   3301  TACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTG  3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  TACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTG  3360

Qy   3361  TTTGCCGTTGCCTGCTTTGGGTAGAAGAGCTGAGCAAGGCCTATGAGGAGGATGATGGTGAC  3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  TTTGCCGTTGCCTGCTTTGGGTAGAAGAGCTGAGCAAGGCCTATGAGGAGGATGATGGTGAC  3420

Qy   3421  GACTACAGCAGCATCATGGTCAAGGCGTCTCAAGGCGCTGGGGACCGGCTGGACGAGGCCTTTGCAGAA  3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  GACTACAGCAGCATCATGGTCAAGGCGTCTCAAGGCGCTGGGGACCGGCTGGACGAGGCCTTTGCAGAA  3480

Qy   3481  GAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGAC  3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  GAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGAC  3540

Qy   3541  GTCGCAGACCTGCCGAAGGTTGCGGTACCAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGC  3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  GTCGCAGACCTGCCGAAGGTTGCGGTACCAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGC  3600

Qy   3601  CAGCCCGACCACACCGAGAAGTCACCATGTGGAGACTCGAGACATCGAGCAGTCTACA  3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CAGCCCGACCACACCGAGAAGTCACCATGTGGAGACTCGAGACATCGAGCAGTCTACA  3660

Qy   3661  GGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTAC  3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTAC  3720

Qy   3721  TTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAG  3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  TTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAG  3780

Qy   3781  GATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGAGACCCATT  3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781  GATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGAGACCCATT  3840

Qy   3841  TTGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTTGCCTTTTATCTTGATGATCC  3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841  TTGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTTGCCTTTTATCTTGATGATCC  3900

Qy   3901  TCAAGGAAATACAACCTAG  3919
           |||||||||||||||||||
Db   3901  TCAAGGAAATACAACCTAG  3919
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RESULT 2
US-10-607-712-75
; Sequence 75, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 3856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(3856)
; OTHER INFORMATION: nnn at positions 2640-2642 is either AAT or no
; OTHER INFORMATION: nucleotides; n at position 2756 is either A or G;
; OTHER INFORMATION: n at position 2758 is either C or G.

US-10-607-712-75

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Query Match        98.3%;   Score 3851;  DB 7;  Length 3856;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches  3851;   Conservative  0;   Mismatches  5;   Indels  0;   Gaps  0;

   64 Qy ATGTCACCCGCCTCCAAGACCTGTCGCAACCCGAAGTCTGAAGAAACCCTGCGGGAT 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1 Db ATGTCACCCGCCTCCAAGACCTGTCGCAACCCGAAGTCTGAAGAAACCCTGCGGGAT  60

  124 Qy GAGATCAATGCCATTCTGCAGAAGAGAGGATTATGGTGTGCTGGATGGGAGGGACCATG 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   61 Db GAGATCAATGCCATTCTGCAGAAGAGAGGATTATGGTGTGCTGGATGGGAGGGACCATG 120

  184 Qy ATCCAGCGGGAAGCTAAAACGAAGAACACTTCCGAGGTCAGGAGTTAAAGATCATGCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  121 Db ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAGTTAAAGATCATGCC 180

  244 Qy AGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACCAA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  181 Db AGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACCAA 240

  304 Qy ATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATGAAACAAATACTTTAGCAGC 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  241 Db ATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATGAAACAAATACTTTAGCAGC 300

  364 Qy ACTAGTATTGCCCAAGCTGACATGGCCTTGAACACTTGGCCTACCCGATGAACATGTGC 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  301 Db ACTAGTATTGCCCAAGCTGACATGGCCTTGAACACTTGGCCTACCCGATGAACATGTGC 360

  424 Qy TCTGCAGGAGTGGCCAGAAAAGTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGAGG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  361 Db TCTGCAGGAGTGGCCAGAAAAGTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGAGG 420

  484 Qy TTTGTGGCAGGGGCTCTGGGTTCGGACTAATAAGACACTCTCTGTGTCCCATCGTGTGGAA 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  421 Db TTTGTGGCAGGGGCTCTGGGTTCGGACTAATAAGACACTCTCTGTGTCCCATCGTGTGGAA 480

  544 Qy AGGCCGATTATAGGACGATCGTTGATGAGCTTGTTGTGAAGCATACCAAGAGCAGCAGCC 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  481 Db AGGCCGATTATAGGACGATCGTTGATGAGCTTGTTGTGAAGCATACCAAGAGCAGCAGGC 540

  604 Qy AAAGGACTTCTGATGGCGGGGTTGATATCTTACTCTACTCTGATATCTGT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  541 Db AAAGGACTTCTGATGGCGGGGTTGATATCTTACTATTTTGATATCTGT 600

  664 Qy AATGCCAAGGACAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  601 Db AATGCCAAGGACAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGG 660

  724 Qy CCTATCTTTATTTCAGGGACGATCGTTGATAAAAAGTGGGACGACTCTTCCGGACAGACA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  661 Db CCTATCTTTATTTCAGGGACGATCGTTGATAAAAAGTGGGACGACTCTTCCGGACAGACA 720

  784 Qy GGAGAGGGATTTGTCATCAGCGGTTGATATCTCATGGAACCACTCTGCATTGGATTAAATTGT 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  721 Db GGAGAGGGATTTGTCATCAGCGGTTGATATCTCATGGAACCACTCTGCATTGGATTAAATTGT 780

  844 Qy GCTTTGGGTGCAGCTGACGCCTTGTTTGCACTTTATTGGAGAAATAATTGGAAATGTACAACAGCC 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  781 Db GCTTTGGGTGCAGCTGACGCCTTGTTTGCACTTTATTGGAGAAATAATTGGAAATGTACAACAGCC 840

  904 Qy TATGTCCTGTATCCCGTTATCCGAGGTCTTCCCAACACCTTTGGTGACTATGATGAAACG 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  841 Db TATGTCCTGTATCCCGTTATCCGAGGTCTTCCCAACACCTTTGGTGACTATGATGAAACG 900

  964 Qy CCTTCTATGATGGCCAAGCACCTAAAGATTTTGCTATGGATGGCTTGGTCAATATAGTT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  901 Db CCTTCTATGATGGCCAAGCACCTAAAGATTTTGCTATGGATGGCTTGGTCAATATAGTT 960

 1024 Qy AGGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  961 Db GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1020
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 1084 Qy TGTAAGCCTAGAGTTCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTCTA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1021 Db TGTAAGCCTAGAGTTCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTCTA 1080

 1144 Qy GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGTTAACATTGGAGAGAAAACCC 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1081 Db GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGTTAACATTGGAGAGCGCGTGTAATGTT 1140

 1204 Qy GCAGGATCAAGGAAGTTGCTAAACTCATCATGGCCAGAAACTATGAGAAGCCTTGTGT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1141 Db GCAGGATCAAGGAAGTTGCTAAACTCATCATGGCCAGAAACTATGAGAAGCCTTGTGT 1200

 1264 Qy GTTGCCAAAGTGCAGGTGGAAATGGAGCCCAGGTGTTGGATGTCAACATGATGATGGC 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1201 Db GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATGGC 1260

 1324 Qy ATGCTAGTAGGTGCTCCAAGTGCAATGACCACAGATTCAACTTAATTGCTTCCGAGCCAGAC 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1261 Db ATGCTAGTAGGTGCTCCAAGTGCAATGACCACAGATTCAACTTAATTGCTTCCGAGCCAGAC 1320

 1384 Qy ATCGCAAAGTACCTTTGTGCATCGACTCCTCCCAAATTTGCTGATTGAAGCTGGGTTA 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1321 Db ATCGCAAAGGTACCTTTGTGCATCGACTCCTCCCAAATTTGCTGATTGAAGCTGGGTTA 1380

 1444 Qy AAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGGACGAC 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1381 Db AAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGGACGAC 1440

 1504 Qy TTCTTGGAAGGCCAGGAAGATTAAAAAAGTATGGAGCGTGCTATGGTGGTCATGGCTTTT 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1441 Db TTCTTGGAAGGCCAGGAAGATTAAAAAAGTATGGAGCGTGCTATGGTGGTCATGGCTTTT 1500

 1564 Qy GATGAAGAAGGACAGGCAACAGGCAACAGAACAGAACAAATCAGAGTGTGCACCCGGCCTAC 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1501 Db GATGAAGAAGGACAGGCAACAGGCAACAGAACAGAACAAATCAGAGTGTGCACCCGGCCTAC 1560

 1624 Qy CATCTGCGTGTGAAAAAACTCGGCTTTAATCCAAATGACACATATTTTTGACCCTAATATC 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1561 Db CATCTGCGTGTGAAAAAACTCGGCTTTAATCCAAATGACACATATTTTTGACCCTAATATC 1620

 1684 Qy CTAACCATTGGGACTGGACTGGAGGAACACAACTTGTATGCCATTAATTTATCCATGCA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1621 Db CTAACCATTGGGACTGGACTGGAGGAACACAACTTGTATGCCATTAATTTATCCATGCA 1680

 1744 Qy ACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTG 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1681 Db ACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTG 1740

 1804 Qy TCCTTCTCCTTCCGAGGAATGGGAAGCCATTCGAGAAGCAATGCATGGGTTTTCCTTTAC 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1741 Db TCCTTCTCCTTCCGAGGAATGGGAAGCCATTCGAGAAGCAATGCATGGGTTTTCCTTTAC 1800

 1864 Qy CATGCAATCAAGTCTGGACATGGAGATAGTGAATGCTGGAAACCTCCGTGTAT 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1801 Db CATGCAATCAAGTCTGGACATGGAGATAGTGAATGCTGGAAACCTCCGTGTAT 1860

 1924 Qy GATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCT 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1861 Db GATGATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCT 1920

 1984 Qy GAGGCCACTGAGAAGTCTTCTAGTTATGCCCAAGGCACAGGAGGGAAGAGAAAGTC 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1921 Db GAGGCCACTGAGAAGTCTTCTACGTTATGCCCAAGGCACAGGAGGGAAGAAAGTC 1980

 2044 Qy ATTCAGACTGATGAGTGAGGAAAATGGCCCTGTCGGAAGAACGCCTTGAGTGTATGCCCTTGTG 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1981 Db ATTCAGACTGATGAGTGAGGAAAATGGCCCTGTCGGAAGAACGCCTTGAGTGATGCCCTTGTG 2040

 2104 Qy AAGGGCATTGAAAACATATTATTGAGGAGTACTGAGGATAAACCAAAAAAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2041 Db AAGGGCATTGAAAAACATATTATTGAGGAGTACTGAGGATAAACCAAAAAAA 2100
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Qy   2164  TATCCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAAAATTGTTGGT  2223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  TATCCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAAAATTGTTGGT  2160

Qy   2224  GATCTTTTTGGAGCTGGAAAAATGTTCTACCTCAGTTATAAAGTCAGCCCGGGGTTATG  2283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGTTATAAAGTCAGCCCGGGGTTATG  2220

Qy   2284  AAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAAGAAGAGAAGAAACCAGAGTG  2343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  AAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAAGAAGAGAAGAAACCAGAGTG  2280

Qy   2344  CTTAACGGCACAGTAGAAGAGGACCCTTACCAGGGCACCATCGTGCTGCCCACTGTT  2403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CTTAACGGCACAGTAGAAGAGGACCCTTACCAGGGCACCATCGTGCTGCCCACTGTT  2340

Qy   2404  AAAGGGCACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTACTGCAATAAT  2463
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  AAAGGGCACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTACTGCAATAAT  2400

Qy   2464  TTCCGAGTTATTGATTTGATTTAGGAGTCATGACTCACTCCATGTGATAAGAGTCGCTCTT  2523
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  TTCCGAGTTATTGATTTGATTTAGGAGTCATGACTCACTCCATGTGATAAGAGTCGCTCTT  2460

Qy   2524  GACCACAAAGCAGATATAATTGGCCTTGTCAGACTCATCACTCCCTTCCCTGATGAAATG  2583
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  GACCACAAAGCAGATATAATTGGCCTTGTCAGACTCATCACTCCCTTCCCTGATGAAATG  2520

Qy   2584  ATTTTTGTTGCCAAGGAAATGTCGAAGGATTAGCTATAGAAGGATTCCATTGTTGATTGGAGGA  2643
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  ATTTTTGTTGCCAAGGAAATGTCGAAGGATTAGCTATAGAAGGATTCCATTGTTGATTGGAGGA  2580

Qy   2644  GCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTA  2703
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  GCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTN  2640

Qy   2704  ATCCATGTCCTGGACGCGTCCAAGGAGTGTGGTGTGTCCCAGCTGTTAGATGAAAT  2763
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  NNCCATGTCCTGGACGCGTCCAAGGAGTGTGGTGTGTCCCAGCTGTTAGATGAAAT  2700

Qy   2764  CTAAAGGATGAATACTTTGAGGAAATCATGAGGAAATATGAAGATATTAGACAGGACCAT  2823
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CTAAAGGATGAATACTTTGAGGAAATCATGAGGAAATATGAAGATATTAGACAGGNCNAT  2760

Qy   2824  TATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTC  2883
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  TATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTC  2820

Qy   2884  CAAATGGATTGGCTGTCTGCAACCTCACCCAGTTATTGGGACCCAGGTC  2943
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  CAAATGGATTGGCTGTCTGCAACCTCACCCAGTTATTGGGACCCAGGTC  2880

Qy   2944  TTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTGAT  3003
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  TTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTGAT  2940

Qy   3004  GTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAACGACAAA  3063
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  GTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAACGACAAA  3000

Qy   3064  ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCTGAACACACTG  3123
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCTGAACACACTG  3060

Qy   3124  ATTAGTCAAAAGAAACTCCGGGCCCGGGGTGGGTTCTGGCCAGCACAGAGTATC  3183
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  ATTAGTCAAAAGAAACTCCGGGCCCGGGGTGGGTTCTGGCCAGCACAGAGTATC  3120

Qy   3184  CAAGACGACATTCACCTGTACGCAGAGGCTGCTGCCCCCAGGCTGCAGAGCCCATAGCC  3243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  CAAGACGACATTCACCTGTACGCAGAGGCTGCTGCCCCCAGGCTGCAGAGCCCATAGCC  3180

Qy   3244  ACTTTCTATGGGTTAAGGCAACAGGCTGAGAGGACTCTGCCAGCACGAGCCGAGCCATACTAC  3303
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Db   3181  ACTTTCTATGGGTTAAGGCAACAGGCTGAGAGGACTCTGCCAGCACGAGCCGAGCCATACTAC  3240

Qy   3304  TGCCTCTCAGACTTCATCGCTTCGGCATCCGTGACTACCTGGCCTGTTT  3363
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  TGCCTCTCAGACTTCATCGCTTCATCCGTGACTACCTGGCCTGTTT  3300

Qy   3364  GCCGTGTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGTGACGAGTG  3423
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  GCCGTGTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGTGACGAC  3360

Qy   3424  TACAGCAGCATCATGGTCAAGGCGTCGGGGACCGGCTGGGCAGTGCCTTTGCAGAGAG  3483
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  TACAGCAGCATCATGGTCAAGGCGTCGGGGACCGGCTGGGCAGTGCCTTTGCAGAGAG  3420

Qy   3484  CTTCCATGAAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGGCAGTGACGTC  3543
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  CTTCCATGAAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGGCAGTGACGTC  3480

Qy   3544  GCAGACCTGCGAAGGTTGCGGTACACAAGGGCATCCGCGACTCGCAGACATCGAGCAGC  3603
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  GCAGACCTGCGAAGGTTGCGGTACACAAGGGCATCCGCGACTCGCAGACATCGAGCAGC  3540

Qy   3604  CCCGACCACACCGAGAAGCTCACCATGTGGAGACTCGGAGACACTGGAGACTCGAGCAGTCTACAGC  3663
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  CCCGACCACACCGAGAAGCTCACCATGTGGAGACTCGGAGACACTGGAGACTCGAGCAGTCTACAGC  3600

Qy   3664  ATTAGGTTAACAGAATCATTAGCAATGCAATGAGTCTCTCAGGGCTCTCTACTTC  3723
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  ATTAGGTTAACAGAATCATTAGCAATGCAATGAGTCTCTCAGCGCTCTCTACTTC  3660

Qy   3724  TCCAATTTGAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT  3783
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  TCCAATTTGAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT  3720

Qy   3784  TATGCATTGAGGAAGAACATATCTGTGCTGCGAGGTTGAGAAATGGCTTGGACCCATTTTG  3843
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  TATGCATTGAGGAAGAACATATCTGTGCTGCGAGGTTGAGAAATGGCTTGGACCCATTTTG  3780

Qy   3844  GGATATGATACAGAGACTAACTTTTTTTTTTTTTTTTTATCTTGATGATCCTCA  3903
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781  GGATATGATACAGAGACTAACTTTTTTTTTTTTTTTTTATCTTGATGATCCTCA  3840

Qy   3904  AGGAAATACAACCTAG  3919
           ||||||||||||||||
Db   3841  AGGAAATACAACCTAG  3856
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RESULT 3
US-10-282-122A-25522
; Sequence 25522, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23

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;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 25522
;  LENGTH: 3786
;  TYPE: DNA
;  ORGANISM: Mycobacterium avium
US-10-282-122A-25522

Query Match        23.3%;   Score 914.6;  DB 7;   Length 3786;
Best Local Similarity 54.8%;   Pred. No. 4.7e-265;
Matches 2055;  Conservative    0;  Mismatches 1634;  Indels   60;  Gaps   10;
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Qy   121 GATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGAGGATGGGACC 180
             ||  ||||||||   |||     ||||          |||||||||||
Db    82 GACGAACTGACGGCGCGCTGCCCAGCCGATCATGGTGATCGACGGCCGCCATGGGCACC 141

Qy   181 ATGATCCAGCGGGAGAAGCTAAACGAAGAAACACTTCCGAGGTCAGGAATTTAAAGATCAT 240
             ||||||||||||   |||||        |||||||||||
Db   142 GCGATCCAGCGGGAGGACCCGCCCCGACGAGGCCGGCTACCGCGGCGGTCAGGTCAGGACTGG 201

Qy   241 GCCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTAC 300
             ||||||||| |||   ||||    |||||||||||
Db   202 CCGAGCGGCATCTGTCGGCAACAACGACCTGCTCAACCTGACGCGACCGCAGATCATCGAG 261

Qy   301 CAAATCCATAAGGAAATACTTGCTCGGGTGCTCGGGCCAGATATCATTGAAACAAATACTTTAGC 360
             ||||||||||||||||||||||||||||||
Db   262 GGCATTCACCGGGAGTACCTCGAGGCGGCGGCCGGCTACCCGGAGATCCTCGAGAACACCTTCAAC 321

Qy   361 AGCACTAGTATTGCCCAAGTGACTACTATGGCCTTGAACACTTGGCCTACCGGATGAACATG 420
             ||||   |||||||||| |||||||||||
Db   322 GCGAACGCGATCTCGCGTGTCCGACTACCGCGGGAGCTGAGCTGAGCTACGAGCTGAACTAC 381

Qy   421 TGCTCTGCAGGAGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTGTGTCCCCATCTGTG 480
             |||||||   ||||||||||||||| ||||||
Db   382 GCCGGCGGCGCCCCTGGCCCGGCGCCGACGAGTTCAGCAGCC---CGCGACAAGCCC 438

Qy   481 AGGTTTGTGGCAGGGGCTCTGGGTCCGGTCCGACTCAGTGTTGTTGAAGCATACCAAGAGCAG 540
             |||||||||||||
Db   439 CGCTACGTCGCGCGAGGGCGGGGGCTCGGGGGCGCTGGGTGGTCGCCGGCCTACCTCGGAGGCG 498

Qy   541 GAAAGGCCGGATTATAGAAGCAATATCACATTGATGAGCTTGTTGAAGCATACCAAGAGCAG 600
             ||||   |||||||||||||||||||||||
Db   499 AACGATCCCGAGTACCCGCGGGGCGTCGGGGGCTCGGGGGCGTGGTCCGCGGCCTACCTCGGAGGCG 558

Qy   601 GCCAAAGGAGACTTCTGGATTGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACT 660
             |||||||||||||||||||||||||
Db   559 GCCAACGGCCTGGTCGACGGCGGTGTCGACCTTCGACCTCTGATCGTCGACGAGCTTCGACACACG 618

Qy   661 GCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAAATCTTTTGAGGAGAAAATATGCTCCC 720
             |||||   ||||||||| |||||||||||
Db   619 TTGAACGCCAAGGCTGCGTTCGCGGACGCGTTCCGAACAGCAGGCCGCGGGCGGCCGC 678

Qy   721 CGGCCTATCTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAG 780
             |||||||   ||||||||||||||||||||||||
Db   679 TGGCCGGTCATCATCTCCGGGCACCATCACCGATGCCCTCGGGGCCCCGGGCCTGTCCGGGGCAG 738
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Qy   781 ACAGGAGGAGGATTTGTCATCAGCGTGTCTCATGGAGACCACTCTGCATTGGATTAAAT 840
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Db   739 GTCACCGAGGACGGCGTTCTGAACTCGATCCGGCCAAGCCGATCGCGGTCGGGGCTCAAC 798

Qy   841 TGTGCTTTGGGTGCAGCTGAGATGAGACGTGCGGCCCTACATCGCCGAGGTGTCCGCAACAACA 900
             |  |||||||||||
Db   799 TGCGCCCTGGGCGGCCCACCCGAGATCGCGGCCCTACATCGCCGAGGTGTCCGCATCGGGAC 858

Qy   901 GCCTATGTCCTGTGTTATCCCAATGCAGGTCTTCCCAACACCTTGGTGACTATGATGAA 960
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Db   859 ACTTCGTCGTCCTGTGCTACCGGAACGCGGCCTTCGGCCCAGAGTGACGGCAGG 918

Qy   961 ACGCCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCCGGCGGCCGGCAATATA 1020
             || |||||     |||||||||||||
Db   919 TCCCCGGAGCCGGTCAGGCCTCCTACATGCCGCGAGACCGGCCGGCCGGGTCAACATC 978

Qy  1021 GTTGGAGGATGCGTGTGGGTCAACACCAGATCATATCACGGGAAATTGCTGAAGCTGTGAA 1080
             |||   |||||||||
Db   979 GTCGGCGGCGGTTGCTGCGGAACCCGCGCCGACGACTCGCTGTTCGTGAACATCGGCGACGACTCGCAGCCGCCACCAAC 1038

Qy  1081 AATTGTAAGCCACCGTAGAGTTCCACCTGCCACTGCTGTTTTGAAGGACATATGTTACTGCTCTGGT 1140
             ||
Db  1039 GGCAAGCCGCGCCGG----GAGGTGCCGGCAGATTCCGGTGGCCACCCG--GCTCTCGGGC 1092

Qy  1141 CTAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAAT 1200
             ||||||   ||||||||
Db  1093 CTCGAGCCGGCTCAACATCCAACATCACCGACGACTCGCTGTTCGTCGTGAACATCGGCGAGCGCCACCAAC 1152

Qy  1201 GTTGCAGGATCAAGGAGGTTTGCTAAACTCATCATCATGGGCAGAAACTATGAAGAAGCCTTG 1260
             ||||||||||||
Db  1153 ATCACCGGCTCGCGGCCCCGGTTCCGCAACCTGATCAAGGGCGAGGACTACGACACCGCGGTG 1212

Qy  1261 TGTGTTGCCAAAGTCGAGGTGAAATGGAGGCCCAGGTGTTGGGATGTGTCAACATGGATGAT 1320
             ||||
Db  1213 TCGGTCGCCCCTGCGCAGCAGGTGGAGGTGCCCAGTGCCAGTGTCATCGACACATGACAGG 1272

Qy  1321 GGCATGCTAGATGTCCAAGTGCAATGACCCAGATTTTGCAACTTAATTGCTTCCGAGGCCA 1380
             ||||||||||||
Db  1273 GGCATGATCGACGGCGTCGCGCGGAGGTGACCCGGTCGATCGACTGAGCCGAGCCGGCCG 1332

Qy  1381 GACATCGCGAAAGTACCCTTGTGCATGCACTCCTCCAATTTTGCTGTGATTGAAGCTGGG 1440
             ||||||||||||
Db  1333 GACATCAGCCGGGTTCCCGGTGATGATCCAAGTGGGAGGTCATCGGAGGTGCATGGCGGC 1392

Qy  1441 TTAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAATAGCATGAACATG 1500
             ||||||
Db  1393 CTGAAGACGTGCAGGGCAGCAAGCCGATCGTCAACTGACATTAAAAGTAAGTTGAGGAGCGAGGAG 1452

Qy  1501 GACTTCTTGGAAGAAGGGTCTCGGGAAGATTAAAAGTATGGCGTGCTATGGTGGTCATGGCT 1560
             ||||||||||||
Db  1453 AAGTTCGTCCGGGAGCGCGGTGCGGTGTCCGCAAGTCAATGGGCCGTGATGGCC 1512

Qy  1561 TTTGATGAAGAAGACAGGCACAACAAGAAATCAGAGTGTGCACCGGGCC 1620
             ||||||||||||
Db  1513 TTCGACAACAGGGTCAGGCGATCAGCCGGAGGTCGGGACAACCTGCGGCGCACGCGCGC 1572

Qy  1621 TACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAAT 1680
             ||||||||||||
Db  1573 TACCGCGTGTGACCCGGAAGAGGTCGGCCTTCCCCGCGGAGAATGACTCTTCGACCCCCAAC 1632

Qy  1681 ATCCTAACCATTGGACTGGACTGAATGTGATGCCAGAGAAACAACTTGTATGCCCATTGTATCCAT 1740
             ||||||||||||
Db  1633 TGCTTGCCGCGGCGGCCGCATCGGAGCCAACTACCGGCCAACCTACTTCATCAGCAG 1692

Qy  1741 GCAACAAAGTCATTAAAGAAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAAC 1800
             ||||||||||||
Db  1693 GCCTTGCCGCGGCGGCCGCATCGTCGCCGGGGGTGCACCTCTCGGAGGCATCTCGAAC 1752

Qy  1801 TTGTCCTTCTTCCTTCCGGGAATGGAAGCCATTGGAGGAGCAATGCATGGGGGTTTTCCTT 1860
             ||||||||||||
Db  1753 GTGTCGTTCGTTCCGGTTCCGGGGGAAACAACCCGTCCGGGGATCCACTCCGGTGTTCCTG 1812

Qy  1861 TACCATGCAATCAAGTCTGCCATGGACATGGAGATAGTGAGATAGTGAGAACTGTGGAAACCTCCCGTG 1920
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Db  2875  GGAATACGGGAATTTCAGGACTACGACCTCGCCGCGAGCTGCGCGAGTACATCGACTGGCAG  2934
Qy  2992  CCTTTCTTGATGTCTGGCAGCTCCGGGCAGCAAGTACCCGAATCGAGGCTTCCCAAGATA    3051
          ||||||  ||||||||||||||
Db  2935  CCGTTCTTCAACGCCTGGGAGAT------------------GAAGGGTCGCTTCCCGACATC  2979

Qy  3052  TTTAACGACAAAACAGTAGGTGAGAGGCCAGGAAGGTCTACGATGATCGCCACAATATG    3111
Db  2980  CTCAACACCCGGCCACCCGGCCGGCCGGCCAAGCTCTACGACGCGCCCAGGAGATG        3039

Qy  3112  CTGAACACACTGATTAGTCAAAAGAAACTCCCGGCCGCCGGGGTGTCGGTTCGGCCA      3171
Db  3040  CTCGACACACCCTGATCAAGGAGAAGTGGCTGACGGCCAACGCGCGATCGGGTTCTTCCCG  3099

Qy  3172  GCACAGAGTATCCAAGACGACATTCACCTGTACGCAGAGGCTCGTCGTGTCCGTCTGCA    3231
Db  3100  GCGAACGCGATCGGCCGGCCGGGTTTCGAAGACATCGAGCTGTACCACCGACGACCCGCACC  3159

Qy  3232  GAGCCCATAGCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACG   3291
Db  3160  GAGGTGCTGACCACGCTGCACAACCTGCCCAGCAGGCGACCACCCGGCCGAATC---      3216

Qy  3292  GAGCCAATACTACTGCCTCTCAGACTTCATCGCTTCCCTTGCATTCTCGGCATCCGTGACTAC  3351
Db  3217  ---CCGAACCGGTGCTGGGCGACTACGTCGTCCGCCCCAAAGAACAGGGGCACCGGGACTAC  3273

Qy  3352  CTGGGCCTTGTTGCCGT----TGCCTCGCTTGGGGTAGAGAGCTGAGCGAGGCTATGAG    3408
Db  3274  ATCGGCGCCTTCGCCGCGGGACCTGGACCGGACCAGGAGCAGCCGGAGATGCGGAGTTCAAG  3333

Qy  3409  GATGATGGTGACGACTACAGAGCATCATGGTCAAGGCGCCTGGGGAGAG    3468
Db  3334  GCGGGCCCCGGACGACTACAGCGGCGATCCTGCTGGAGTCGATCGCCGGGCTGGCGGAG  3393

Qy  3469  GCCTTTGCAGAGAGCTCCATGAAGAAGAGTTCCGCGAAGAGTTCCGCAGTCGTGGCAGT   3528
Db  3394  GCGTTCGCCGAACGGATGCACCAGCCGGTCCGCAAGGAGTTCTGCGGGCTACCAGCCGAC  3453

Qy  3529  GAGCAGCTGGACGTCGCGAGACCTGCGGTTGCGTACAAGGCATCCCGGCTCCT    3588
Db  3454  GAGCAACTGGACAACGACGACACCACTCATCATCGAGAAGAAGTACCGGGAATCCGGCCCGCCG  3513

Qy  3589  GGCTACCCCAGCCAGGCATTAGGTTAACAGAATCATTAGCACCTGCTTCAGCAGTC    3648
Db  3514  GGCTACCCCGGCGGCCTGCCCGGAGCACATCGATCGGCCGGCGACGTGATGGACGTC  3573

Qy  3649  GAGCAGTTCGCAGGGATTAGGTTCAAGGACTGAGAGATTAGCTATATAGCCGAGATC    3708
Db  3574  AAGGAGCGCCACCGGACGTCGCATCGGAGCTGCGATGGCCCATGTGGCCCGCGCCGTC  3633

Qy  3709  TCAGGGCCTCTACTTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAG   3768
Db  3634  AGCGCGGTTGGTATTTCTCGACCCAGTCGCAGTACTTCGTGTCGTTGGCCCAG    3693

Qy  3769  GATCAGGTTGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGAGAAATGG   3828
Db  3694  GACCAGTCGCCGCGACTACGCGAAGGCGCTGGAGACGCTGGCCGAGGCGCGCTGG  3753

Qy  3829  CTTGGACCCCATTTTGGGATATGATGATACAGA  3857
Db  3754  CTGGCCCCCCAACCTCGCGCTACACAACCCCGA  3782
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RESULT 4

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Db  1813  TTCCACGCCATCAAGGCCGGCCTGGACATGGGCCGGCATCTCTGCTGAAGATCTCAACGCCGCGCGCCTGGTGCCCC  1872
Qy  1921  TATGATGATATCCAGCTTCGCAGTTCTGTGTGAAGATCTCATCTGAATAAAGAC    1980
Db  1873  TACGACTCGATCGACCCGAGCTCGCGGGACCCGCATCCGAGACGCGTCGTGCTGAACCGGCCGC  1932

Qy  1981  CCTGAGGCCACTGAGAAGCTCTTACGTTATCGCCAG------ACTCAAGGCACAGAGAGGG   2034
Db  1933  GAGGACGGCGGCCGAGGAGGCTGCTGGAGATCGCCGAGCGGTTCAACAAGTCCGCAGATGCT  1992

Qy  2035  AAGAAAGTCATTCAGACTGATCAGTCAGTGGCCCTGTCGAAGAACGCCTTGAGTAT    2094
Db  1993  TCGGAGGATTCGGCGCGGGGCCGAGGTGCGCGGGCCTGCCGGTTCGCCGAGCGGATCACGCAC  2052

Qy  2095  GCCCTTGTGAAGGGCATTGAAAAACATATTATTGAGGATACTGGAGGAAGCCAGG---TTA   2151
Db  2053  GCCCTCGGTCAAGGGCATCGACACCCCCAGTCGACGAGGACACCGGAGGAGTTGCGGGCCGAG  2112

Qy  2152  AACCAAAAAAAATATCCCGACCCTCCAATATAATTGAAGGACCCCTGATGAATGAAATG    2211
Db  2113  ATTGCCGCCCGCGGGTGCCCGGCGATCGAGGTGATCGAGGGGCCCGGTCTGATGGACGGCATG  2172

Qy  2212  AAAATTGTTGGTGATCTTTTTGGAGCTGGAAAAAATGTTTCTACCTCAGGTTATAAAGTCA   2271
Db  2173  AACGTCTCGGCGGACCCTGTTCGGCTTCGGCTCCTGCTCCGGCAAGATGTTTTTGCCCCAGGTGGTGAAGTCG  2232

Qy  2272  GCCCGGGTTATGAAGAAGGCGTGTTGCCGCACCTTATCCCTTTCATGAAAAAAGAAGAGAA   2331
Db  2233  GCCCGGGTGATGAAGAAGGCCCTGCCTACCTGCTCGTTCATCGAGGCCGAGAGGAA  2292

Qy  2332  GAAACCAGAGTGCTTAACGGCACAGTAGAAGAGAGAGACCCTTACCAGGCCACCATCGTG    2391
Db  2293  AGGACACCAAACGGCACCATCGTG--------AGTCCGGCGTGTCCGGTTCCA  2337

Qy  2392  CTGGCCACTGTTTAAAGGCGACGTGCACGACATAGTTGGAGTAGTTCTT    2451
Db  2338  ATGGGCGACCGTCAAGGGCGACGCACGTCCACGAACAATCGGCACACTGTCTCTTG  2397

Qy  2452  GGCTGCAATAATTTCCGAGTTATTGATTAGGAGTCATGACTCCATGTGATAAGATACTG   2511
Db  2398  CAGTGCAACAACTTCGAGGTGATCGACCTTCGGTGTGATGGTGCCGGCCAGAAGAGATCCTC  2457

Qy  2512  AAAGCTGCTCTTGACCAAAGACAGATGAAATGGCGTGTCAGGACTCATCATCACTCCTTCC    2571
Db  2458  GATGCTGCGAAAAGAGCACGACGACGCACATCATCGGGCGTGTCCGCCGGGTTAGGACTTCACACCCGTCC  2517

Qy  2572  CTGGATGAAATGATTTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTG   2631
Db  2518  CTGGGACAGAGATGGAACGGAACGGAACGCGGAGATGGAACGGGCGGCCTGCAGATCCGCTG  2577

Qy  2632  TTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATAC    2691
Db  2578  CTGATCGGCGGCGGCGGACCACCTCCGCGCGGCCGTGAAGATCTCGCCGGCGCGT-  2637

Qy  2692  AGTGCACCTGTAATCCATGTCCTGACGCGTGGTGGTGTTGTTCCCAGCTG    2751
Db  2638  TCCGGGCCCCGGTGGTCTGGGTCAAGGACGCGCTCCCCGCGCGGTGCGGTGCCGCGCTG  2697

Qy  2752  TTAGATGAAAATCTAAAGGATGAAATACTTTGAGGAAATCATGGAAATATGAAGATATT   2811
Db  2698  CTGGACGACAAGCAGCGCGGCGGCCGCCCCTGCTGACGGAGGCCACCGAGAGGACTACGCGT-  2756

Qy  2812  AGACAGGACCATTATGAGTCTCTCAAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGA   2871
Db  2757  --GGGGAACGGCACGCCCCAGAAGAACGAGGCGGCCGATGGTGACGCTGGAAAAGGCCCGC  2814

Qy  2872  AAAAGTTGGTTTCCAAATGAGATTGGCTGTCTGTCAAGACCTGAGAAGCCCACGTTTATT  2931
Db  2815  GCCAACCGGACGCCGATCGCACTGGGAGACGGCTACACGCCCGGTCCGGATCGGTGCG  2874

Qy  2932  GGGACCCCAGTTCTTTGAAGACTCTTTGAAGACTATGACCTGCCGAGAAGCTGGTGGACTACATTGACTGGAAG  2991
Db          ||| ||| ||||||
```

```
, APPLICANT:  Zyskind, Judith
, APPLICANT:  Wall, Daniel
, APPLICANT:  Trawick, John
, APPLICANT:  Carr, Grant
, APPLICANT:  Yamamoto, Robert
, APPLICANT:  Forsyth, R.
, APPLICANT:  Xu, H.
, TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
, FILE REFERENCE: ELITRA.034A
, CURRENT APPLICATION NUMBER: US/10/282,122A
, CURRENT FILING DATE:  2003-02-20
, PRIOR APPLICATION NUMBER: 60/191,078
, PRIOR FILING DATE:  2000-03-21
, PRIOR APPLICATION NUMBER: 60/206,848
, PRIOR FILING DATE:  2000-05-23
, PRIOR APPLICATION NUMBER: 60/207,727
, PRIOR FILING DATE:  2000-05-26
, PRIOR APPLICATION NUMBER: 60/230,335
, PRIOR FILING DATE:  2000-09-06
, PRIOR APPLICATION NUMBER: 60/230,347
, PRIOR FILING DATE:  2000-09-09
, PRIOR APPLICATION NUMBER: 60/242,578
, PRIOR FILING DATE:  2000-10-23
, PRIOR APPLICATION NUMBER: 60/253,625
, PRIOR FILING DATE:  2000-11-27
, PRIOR APPLICATION NUMBER: 60/257,931
, PRIOR FILING DATE:  2000-12-22
, PRIOR APPLICATION NUMBER: 60/267,636
, PRIOR FILING DATE:  2001-02-09
, PRIOR APPLICATION NUMBER: 60/269,308
, PRIOR FILING DATE:  2001-02-16
, Remaining Prior Application data removed - See File Wrapper or PALM.
, NUMBER OF SEQ ID NOS: 78614
, SOFTWARE:  PatentIn version 3.1

; SEQ ID NO 8842
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-10-282-122A-8842

Query Match          23.3%;    Score 911.8; DB 7;  Length 3684;
Best Local Similarity  55.3%;  Pred. No. 3.3e-264;
Matches 2070;  Conservative   0;  Mismatches 1557;  Indels 114;  Gaps  11;
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Qy  128  TCAATGCCATTCGCAGAAGAGGATTATGGTGCTGAGGAGGATGGGACCATGATCC  187
              ||| || ||  |||||||||| || | || ||||  ||  || | |||||||||
Db   20  TAAAAGCGCTTCTTGCTAAACGCATTCTGATTATTGATGGTGCAATGGGAACCATGATCC   79

Qy  188  AGCGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAATTTAAAGATCATGCCAGGC  247
              || |||| |||  ||| | || ||||| || |||   || |||| ||||| ||||
Db   80  AGCGGCCATAAAATTGGAAGAAGCTGACATCGTCGTGTGAGCGTTTGCTGATTGGCACATG  139

Qy  248  CGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTACCAAATCC  307
              | ||||| || || |  | |||  || |  || |||| | |||||  ||||||||||
Db  140  ACTTAAAAGGTAACAATGACCCTTTGGTTCTAACACAGCCTCAAATCATTCAAGGTATTC  199

Qy  308  ATAAGGAATACTTGCTGCGGCGCAGATATCATTGAAACAACAAATACTTTTAGCAGCACTA  367
              || || |||| || |||  || ||| ||||| |||| |||| |||| ||  || |||
Db  200  ATGAAGCCTACCTTCGATGCTGGTGCAGACATTATTGAAACCACAGCTTTAACGGTACAC  259

Qy  368  GTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGATGAACATGTGCTCTG  427
              | |||| ||||| ||| || |||||||||||||  || |  |  ||   ||||| |||
Db  260  GTGTTTCAATGTCTAAGCACATGATCACCGGTTGTTAACTCAATTTCCTTAAAAGAAGGC  319

Qy  428  CAGGAGTGGCCAGAAAAAGCTGCCGAGAAAGCTGCCGAGAGGTAACTCTCCAGACAGGA  487
              |||  || | |  ||  |  || ||| ||  || ||| || ||  || || || |||
Db  320  CACGTTTAGTAGCTGGGCAACATCTCGTACATGCCAACATCTCGCTACATGTTCAATCTCT  376

Qy  488  TGGCAGGGGGCTCTCGGGGTCCGACTAATAAGAACACTTCTCTGTGTCCCCATCTGTGAAAGGC  547
              || | ||| |||  ||  | |||  |||||||   |||| || || ||| || |||||||
Db  377  TGGCAGGTGTACTTGGGCAACATCTCGTACACATGTTCAATCTCTCCAGATGTGAACAACC  436

Qy  548  CGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGCAGGCCAAAG  607
              |||  || |   | ||| |||  | ||||||||||||||  ||||| ||||| |||
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Db  437  CTGCTTTTCGTAACATTAGCTTGATGAACTAAAAGAAAAATTATATATTGAAGCGACTCATG  496
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Qy  608  GACTTCTCGATGCGCGGGTTGATATCTTACTCATTGAAACATATTTTGATACTGCCAATG  667

Db  497  CACTAATTGAAGTGGTGCAGACATTATCCTGATTGAAACTGTATTTGATACTTTAAACT  556
              || |||||||||||||||||||  || ||||||||||||  |  ||||||||  |||||
Qy  668  CCAAGGCAGCCTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCGGCCTA  727

Db  557  GTAAAGCAGCGATTTTTGCAGTCAGAGAGTCTTAAACAAATTGGTCGCGAATTACCAA  616
              || ||| | || |  |  ||  || ||   || |||| |||||||  |||||||||||
Qy  728  TCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCCTTCCGACAGACAGAG  787

Db  617  TTATGATTTCAGGGACCATTACCGATGCATCAGGCCGTACTTTAACAGGTCAGACAGCGG  676
              | | | |||||||| |  | || |||   ||||| ||||| ||||||  |||||||||
Qy  788  AGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGTGCTT  847

Db  677  AAGCTTTCTGGAACTCCGTTCGTCATGGCGATTTGCTTTCAATCGGTTTTAACTGTGCCC  736
              |||||||||  || |||||||||||||| || ||||||||||||||||||||||||||||
Qy  848  TGGGTGCAGCTGAGATGAGACCTTTATTGAAGTAATTGGAAATAATGTACAACAGCCTATG  907

Db  737  TTGGTGCAGATGCCATGCGCCCCTCACGTAAAAACTATTTCCGATGTCCGAGATACCTTTG  796
              || |||||| |||||| | |||| ||||||||| |||||||||||| |||||||||||||
Qy  908  TCCTCTGTTGTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAACGCCTT  967

Db  797  TTTCAGCGCACCCAAATGCAGGCTTACCAAACGCATTGGTGAATATGACGAAACTCCAG  856
              ||||||||  || ||||||||| ||||| || |||||||||| |||||||||| ||||
Qy  968  CTATGATGGCCAAGCACCTAAAGATTTTGCTATGGATGGCTTGGTCAATATAGTTGGAG  1027

Db  857  AGCAAACTGCAGCTTTCTTAAAAGAGTTGCTGAAAGCGGGTTTGATTAACATTACTCGTGTG  916
              ||||||||||| |||||||||||||||||||||||||||||| |||||||||||||||||
Qy  1028 GATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATTGTGCAG  1087

Db  917  GTTGCTGTGTACGGACACCAGACCATATTCGACTATTGCCAATGCGCTATTGCGGTAAAAGACACATTG  976
              ||||| | | |  || | |  ||| ||| |  || ||| ||||||    |||||||||||||||
Qy  1088 AGCCTAGAGTTCCACCTGCCACTGCGTTTGAGGACGATATGTTACTGTCCGTCTAGAGC  1147

Db  977  CGCCTCGCCAAGTGCCTGAAACCGTACCTGCTTGCC------GCTTAAGTGGTTTAGAAC  1030
              || || | ||||| || |||||||  | | || ||       ||||||| |||| ||||
Qy  1148 CCTTCAGGATTGGACCGTACACCAACCTTGTTAACATTGTGATTGTTAAGCGCGCTGTAATGTTGCAG  1207

Db  1031 CATTTAATATTTATGATGATTCATTGTTCGTAGTCAAACGTTGGGGAGCGTACTAACGTTACCG  1090
              || |||||  || | |||| || ||||||||||| ||||||||||||| | |||| ||| ||
Qy  1208 GATCAAGGAAGTTTGCTAAACTCATCATGCAGAAACTATGAAGAAGCCTTGTGTTG  1267

Db  1091 GTTCTAAAAAATCTTAGTCTCATTCGTGAAGAAAAACTTTGCGAAGAAAACTTTAGAAGTTG  1150
              | ||  |||||  || |||| || ||||||  ||||||| || ||||||||   ||| |||
Qy  1268 CCAAAGTGCAGGTGGAAATGGGAGCCCCAGGTGTTGGATGTGTGGTCAACATGATGGCATGC  1327

Db  1151 CACAGCAGGTTGAGCGTGGCGCACAGATTATCGACATTAACATGATGAGGGGATGC  1210
              || ||||||| |||| | |||| |||| | |||| ||| ||||| |||| |||||||
Qy  1328 TAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCAGACCATCG  1387

Db  1211 TCGATTCGCAAAATGCGATGGTGCATTTCTTAACCTTGTCTGTCTAGCATCCATGAACCGGACAATTT  1270
              || | | || ||||| || ||| |||| || |  || |  | ||||| |||| | |||||| ||||
Qy  1388 CAAAGGTACCTTTGTGCATCGACTCCTCCAATTTGCGTGTGATTGAAGCTGGGTTAAAGT  1447

Db  1271 CACGTGTACGATCATGATTGACTCATCGAAATCGGAAATCATTGAAGCCGGCTTAAAAT  1330
              || ||| | ||||||||||||| |||| || |||||||| |||||||| || ||||| |
Qy  1448 GCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAGAGGAGGACGAGTTCT  1507

Db  1331 GCGTACAAGGTAAACCGGTTGTTAACTCAATTTCCTTAAAAGAAGGTTATGACGAGTTTG  1390
              || || ||||| ||| ||| ||||| | ||| ||| || |||||||| ||| |||||||
Qy  1508 TGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGCTGGTCATGGTCGTAAAGGC  1567

Db  1391 TTGAAAAGGCCCGGCCTTCGCCGTCAATATGGTGCTGCAATTATTGTGATGGCCTTTGACG  1450
              || ||||| |||  || | || || | || || ||| | | ||| || | || || | ||
Qy  1568 AAGAAGGACAGGCCAGGAAGATTAAAACAGACAACAAAATCAGAGTGTGCACCCGGCCTACCATC  1627

Db  1451 AAGTAGGTCAGGCCGACACTGCTGACGTAACGTGAAATCTGAAATCGTATGACA  1510
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Qy  1628 TGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATCATTTTTTGACCCTAATATCCTAA  1687
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Db  1570 TTTTGGTTAACGAAGTAGGCTTCCCTGCTGAAGATATTATTTTGACCCGAACGTGTTG 1570
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Qy  1747 CCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATGCAACAA 1688

Db  1630 CAGTTGCGACTGGTGGTATTGAAGAACATAACTACGCAGTCGATTTTATTGAAGCAACGG 1571
         |||  |||||||||| ||||||||||||||  ||||| ||||||||||||||| |||||
Qy  1807 AGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTAGGCAATGCATGGGGTTTCCTT 1748

Db  1690 GCTGGATTAAACAGAACTAACGACACCCATCAGTTTTCTGGTGTGTCTCAACGTTTCGT 1631
         ||||| ||||| |||  ||||||||||||||||||||| |||||||||||| ||||||
Qy  1867 TCTCCTTCCGAGGAATGGAAGCCATTGCGAGAAGCAATGCATGGGGTTTCCTTCCATG 1808

Db  1750 TCTCATTCCGTGCAATGAACCAGTTCGTGAGGCCATTCACTCTGTATTCTTGTACCATG 1691
         |||||||||||||  |||| |||||||| ||||||||||| |||||| |||||||||
Qy  1927 CAATCAAGTCTCGCATGGACATGGAGATAGTGAATGCTGAAACCTCCCTGTGTATCGATG 1868

Db  1810 CCATCAAGCAAGGCATGACCAGTTGTATTGTTGAACGGCAGGTCAAATGGCTATTTATGATG 1751
         |||||| |||||||| ||||||||||| ||||| || |||||| ||||||| |||||||||
Qy  1987 ATATCCATAAAGGAAGTCATCTGAAGATCTCATCTGGAATAAAGACCCCTGAGG 1928

Db  1870 ATATTCCTACCGAGCTAAAAGAGAGCGGTTGAAGATGTCATTTAAAACCAAAATCAAGGTG 1811
         ||||||| |||||| ||||||||  |||| ||||| || ||||||||||| ||||||||
Qy  2028 CCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACA 1988

Db  1930 AGTTCTGGTCAAGTCGCGACTGCAGAAACTACTTGAAGTTGCAGAAAAAATACCGTGACAAG 1871
         || |||||  ||||  || ||||||||  |||||||| |||| ||||||||||||| |||||
Qy  2086 --GGAGGAAGAAAGTCATTCAGACTGATGAGTGGGAAAGTGCCCTGTCGAAGAACGCC 2029

Db  1990 GTGGGTGCAACAAAGAGAGCCGAGAACTTGATGGCGTAATAGTCAGTGAATGGGCTA 1931
         ||||| ||||| |||||||| |||||  |||| | ||| |||| ||||||||||
Qy  2146 TTGAGTATGCCCTTGTGAAGGCCATTGAAAAACATATTTATTGAGGATACTGAGGAAGCCA 2087

Db  2050 TTGAATATGCCTTGGTTTAAAGGTTATTACGACTTTATATTGACCAAGACACCGAGAGCCC 1991
         |||| ||||||  |||||||||||||||| |||||| ||||||| |||||||| |||||
Qy  2206 GGTTAAACCAAAAATATCCCCGACCTTCAATAATTGAAGGACCCCTGATGAATG 2147

Db  2101 GCTTAAAAATCAAA--------CGTCCTTTAGATGTAATTGAAGGGCCACTGATGGACG 2051
         ||||| ||||||          ||||| ||||||||||||||||||||||||| |||
Qy  2266 GAATGAAAATGTTGGTGATCTTTTTGGTGAGCTGAAAAAATGTTCTACCTCAGGTTATAA 2207

Db  2161 GCATGAACGTCGGTGGTGTTCGTTCGGTTCAGGCAGGTTAAAAATGTTCTGCCACACAAGTGTAA 2102
         |||| |||||| ||||||| ||  ||||| || | |||||||||||||||||| ||||||||
Qy  2326 AGTCAGCCCGGGTTATGAAGAGGCTGTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAA 2267

Db  2221 AATCTGCCCGAGTCATGAAACAGCAGTAGCACTTGGCTAATATGGCGTAATCGAAGCTGAA 2162
         ||||||||||||||| |||||||||||  ||||| || ||||| |||||||| |||||
Qy  2386 GAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAAGAAAGAGGAGGCACCA 2327

Db  2248 --------AGACCGAAGGACAGTCTAAAGGTAAAG 2222
         
Qy  2446 TCGTGCGTGGCCACTGTTAAAGGGACGTGACGTGCACGACATAGGTTGGAGTAG 2387

Db  2308 TCCTAATGCAACGGTTTAGTGATGTGTTGCTAAAGAAATGGTAAAATATTGGTAGGGCGTAG 2249
         || ||||| |||||| |||| ||||| || ||||||||  |||||||||||||| ||||
Qy  2506 TCCTTGGCTGCAATAAATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGA 2447

Db  2368 TACTTGGCTGTAATGGCTCATGACATTGTACCTTGGCCTGTAATCCCTTGGCGTAAA 2309
         ||  |||||||| |||||||| |  || ||||||| ||||| | |||  |||  |||
Qy  2566 GAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAAGAAAGAGGAGGCACCA 2507

Db  2428 TCTTACAAACTGCAATTGCATGATGAAAATGTGACATCATTGGACATTCTTCGTCGATCACCC 2369
         || || ||| |||||||| |||| ||||| || || |||||||| |||| |||||||||
Qy  2626 CTTGAAAGTTTGTCCGCCACTGTTAAAGGGACGTGACGTCAAGGATTAGCTATAAGGATTC 2567

Db  2488 GTTCTACCGGACAAAATCGGTATTTTGTTGCTAAAGAAAATGCAGCGTAAAGGCTTTAACATTC 2429
         ||| || |||| ||||  ||| ||| |  |||||||||| |||| |||||| ||||  |||||
Qy  2683 CATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAG---CTC 2627

Db  2548 CTTTATTAATTGGTTGGTGGCCGACTACTTCTAAAGCACATAACAGCAGTAAAAATTGACCCTC 2489
         ||||| ||||||| ||||| | ||||| || |||||||| || || |||||||||||||||||
Qy  2743 CCAAGGATCAGGTTGAGGATTATGCATTGAGGATTATGCCAAAATCTGGTGGTGTGTGTT 2684

Db  2608 AGTATCAAAACGATGCGGTAATTTATGTGCCGATGCTTCACGTGCTTCAGTGTTGGTGTAGCGA 2549
         || | || | ||||||| ||||||  ||| ||  ||||| |||| ||||| |||||||||| |
Qy  2803 CCCAGCTGTTAGTAGAGTGAAAATCTAAAGGTGATGACTTTGAGGAAATCATGGAAGAATATG 2744
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Qy  2803 CCCAGCTGTTAGTAGAGTGAAAATCTAAAGGTGATGACTTTGAGGAAATCATGGAAGAATATG 2744
Db  2668 CAACCTTGCTTTCGAAAGAAATGCGTGGAGCATTATTGAAGAGGAGCATCGTGCTGAATATG 2609

Qy  2863 AAGATATTAGACAGGACCATTATGAGTCTCTCAAGGAGGAGGATACTTACCCTTAAGTC 2804
Db  2728 CCAAAATTCGTGAGCGTTAGCGGCGTTAGCCACAACAAAGCCAAAAGCAACTGACTTATAAAG 2669

Qy  2923 AAGCCAGAAAAGTGGTTCCAAATGATTGGCGTGTCTGAACCTCACCCAGTGAAGCCCA 2864
Db  2782 AGTCGGTTGAAAATGGTTTAAAATTGATGAAGAAACTACGTGCCAC------CAAAACCAA 2729

Qy  2983 CGTTTATTGGGACCCCAGTCTTTGAAGACTATGACCTGCAGAGAGCTGGTGGACTACACATTG 2924
Db  2842 ATCTTTTTGGGACACAAGTTTTAAAGAATTATCCGCTTGCTACACTCGTGGATTATTTTTG 2783

Qy  3043 ACTGGAAGCCTTTCTTTGATGTCTGGCAGCTCGCCTCCGGGCAAGTACCCGAATCGAGGCTTCC 2984
Db  2887 ACTGAGACGGCCATTCTTTATTTCTTGGAGTTAACTGGCAA------ATTCC 2843

Qy  3103 CCAAGATATTTAACGACAAAACAGTAGGTGAGAGGCCAGGAAGGTCTACGATGATGCCC 3044
Db  2947 CGAAAATTTTAGAAGATGAAGTGTCGCGGAAGCAGCAGCTGACCTTTACAACCAGGCAC 2888

Qy  3163 ACAATATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGCGCCCGGGGGTGTTGGTTGGGT 3104
Db  3007 AAGCGATGTTGAAAGATATTATTATCGACAAACAATCGTTTTGATGCTCGTCGTGCTGTATTTTGTA 2948

Qy  3223 TCTGGCCAGCACAGAGTATCCAAGACGACATTCACCTGTACGGAGGCTGCTGTGCCCC 3164
Db  3067 TGTTCCCGTGCTCAGCGTACAGACGCAGATACCCTCAGCGTATTGGAGGTTGCTGGTCAAA 3008

Qy  3283 AGGCTGCGAGAGCCCATAGCCACTTCTATGGGGTTAAGGCAACAGCTGAGAGGACTCTG 3224
Db  3118 -----TACTTTGAGCACTTACGCCAGCAATCTGACAAGGTGACAG 3068

Qy  3343 CCAGCACGGAGCCACCATACTACTGCCTCTCAGACTTCATCGTCCCTTGCATTCTCGGCATCC 3284
Db  3169 AACCAAATTTATCCTTCCTGGCAGATTACAT---TCGAGCTGATCGCCGAGCAGC 3119

Qy  3403 GTGACTACCTGGCCGTCTGTTGCCGTTGCCGTTGGGGTAGAAGAGCTGAGGCAAGGCCT 3344
Db  3229 AAGAACTACTTGGGCGGATTCACTGTATCGATTTTGGTGCAGAAGAACTGGCAAATGAAT 3170

Qy  3463 ATGAGGATGATGGTGACGACTACAGCAGCATCATGGTCAAGGCGCGCTGGGGGACCGGCTGG 3404
Db  3289 ACAAAGCCAAAGGTGATGATGAAGAAAGAGAGTCATTAGTTGCAGTCATTATTAGTCAGTT 3230

Qy  3523 CAGAGGGCCTTTGCAGGGAGAGTTCGCCGGCAGAACTGGCGCTGGGGTGGGAAACTGTGTG 3464
Db  3349 CCGAAGCTTTTGTCCGGAACACTTTACATGAACGTATTCGTAAAGAGTTCTCGGGGCCTAG 3290

Qy  3583 GCAGTGAGCAGCTGGACGTGGCGCCTCGCGAGGTTGCGGGTACAAGGGCATCCGCCCCG 3524
Db  3409 CTGATGAGCAGCTCAGCAATGCATCATCCTCAGAGTGATTAAAACTTTCGCCCCTG 3350

Qy  3643 CTCCTGGCTACCCCAGCCGACAGTCTAAATTGGCCTGTCGTCAGGACTCATCACTC 3584
Db  3469 CACCAGGCTACCCCTCCCGCTGCTGCCAGAGACTCTGAAAAAGCAGTCTAAAGGTAAG 3410

Qy  3703 ACATCGAGCAGTCTACAGACGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAG 3644
Db  3529 GTTCTACCGGACAAAATCGGTATTTTGCTAAGGATGATGCCCCATCTT 3470

Qy  3763 CAGTGTCTCAGGCCTCTACTTCTCCAAATTGTCGTGTGGGAAGATTT 3704
Db  3589 CAGTAAGTGGTTTCTATTATTCTCATCCTCAGAGTGAATACTTTAACGTGGGTAAAAATCT 3530

Qy  3823 CCAAGGATCAGGTTGAGGATTATGCATTGAGGATTATGCCAAAATCTGGTGGTGTTGAGA 3764
Db  3649 CTCAAGACCAACTTGAAGATTATGCCACTGATGATGAGCGGAAGC 3590
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Qy   3824 AATGGCTTGGACCCATTTTGG 3844
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Db   3650 GTTGGTTAGCTCCGAATTTAG 3670

RESULT 5
US-10-282-122A-32592
; Sequence 32592, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32592
; LENGTH: 3669
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-10-282-122A-32592

Query Match   23.0%; Score 902.6; DB 7; Length 3669;
Best Local Similarity   55.0%; Pred. No. 2e-261;
Matches 2046; Conservative   0; Mismatches 1574; Indels   99; Gaps   10;

Qy   145 AAGAGGATTATGGTGCTGGAGGATGGGACCATGATCCAGCGGGAGAAGCTAAAC 204
           ||| ||||| ||| ||||||||| |||||| ||||||| |||
Db   34 AAACGGATCTCAGTCCTTGATGCGCAATGGAACCATGATCCAGCAATATCAGCTGGCA 93

Qy   205 GAAGAACACTTCCGAGAGTGTTGGAGGTTAAAGATCATGCGAGGCGCTGAAAGGCAACAAT 264
           |||| |||| |||||||| |||||||||||||| |||| ||||| ||||
Db   94 GAAGAAGATTACCGAGGTGAACGTTTTGCCCATTGGCAATGTGATGTTAAAGGGGAATAAT 153

Qy   265 GACATTTTAAGTATAACTCAGCCTGATGTCATTTACCAAATACCATAAGGAATACTTGCTG 324
           ||| ||| | ||| ||||| |||| ||| |||| | |||||| ||
Db   154 GACCTTTTAGTCTTGACGCAGCCGCAGATCATTACTGAAATTCATAAATGCTTATTTTGAA 213

Qy   325 GCTGGGGCCAGATCAATCATTGAAACAAATACTTTTAGCAGCACTAGTAGTTGCCCAAGCTGAC 384
           ||| |||||| || || | || ||||| | | | | | |||| ||||
Db   1288 ATGATTGACTCGTCAAAATGGCAAGTTATTGAGAAGGATTGAAAATGTATTCAGGGTAAA 1347

Db   214 GCCGGTGCAGATATCGTGGAAACAAACACCTTTAATGCAACCTCTATTGCCATGGCTGAT 273

Qy   385 TATGGCCTTGAACACTTGGCCTCCGATGAACATGTGTCTCTGCCAGGAGTGGCCAGAAAA 444
           |||| ||||||| || || ||| ||| || ||| |||| || ||||
Db   274 TATCAGATGGAAGGGTTATGTGCAGAATTGAATGAAGAGGGCTGTAAACTTGCCAGAGCC 333

Qy   445 GCTGCCGAGGA--GGTAACTCTCCAGACAGGATGTCCCATCTGTGGAAAGGCCGGATTATAGGAAC 501
           ||||| ||||| ||||||| ||| |||||| |||||| |||| |||| ||||| ||||
Db   334 TGTGCTGATAAATGGAGTGCATTAACGCCAGATAAACCACGTTATGTGTGCAGGGTATTA 393

Qy   502 GGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGGAAAGGCCGGATTATAGGAAC 561
           ||||| |||||||||||| | | | ||||| | |||| ||||||| ||||| ||||
Db   394 GGGCCGCCAATAGAACAGACATCCATTTCCTGATGTTAACCATCCCGCGTTTCGTAAT 453

Qy   562 ATCACATTGATGAGCTTGTTGAAGCATCACCAAGAGCAGCCAAAGGACTTCTGGATGGC 621
           || ||||| || || | | | |||| ||||| ||||||||| |||| ||||
Db   454 ATCTCATTTGATACATTGGCTTATCGAGAGGCGATCTGCCGGACTCATTAAAGGA 513

Qy   622 GGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTGCCAATGCCAAGGCAGCCTTG 681
           ||| || || || || | ||| || | | ||||| ||| || |||| |||||||
Db   514 GGGGTGGATTAATTATGTGAAACCATTTTTGCACCCTAAATGTCAAAAGTGCTATT 573

Qy   682 TTTGCACTCCAAAATCTTTTTGAGGAGAAAATATGTCTCCCCGGCCTATCTTTATTTCAGG 741
           ||| | |||||||||| | ||||| ||||| ||| | | || |||| | ||||||||
Db   574 TTTGCGATTAAATGTGAGTTTGATAATCTTAATATTAAATATTACGGTGATGTCTCAGGG 633

Qy   742 ACGATCGTTGATAAAGTGGGCGGACTCTTTCCGGACAGCAGGAGGAGGGATTTGTCATC 801
           || || | ||| || | || | || |||| || || | || |||||||
Db   634 ACTATCACTGATGCGTCAGGTAGAACATTAACAGGGCAAACCACAGAAGCCTTTATCAC 693

Qy   802 AGCGTGTCATGGAGAACCACTCTGCATTGGATTAAATTGTGCTTTGGGTGCAGCTGAG 861
           |||||| || || || ||| | ||||| |||| | | |||| |||| || |||
Db   694 TCACTACGTCATGCCGACGCGTTATCATTTGGTTTAAATTGTGTGCCTAGGGGCCAAAGAA 753

Qy   862 ATGAGACCTTTTATTGAAATAATTGGAAAATGTACACAGCCTATGTCCTCTGTTATCCC 921
           ||||| ||| | |||| ||||| ||||| | | |||| | | ||| |||||||
Db   754 TTACGCCAATATATTCAAACTCTCTCCCAAATATCAGAGAACTTATGTCAGTGCTCACCCT 813

Qy   922 AATGCAGTCTTCCCACCAACACTTTGGTGACTATGATGAAACGCCTTGTCATGATGGCCAAG 981
           |||||| | | | || |||| ||| || || |||| |||| |||| || ||||||||
Db   814 AATGCTGGCTTACCTAATGCCTTTGGCGGATATGATTTAGATGCCAATGACATAGTGCCGAA 873

Qy   982 CACCTAAAGGATTTTGCTATGGCTATGGCTGGTTTCTATAGTTGGAGGATGCTGTGGGTCA 1041
           ||| ||||| | ||| | ||| || | || | ||| | | | ||||| || |
Db   874 CAAATCAAGGAGTGGGCCCAAGCTGGGTTTCTTCAATATTGTCGGTGGTGTTGTGGCACA 933

Qy   1042 ACACCAGATCATATCAGGGAGAATTGCTGAAGCTGTGAAAAATTGTAAGCCTACGAGTTCCA 1101
           | || || | | ||||| |||||| | ||| ||| | ||| | | ||| ||||||
Db   934 ACCCCTGCCCATATTCAGGCTATTGCTCAAGCGGTTGATGGCATAGCACCTAGAACATTA 993

Qy   1102 CCTGCCACTGCTTTGAAGGACATATGTTACTGTCGTCTGGTCATGATGTTCGAGATCAAGGAAGTTT 1221
           ||||| | ||| | | ||| ||| |||| | ||||| |||||| |||||| |||||||
Db   994 CCTGTCA------TTAAAAAGCCTGTCGCACTCTCAGGTCTTGAGCCTTTGGTCTCATTGAT 1047

Qy   1162 CCGTACCACCAACTTGTTAACATTGGAGAGCGCTGTAATGTTGCAGGATCAAGGAAGTTT 1221
           |||| | | || | | | ||||||||| || | | ||||| | ||| |||||
Db   1048 GATAATTCGCTGTGTCGTCAATGTGGGGGAACGAATGTTGACAGGTTCGGCTAAATT 1107

Qy   1222 GCTAAACTCATCATGGCAGGAAACTATGAAGAAGACCTTGGTGTTGCCAAAGTGCAGGTG 1281
           ||||| | || || |||| ||| | | |||| | ||| |||| | ||| |||
Db   1108 AAACGTTTAATAAAAGAGGTAATTACCAAGAACCCGTGTTGCTCGTCGTCAGCAAGTT 1167

Qy   1282 GAAATGGGAGCCCAGGTCGTTGGATGTCAACATGCGCTGAAAGGCAACAAT 1341
           |||| || |||| || |||| ||||| | || |||| ||||| |||||
Db   1168 GAAAACGGTGCTCAAATATCAATCAATATCGATGAAGGCATGTTAGATGCGAATATAAT 1227

Qy   1342 GCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCAGAATCGCAAAGTACCTTTG 1401
           |||| | || | | ||||| | || || || | ||| || || ||||
Db   1228 GCAATGACACACGTTTTCTTAATCTTATTGCGGGTGAACCCGATATTGCCAAAGTCCCGATT 1287

Qy   1402 TGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTTAAAGGCGTGGTGCAAGGGAAG 1461
           || | |||| || ||| || | || |||||| || || ||| |||||| ||||| |||
Db   1288 ATGATTGACTCGTCAAAATGGCAAGTTATTGAGAAGGATTGAAAATGTATTCAGGGTAAA 1347

us-10-607-712-1.rnpbm

Qy 2536 GATATAATTGGCTGTCGAGGACTCATCACTCCTTCCCTGGATGAAATGATTTTTGTTGCC 2595
         ||| |||||| |||| ||||||||||||| ||| ||||| ||||||||| ||| |||
Db 2386 GATATTATTGGATTGTCTGGATTGATCATCACCCCATCACTGGATGATGAGATGGTGAATGTTGCT 2445

Qy 2596 AAGGAAATGAGAGAGATTAGCTAGTAGCATTCCATTGTTGATTGGAGAGCAACCACTTCA 2655
         ||||||||| |||| |||| | || |||||||||||||||||||||||||| || ||
Db 2446 AAAGAGATGGGAAAGACGCGGTTTTCTTCCTTAATGATGGTGCGGCAACATCG 2505

Qy 2656 AAACCCACACAGCAGTTAAAATAGTCCGAGATACAGTGCACCTGTAATCCATGTCCTG 2715
         |||||||| ||| ||||||| | |||| |||| |||| |||||||||||| | ||||
Db 2506 AAAGCGCACACCGCGAGTAAAAATTGAGCCTAATTACAGCCCACCCACCCGTTTATGTGCAG 2565

Qy 2716 GACGCGTCCAAGAGTGTGGTGGTGTGTCCAGCTGTTAGATGAAATCTAAAGGATGAA 2775
         || | ||||| ||| |||| || || | |||||||| ||||||| |||||| ||
Db 2566 AATGCGTCAAGGACGGTCGGGTGGTCCTGCGCATTAATTATCGCCACACAAAGGCTGAT 2625

Qy 2776 TACTTTGAGGAAATCATGACGTGTATGCCATTAATTTTATCCATGCAACAAAGTCATTAAAGAA 2835
         | |||||| | |||| ||| || ||||| |||||| ||||||| || || ||||
Db 2626 TTTGTGCTAAAACACGCCCGTGAATATGAAGTGGTACGTCAGCAGTATGCGAGAAAAAAA 2685

Qy 2836 AAGGAGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGATTGG 2895
         ||||| |||| ||||| | ||||| ||| | ||| || |||||||| | |||
Db 2686 CCGCGTACGCCTCCCGTTTCCTTAGCGAAAGCTCGTGCCAATGCCAGTTGACTGG 2745

Qy 2896 CTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGACCCGGTCTTTGAAGACTAT 2955
         |||||| |||||||| |||||| |||||| |||| |||| |||| ||| ||||
Db 2746 CAACACTATACGCCACTTAAGCCGAACAATTAGGGGTACAACAAGTTACAGGCCAATATT 2805

Qy 2956 GACCTGCAGAAGCTGGTGGACTACCGGAATCGAGCGTTCTTCTTGATGTCTGGCAGTC 3015
         ||| ||| || | ||| | ||||| | | || |||| |||| || |||||||
Db 2806 GAA------ACTTACGTGAGTATATCGACTGGACGCCTTTCTTTATGAGTTGGTCATTGG 2859

Qy 3016 CGGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTAACGACAAAACAGTAGTGAA 3075
         | |||| ||| | | || ||||||| ||||| | | |||||
Db 2860 GCGGGAAATATCCACGT---------ATATTAGAAGATGAGGTTGTCGGGGAA 2904

Qy 3076 GAGGCCAGGAAGGTCTACGATGCTGGAACACACTGATTAGTCAAAAG 3135
         |||| ||| || |||| ||| ||||| |||||| || |||||
Db 2905 GAGGTAAGACGCGTTTTTGCAGATGCCATGTTGATAAACTCAGCCGTGAAAAA 2964

Qy 3136 AAACTCCGGGCCCCGGGCGTGTGGTGTTCTGGCACAGAGTATCCAAGACGACATT 3195
         ||| ||| || ||| | |||||||| || |||| |||| ||| ||| ||||||
Db 2965 TTACTGACACCGAAAGGTATCGTTGGTTTATTCCCGTGGTCGCCTTGGTGTGATGACATT 3024

Qy 3196 CACCTGTACGCAGAGGCTGCTGCGTGCCCCAGCGTGCGAGAGCCCATAGCCACTTCTATGGG 3255
         | | ||| ||| ||| ||| | ||||||| |||||| | ||| |||||
Db 3025 ATTATTACCAAGATGAAACGGCACAGCATG---------AGTTATTACGTTGTTGCCAT 3075

Qy 3256 TTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCAGCCAATACTGCCTCTCCGAGAC 3315
         || |||| || || ||| |||||| |||| |||| |||| | | ||| | |||
Db 3076 TTACGCCAACAACAGAAAAAAAGA-------GTACCCTAACTATTGCTTAGCAGAC 3126

Qy 3316 TTCATCGCTCCCCTTGCATTCTGGCATCCGTACCTGGGCGTCGTTGGTGCTTGCCTGC 3375
         ||||| | | || ||| |||| | || ||| ||||| |||| ||| |||| | ||
Db 3127 TTTATTGCCCCGTGGATAGTGGTCTTGCTGGACTATTTGGGCTTTTGCAGTTACCGGC 3186

Qy 3376 TTTGGGGTAGAGA---GCTGACAAGGCCTATGAGGATGGTGACGACTACAGCAGC 3432
         || | |||||| |||| ||| | | |||||| | | |||||| |
Db 3187 GGTCTAGAAGAGAATGCTCCACTCCGTAATGGGTATATAATGCTTCATGATGATTACAATAAA 3246

Qy 3433 ATCATGGTTCAAGGCGTCGGGGACCCGGCTGGGAGAGGCCTTTGCAGAAGAGCTCCATGAA 3492
         || ||||| | ||||| | | |||| || || |||| ||| |||| | ||| ||||||
Db 3247 ATTATGTGTAAAAGCGCTATCCGATCGTCTTGCGAGAACGTTTTGCCGAATATTTGCATCAA 3306

Qy 3493 AGAGTTGCCAGAAGAACTGTGGGCCTACTGTGGCAGCTGGCAGTGCTGCAGACCTG 3552
         | ||| | ||| | |||| || | ||| |||||| ||| |||||||| ||||
Db 3307 CAAGTGAACCAAGATTTGGGGTTACAGTCCTGACGAAGCGCTCTCTAATGACGAGTTG 3366

Qy 3553 CGAAGGTTGCGGTACAGGGCGTACAGGGATATCGGCGCTCACCCAGCCAGCAGCCACCAC 3612
         | ||| | | ||| | |||| | |||||||| |||| | || || ||||| ||
Db 3367 ATTAGACAGAAAAAATCAAGGACACCGGGATATGCGGCGCTTGCCCAGACGAC 3426

Qy 3613 ATTAGGAGTCATGACTCCATGTGATAGTGGACTGGTCTCTTGACCACAAAGCA 3672
         |||| |||| |||| ||||| || | | ||| ||| |||| ||||||||
Db 3427 ACCGAGAAGCTCACCATGTGAGACTCCGCAGACATCGAGCAGTCTTACAGGCAGTCTTACAGGCATTAGTTA

```
Db   3427 ACAGAAAAAGCAAAATTTGGCAACTGGTTAAATGTAGAAAAATCGCATTGGTATGGAAGCTT 3486
          ||| ||       |||        ||||        |     ||| ||    |||||
Qy    173 TGGGGACCATGATCCAGCGCGGAGGAAGCTAAAGCAGGAGAAGAGAACACTTCCGAGGTCAGGAAGTCAGGAATTA 232

Db   3673 ACAGAATCATTAGCAATGCCACCTGCTTCAGCGAGTCTCAGGGCCTCTACTTCTCCAATTG 3732
          |||             ||       |||        |||          ||||
Qy     89 TGGGCACCATGATCCAGAGCTACAAGCTGGAAGAGAGGCCGACTACCGGCGCGAGCGCTTCG 148

Db   3487 ACTGGATCGCTTACGCGATGTGGCCGGCGGGCTTCGGTATCGGGTTGGTATTTTAGTCATCCT 3546
          |||             |||       ||||        ||||        |||||
Qy    233 AAGATCATGCCAGGCCGCTGAAAGCCGTGAAAGGCAACAATGACATTTAAGTATATAACTCAGGCTGATG 292

Db   3733 AAGTCCAAATATATTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGATTATGCATTG 3792
          |||             |||       ||||        ||||        |||||
Qy    149 CCGACTGGCCGGAGCGACGTGAAAGGCGAAAAGGCAACAACGACACCTCTTGCTGCTGAGCCGCCCGCCGACG 208

Db   3547 GAAAGTAAATAATATTTGCCGTCGCTCAAATTCAAAAGATCAGTAGAAGATTACGCCAAA 3606
          |||             |||       ||||        ||||        |||||
Qy    293 TCATTACCAAATCCATAAGGAATACTTGCTGTGGGGCAGATATCATTGAAACAAATA 352

Db   3793 AGGAAGAACATATCTGGCTGAGGTTGAGAAATGGCTTGAGACCCCATTTGGGGATGA 3851
          |||             |||       ||||        ||||        |||||
Qy    209 TGATCCAGGCCATCGACCTCGACGGCGGCGGGCCGGGCCGGATGGCCTTGAACACTTGGCCTGGCCCTCACCGGA 268

Db   3607 CGTCGGTGGTATGAGTGTGAGTGAAGTTGAGCGGTTGGTTAGCCCCTAATTTAGGTTATGA 3665
          |||             |||       ||||        ||||        |||||
Qy    353 CTTTTAGCAGCACTAGTATTGCCCAAGCTGACTATGGCCTGACACTTGCGCTGCGCCACGAAC 412

Qy    269 CCTTCAACGCTGTCCCAGGCCACCCAGGTGTCCAGGAGTGGCCCAGGAGGTAACTCTCCAGA--- 328

RESULT 6
US-10-282-122A-30149
; Sequence 30149, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE:   2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30149
; LENGTH: 3705
; TYPE: DNA
;. ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-30149

Query Match      23.0%;  Score 901.4;  DB 7;  Length 3705;
Best Local Similarity   55.2%;  Pred. No. 4.7e-261;
Matches 2073;  Conservative   0;  Mismatches 1581;  Indels 103;  Gaps  12;

Qy    413 TGAACATGTCTGCTTCGCAGGAGTCGGCCCAGAAAAGCTGCCGAGGAGTAACTCTCCAGA--- 469
          ||| ||       |||        ||||        ||||        |||||
Qy    470 CAGGAATTAAGAGAGTTTGTTGCAGGGGCTTCTGGGTCCGACTAATAAGACACTCTCTGTGT 529

Db    329 TCAACGTCGAAGGGGCCGCTGGCCCTGGCGATCTTCGCCCGTCCAGGGCGTGTTCGAGGAAC 388
          ||| ||       |||        ||||        ||||        |||||
Db    389 CGGACAAGCGCCGGTTTCGTCGGCGTGCGGCCCCGGCGTCTGGCGCCCGACCACGCCCACCGTCTCTCGATTT 448

Qy    530 CCCCATCTGTGAAAGGCCGGATTATAGGAACATCACATTTGATGAGCGTTGTTGAAGCAT 589
          ||| ||       |||        ||||        ||||        |||||
Qy    590 ACCAAGAGCAGGCCAAAGGACTTCTGGATGCGGGGGTTGATGTCTTACTCATTGAAACTA 649

Db    449 CCCCGGAGTGAACAACCCCGGCTACCGCAAGGTCACCTTCGACGAACTGGTGGAGAACT 508
          ||| ||       |||        ||||        ||||        |||||
Db    509 ACGTCGAGGGCGACCCGGAGGCCTGATCGAAGGCGGCGGCCGACCTGATCCTGATCGAGCGACCA 568

Qy    650 TTTTGATACTGCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGA 709
          ||| ||       |||        ||||        ||||        |||||
Qy    710 AATATGCTCCCCGGCCTATCTTTATTTCAGGACGACGATCGTTGATAAAAGTGGGCGGACTC 769

Db    569 TCTTCAACACCCTCAACGCCAAGGCGGCGGATCTTCGCCGTCCAGGGCGTGTTCGAGGAAC 628
          ||| ||       |||        ||||        ||||        |||||
Db    629 TCGGCGTGGAGCGTGCCGATCATGATCTCCGGAACATCACCGACGGCCGCCTCTCGGCGCACCC 688

Qy    770 TTTCCGGACAGAGAGGAGGAGATTTGTCATCAGCGTGTCTCTGGAGAACCACTCTGCA 829
          ||| ||       |||        ||||        ||||        |||||
Qy    830 TTGGATTAAATTGTGCTTTGGGGTGCAGCTGAGATGAGACCTTTTTATTGAAATAATTGGAA 889

Db    689 TGTCGGGGCCAGACCACCGGAGGCCTTCTGGAACTCGGTTGCGGCATGCCCGGCCGATCTCGG 748
          ||| ||       |||        ||||        ||||        |||||
Db    749 TAGGCCTGAACTCGCCCCTCGGCGCCCAAGGAATTGCGGCCGTACATCGAGGACACTGTCGA 808

Qy    890 AATGTACAACAGCCTATGTCCTCTGTTATCCCAATGCAGAGTCTTCCCAACACCTTTGTG 949
          ||| ||       |||        ||||        ||||        |||||
Qy    950 ACTATGATGAAACGCCTTGTGGTGGTCAACACCAGTCATATCAGGGAAAATTGCTG 1009

Db    809 CCAAGGCGACACTCACGCCTCGGCCTGCCCACCCAAGCGGCGGCCGCCGGCCCTTCGGCG 868
          ||| ||       |||        ||||        ||||        |||||
Db    869 AATACGACGAATCGCCGGCGGGCGGAAATGGCCGTGTGGTCGGAGGAAACGTTCGCCGCGGATGAATTCGCCCGCCGGCT 928

Qy   1010 TGGTCAATATAGTTGGAGGATGCTGTGGTCAACACCAGCATCATCAGGGAAATTGCTG 1069
          ||| ||       |||        ||||        ||||        |||||
Qy   1070 AAGCTGTGAAAATTGTAAGCCTAGAGTTCCACCTGCGCTTTTGAAGGACATATGT 1129

Db    929 TCCTCAATATCGTCGGCCGCTGCTGACGGGCCATCCCGAGGATCGCGCCACCCGCGCACATCGGCGATCGCCA 988
          ||| ||       |||        ||||        ||||        |||||
Db    989 AGGCAGTGCCAAGTACCCGCGGGCATCCCGGAGATTCCCCGGGCCTGTC------ 1042

Qy   1130 TACTGTCTGGTCTAGAGCCCTTCAGGATTGGACCGTACCACCAACTTGTTAACATTGGAG 1189
          ||| ||       |||        ||||        ||||        |||||
Qy   1190 AGCGCTGTAATGTTGCAGGATCAAGGAAGTTTGTAAACTCATCATGGCAGGAAAACTATG 1249

Db   1043 GCCTGTCCGGCCGTTCGGAGCGTTCACCATCGACCGGCAGCTGCGTGTTCGTGTTCGTCAACGTTCGGGG 1102
          ||| ||       |||        ||||        ||||        |||||
Db   1103 AGCGCCACCAACATCACCGGTTCGGCCAGTTCGCCCGCGTATCCTGATCCTCGATGCGCGGCA 1162

Qy    113 CCCTGCGCGGATGAGATGACCAATGCCATTCTGCAGAAGAGAGATTATGGTGCTGATGAGGAGGA 172
          ||| ||       |||        ||||        ||||        |||||
Db     29 CCCGGCCTGCAAGCCTGCACCGCACGCCCTCAGCGGAACGTATCCTGATCCTCGATGCGCGGCA 88
```

Qy   1250 AAGAAGCCTTGTGTGTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCGCCCAGGTGTTGGATGTCA 1309
          |||||| || | |||||| ||||| | || || || | ||||| |||| || || ||
Db   1163 CGGAAGCTCTCGAGGTCGCCAGCAGCAGGTGGAAGCGCCGGCCGCCCAGGTATGAGGCTGACATCA 1222

Qy   2234
                                                    || |||
Db   2234 AAGGCGACA----------------------------------AGCCGGAGCCAAGGCAAGA 2263

Qy   1310 ACATGATGATGGCATGGCTAGTAGTGGTTCCAAGTGCCAATGACCAGATTTGCAACTTAATTG 1369
          |||| ||||| | || ||||||| || | ||||| ||| ||| || ||| |||||| |||
Db   1223 ACATGACGAAGGCATGCTGGACTCTGAAAGGTACCTTTGTGCATCGATCGATCGTGATCG 1282

Qy   2387 TCGTGCTGGCCACTGTTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAG 2446
          | ||| |||||||||| | |||||| ||| || | |||| ||| ||||| ||||
Db   2264 TCCTGATGGCCACGGTCGAAGGGCGACGTGCAAGCAGCATCGTCGGCGTGG 2323

Qy   1370 CTTCCGAGCCAGACATCGCAAAGTACCTTTGTCATCGACTCCTCCCAATTTTGCTGTGA 1429
          | |||| || || |||||| |||| ||| || ||| || || | || || ||||
Db   1283 CCTCCGGAGCCGACCATCTCCGCCGTGATGATGATCGACTCCTCCAAGTGGGAAGTGA 1342

Qy   2447 TCCTTGGCTGCAATAATTCCGAGTTATTGATTTAGGAGTCATGACTTCCATGTGATAAGA 2506
          | || | ||| | ||| | || | |||| ||| || |||| ||||||| |||||||
Db   2324 TGCTCGGCTGCAACGGCTATGACGTGTCGACCTGGGTGTGCGGGGAGAAGA 2383

Qy   1430 TTGAAGCTGGGTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTTCTGAAGG 1489
          | ||| ||| || ||| || |||||| ||| | || ||| || |||||| || ||||
Db   1343 TCGAGGCCGGCCCGGGCGAGCTGGCAACGGGCAATGCGCAGTAGCATTCTCGATGAGG 1402

Qy   2507 TACTGAAAGCTGCTCTTGACCAAAGCAGATATAATTGGCTCGTGTCAGGACTCATCACTC 2566
          |||||| ||| ||| ||||| |||| || | | | ||| ||||||||||| ||| ||
Db   2384 TCCTGCAGACCGCCGCCATCGGCCTGTCTCGGCCTCGTGTCTCGGACTCACGC 2443

Qy   1490 AAGGAGGAGGACTTCTTGACAGAAGCCCAGGAAGATTAAAAAGTATGGACGTGCTATGG 1549
          |||| ||||| | || |||||| | |||| ||||||||||| || ||| || ||||
Db   1403 AAGGCGTCGAGGCCTTCAAGCACCATGCCCGCTGTGCAACGCGACACCCCGGTGG 1462

Qy   2567 CTTCCCTGGATGAAATGATTTTTGTTGCCAAGGAAATGGAGATTAGCTATAAGGAATTC 2626
          | ||||||| ||| || || | |||||||| || || || || ||| ||| || |
Db   2444 CGTCGCTGGACGAGATGTTCACGGCGGCCAACTCGAGAAATGCAGCAGAATTTCCAGTTGC 2503

Qy   1550 TGGTCATGGCTTTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTT 1609
          ||| ||| || || || ||||| |||| | |||| | ||| ||| |
Db   1463 TGGTGATGATCGGCGGCGTCCTACGCACATCT 1522

Qy   2627 CATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACACAGTTAAAATAGTCCGA 2686
          ||| |||||| ||| |||| | ||||||||| | ||| | | ||||||||||||||
Db   2504 CGCTGATGATCCGCGGCGGCCCACTACCTCGAAGGCGCGCATACGCGGTGAAGATCGATCCGC 2563

Qy   1610 GCACCCGGGCTACCATCTCGTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATT 1669
          ||| || || |||||||| || || ||||||| ||| ||||| | ||| |||
Db   1523 GCAAGCCGCCTTCGAGCAGTGCGTGAAGGCCATCTCCGCCGTGATGGAAGATCATCT 1582

Qy   2687 GATACAG---TGCACCTTGTAATCCATGTCCTGACGCGTCCGAGGAGTGTGGTCGTGTTT 2743
          || || | | || | || |||||||| |||||| ||| ||||||| ||| | |||
Db   2564 AGTACAGCAACGACGACGCGGTGGTCTACGTCACGGAGAGCCTGCGCGGTAGGCGTGGCCA 2623

Qy   1670 TTGACCCTAAATATCCTAACCATTGGAATGGAGGAACAACAACTTGTATGCCATTA 1729
          || || || | |||| || |||| || ||| |||| |||| ||| | |||||||
Db   1583 TCGATGCGAACATCTTCGCCATCGCCATCGAGGACTGAAGGCCATCTCCGCCGTCACG 1642

Qy   2744 CCCAGCTGTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATG 2803
          ||| | || | ||| | || ||| ||||| || || |||| | ||| || ||||
Db   2624 CCAGCCTGTCCAAGGAGCTGCGCGGCGTCGAAGGCCACCCGCCGCCGCCGACTACG 2683

Qy   1730 ATTTTATCCATGCAACAAAAGTCATTAAAGAACCATTACCTGGAGCCAGAGAAAGTGGAG 1789
          | ||| || ||||| | | ||| || ||||| | | ||| |||||| |||||| |||
Db   1643 ATTTCATCAAGGCCTCTACAGCGTCCTACGCCGCCCTGCCGAGCTCCCCTGGAGCTCG 1702

Qy   2804 AAGATAT------TAGACAGGACCATTATGAGTGTCTCTCAAGGAGGAGGAGATACTTACCCTT 2858
          ||||||| |||| ||| || | | ||||| || |||| || || || || ||| |
Db   2684 CGGTGGTCCGGAACCGCACGGCCAACCGCGCCGAGCGGCTGCGCGGCGCTGCGCTACGAAC 2743

Qy   1790 GTCTTTTCCAACTGTCCTTCCTTCCTTCGTTTCCGCGGCAACACCCGTACGGCGAGGCGATCCACT 1849
          || ||| |||| || || ||| | || || ||||| ||| | ||| || || || ||| ||
Db   1703 GGGTGTCAAGCGTGTCCTTCTTCGGTCCTTCGGGCGGCATCGACCGGGTCGGAGGCTCGGGGCG 1762

Qy   2859 AAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGATTGGGCTGTGTCGAACCTCACCCAGTGAA-------- 2918
          |||| |||| ||| ||| | | || ||||| ||| | |||||| || || || |||||
Db   2744 AGGCGATCGCCAACAGCCGCCGGTTCTCCGGCCGTCGCTCGGGCCGGGTACCGCCCGGCCGAC 2795

Qy   1850 GGGTTTTCCTTTTACCATGCAATCAAGTCTGCAATCAAGTGACATGGACATGTGATGAGAGTGAATGCTGGAA 1909
          |||| |||| || ||| ||| || |||| || || ||| |||| || |||||| | ||||| | |||||
Db   1763 CGGTGTTCCTCTACTACGGCGATCCGACCGATCCGACGCGTCGAACGTGATCGTCAACGCGGAGTA 1822

Qy   1910 ACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCTTCTGTGTGAGATCTCATCT 1969
          || || | | | | ||| ||| || ||| || || |||||| || | || |||| ||
Db   1823 AGCTGACTGGCGCGTCGTGTGCGCGAAGGCCTGCGAAAGCCTGCGAGGTCGAGGACGTGTGC 1882

Qy   2919 GCCCACGTTTATTGGACCCAGGTCTTCTTGAAGACTATGACCTTGCAGAAGCTGCTGGACTA 2978
          || ||| || || || |||| | || ||||| ||| ||| || ||| || ||| || |
Db   2744 AGGCGATCGCCAACAGCCGCCGGTTCTCCGGCCGTCGCTCGGGCCGGGTACCGCCCGGCCGAC 2795

Qy   1970 GGAATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGAGACTCAA---GGCA 2026
          | |||| |||| || |||||| | | ||| | | || | |||||| ||||| ||||
Db   1883 TCAACCGCACCGCCGGCGCCCGGCGTCCGGATCGCCGACGACTACAAGGGCG 1942

Qy   2979 CATTGACTGGAAGCCTTTCTTCTTTGATGTCTGGCAGCTCCGGGGCAAGTACCAGGCAAGTACCCG--------- 3038
          |||| | ||| || || | | |||| | || ||| || || || || || || || ||||
Db   2856 CATCGACTGGACGACGCCGTTCTTCCTGGACGTCTGGCAGCTGCCGGGACCTGCCGCGGACCGAGTACGGACTACG 2907

Qy   2087 TTGAGTATGCCCTTGTGAAGGGCATTGAAAACATATTATTGAGGATACTGAGGAGGCCA 2146
          | ||| |||||| |||| |||| || || |||| | | || ||||| ||||| | |
Db   2003 TCGAGCATGCGCTGGTCGGGCGTGGCCAGGGCATCAACCACCTGGATCGTCGTGAGGTGTGC 2057

Qy   3039 CTTCCCAAGATATTTAACGACAAAACAGTAGGTGAGGCCAGGAAGGTCTACGATGA 3098
          | || | | ||| |||| | | || | |||| |||| || |||| |||| |||
Db   3021 CGGCTTCTCGGCGGCCGGATCGCGCCGGGATCCGCCGGAGGTCTACGGCGGCCGATGG 3080

Qy   2147 GGTTAAACCAAAAAAAATATCCCGACCTCTCAATATAATTGAAGGACCCCCTGATGAATG 2206
          | ||| ||| ||| ||||| ||| | | || |||| |||| | | |||
Db   2058 ----ATGCGGCCAGCAGTGTGCGGTCCCGGTCCCATGCTGGTCCG 2113

Qy   3099 TGCCCACAATATGCTGAACACACTGATTAGTAGTCAAAGAAACTCCGGGCGTGTGT 3158
          | ||| | || ||| |||||| || | | || || | |||| ||| || || ||
Db   3081 C------GAGACCCTGCCACCCTGCACCACGGGTAAGCCAGCAGCGACGATCAAGCC 3128

Qy   2207 CAGGAGGGAAGAAAGTCATTCAGACTGATGACTGATAGTGAGAAATGGCCCTGTCGAAGGACGCC 2266
          ||||| || |||| | || |||| | || | || | || |||| | || ||| | ||| ||
Db   2114 GCGGGCGCCGGTGATCGCCGAGGGCATGCGCCAGCTACAGCGTCGAGAAGCGCGCC 2173

Qy   3159 TGGGTTCCAGCACGACGGCCAGCCGGTATCCCAAGAGACGACTTCACCTGGAGGAGCCA 3218
          | || ||| || | ||| ||| || | ||||||| |||| || || |||||| ||
Db   3021 CGGCTTCTCGGCGGCCGGATCGCGCCGGGATCCGCCGGAGGTCTACGGCGGCCGATGG 3080

Qy   2267 AGTCAGCCCGGGGTTATGGAAGGGCATTGAAGGCGCGTTGGCCCACCTTCATGGAAAAAGAAA 2326
          |||| ||| || || | ||| ||| || | ||| || || ||||| |||||| |||||
Db   2174 AGTCCGGCGAGTGATGAAGCAGCAGGGCGTGGCGCCCACCTTCCACTGATTCCTTCATGGAGGAGA 2233

Qy   3219 GCCCCAGGCTGCAGAGCCTGCAGAGGCCCATAGCCACTTTCTATGGGTAAGGCAACAGGCTGAGAAGGA 3278
          || || | |||||||||| || | || ||| || || || | || |||| ||| || ||||||
Db   3183 CGTGGCGCGAGTGATGAAGCAGCAGGGCGTGGCGCCCACCTTCCACTGATTCCTTCATGGAGGAGA 3242

Qy   2327 GAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAAGAGAGAGACCCTTACCAGGGCACCA 2386
          ||| || ||| |||| | | || ||||| | |||||||| || || |||| |||| ||
Db   2327 GAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAAGAGAGAGACCCTTACCAGGGCACCA 2386

Qy   3279 CTCTGCCAGCACGGAGCCATCACTGGTCATCGATCGTCTGCGGTTGGGGCTGTGTGGTCGTGTGT 3338
          || |||| || || || ||| | || || ||||| | |||| | ||||| |||| ||||||
Db   3129 GGACGGCA------AGCCGAACCTGTCGTGGCCGATTTCGTTGCGCGGGGAAAGCGG 3182

Qy   3339 CATTCCGTGACTACCTGGGCCTGTTG---CCGTTGCCTGCTTGGGTGGGCGGCCGCCGATGG 3395
          | | | | |||||| |||| |||
Db   3183 CGTGGCGCGAGTGATGAAGCAGCAGGGCGTGGCGCCCACCTTCCACTGATTCCTTCATGGAGGAGA 3242

Qy   3396 CAAGGCCTCATGAGCGATGAGATGGTGCACGTACAGACTACGCATCAGTGTCAAGGCGCTGGGGGA 3455
          ||| | |||||| | ||| | |||||||| |||||||| || | |||| ||||| || | |||

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;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 19987
;  LENGTH: 3681
;  TYPE: DNA
;  ORGANISM: Enterobacter cloacae
US-10-282-122A-19987

Query Match             22.9%;  Score 899;  DB 7;  Length 3681;
Best Local Similarity   55.1%;  Pred. No. 2.5e-260;
Matches 2053;  Conservative   0;  Mismatches 1570;  Indels 102;  Gaps 11;

Qy     149 GGATTATGGTGCTGGATGGAGGGATGGGGACCATGATCCAGCCGGAGAAGCTAAACGAAG 208
           ||||||    || |||||| ||||  | | |||||||||||||||||||    ||||||||
Db      44 GAATTCTGGTGCTGGACGGCGGCGCATGGCCACCATGATCCAGGGTATCGTCTGAGTGAAG 103

Qy     209 AACACTTCGAGTCAGGAATTTAAAGATCATGCCAGGCGCTGAAAGGCACAATGACA 268
           || ||||| ||  ||| ||   |||  | |  |  || | || ||  |  |  |||
Db     104 ACGATTTCCGCGCGAGCGCTTTGCCGACTGGCCCTCGAAACCATAAGGAACAACGATC 163

Qy     269 TTTTAAGTATAACTCAGCCTGATGTCATTTACCAAATCCATAAGGAATACTTGCTGGCTG 328
           |||| |||||  || |   |   | |||| | || || ||| | || | | |  | | ||
Db     164 TGCTGGTGCTCAGCAAGCCGTCCGTCATTAAGGATATCCACAACGCCTACTTCGAAGCGG 223

Qy     329 GGGCAGATATCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCAACTGACTATG 388
           | ||  | || ||| || | | || |||  | | |    || ||| |  |||| | ||
Db     224 GTGCGGATATCGTTGAGACCACCTTAACTGACAATGAGCAATCAACTGAAGCGCCTGCG 283

Qy     389 GCCTTGAACACTTGGCTACCGGATGAAGCTGCTCTGCAGGAGTGGCCAGAAAAGCTG 448
           ||||||||| |  | ||     |||||    |  ||   |||||| | |  || | ||
Db     284 AGATGGAATCCCTGCGGCGGAAATCAACCTGAAGCCGGAAGCCGGAAGTGCCGCCTGCG 343

Qy     449 CCGAGGAGGTAACTCTCCAGACAGGAGGATTAAG--AGGTTTGTGGCAGGGGCTCTGGGTC 505
           |||||  || | | |    | | ||| | ||||    ||  |   || | || || | | |
Db     344 CCGACGAGTGGACGGCACGGTACGTCCGGACCAGCCTTGGCGGGTGCTTGGCC 403

Qy     506 CGACTAAATAAGACACTCTCTGTGTCCCCATCTGTGGAAAGGCCGGATTATAGGAACATCA 565
           ||  |  |    |  |  |  ||| |||  | | |||   |   || | || | |   |||
Db     404 CACGAACCGAACCGGTCGATTTCACCGGACGTCAACGACCACCCGGCGTTTCGTAATATCA 463

Qy     566 CATTTGATGAGCTTGTTGAAGCATACCAAGAGACAGGCCAAAGACTTCTGGATGGCGGGG 625
           || | ||  | |  ||    | | | |  ||| | | || ||| | | | |||  | || |
Db     464 CCTTCGATCAGCTCGTTGCGGCCTACCGTGAATCGACCCTCAAAGCGCTGGTGGAAGGCGGTT 523

Qy     626 TTGATATCTTACTCATTGAAAATCATTTTGATACTGCCAATGCAAGCACCGCCTTGTTTG 685
           || | |||  |||   | || || |  |||||| | |   | | || | |  || | || |
Db     524 CCGATCTGATCCTGATAGAAACCGTATTCGACACCCTTAACCGCAAAGCCGGATTTACG 583

Qy     686 CACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGGCCTATCTTTATTTCAGGGACGA 745
           | |||  ||| |  |||| ||| ||||  |   || |  | |   | |  ||| || | |
Db     584 CGGTGAAAGAGGAGTTGAGGGCTGGAGCTGGCGTTGACCTGCCGATCATGATGATTCCGGCACCA 643

Qy     746 TCGTTGATAAAGTGGGCGGACTCTTTCCGGACAGAGGAGGATTTGTCATCAGCG 805
           | ||| |  | ||   | | || | | ||  | | | || | | |  | || ||
Db     644 TCACCGAGCCTCCGGCGTCGATTTCACCCGTCTCGGTGGTTTATAACTCTC 703

Qy     806 TGTCTCATGGAGCCACCACTTCGATTCTGCATTGGATTAAATTGTCTTTGGGTGTGGAGATGA 865
           || ||| | | ||||| ||  | || | | |  ||| | ||  | |  | || || || | ||
Db     704 TGCGCCACGCCGAAGCGCTCTCCTTGGCTCTCTTGGCCTGAACTCGTGATGAGCTGC 763

Qy     866 GACCTTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTGTTATCCCAATG 925
           || | |  |||  ||| ||   || | ||| |  | | || || ||  |   || | ||
Db     764 GCCAGTACGTGCAGGAGCTTTCCCGTATCGCGGAATGCTACGTCACCGGGAACG 823

Qy     926 CAGGTCTTCCCAACACCTTGGTGACTATGATGAAACGCCTTCTATGATGGCCAAGCACC 985
           ||| || |  | | |||  || |  || ||  ||||| |  || | || | || || |||
Db     824 CCGGTCTGCCGAACGCGTTCGGTGAATACGATCTTCGATGCCCGACACCATGGCGCGCAAA 883

Qy     986 TAAAGGATTTTGCTATGATGGCTTGGTCAATATAGTTAGTTGGAGATGCTGTCGGCAACAC 1045
           | ||| || |  | | |  | ||  |  |  |  | ||   |  | |  | |  || |  |
Db     884 TCCGCGAGTGGGCCGAGTCTGGCTTCCTGAACATCGTGGCTTGGTCGGTGCTGCGCGCCACCG 943

Qy    1046 CAGATCATATCAGGGAAAATTGCTGAAGCTGTGAAAAATTGTAAGCTAGAGTTCCACCTG 1105
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Db   944 CGGAGCACATCCGCGGCCATGAGCAGCAACGCGTCGCCGCGACTGCTGCCGCAAGCTGCCCG 1003
             || |||| |||| ||          |||           |||||||||||||||||
Qy  1105 CCACTGCTTTTGAAGGAACATATGTTACTGTCTGGTCTTAGAGCCCTTCAGATTGACCGGT 1165

Db  1004 AGCTTCCGGTTGCCTGTTCGT------CTGTCCGGCCCTTGAGCCGTTGAACCATCGGCGACG 1057
             || |||| |||||           |||||||| ||||| |||||||||||||
Qy  1166 ACACCCAACTTGTTAACATTGCAAGAGCGCTGTAGGATCGGATCAAGGAAGTTTGCTA 1225

Db  1058 ACAGCCTGTTTGTGAACGTGGGTGAGCCGTACTAACGTCACAGGTTCTGCAAGTTCAAGC 1117
             ||||||||| |||||||||| |||| ||||||||||||||||||
Qy  1226 AACTCATCATGGCAGGAAACTATGAAGAAGAAA 1285

Db  1118 GCCTGATCAAAGAGAAGAAATACAGCGAAGCGAAGAAATACAGGCTGGAAA 1177
             |||||||||||||||||||||||||||||||||
Qy  1286 TGGGACCCAGTGTTGGATGTCAACATGGATGATGCCATGGCTAGATGGTCCAAGTGCAA 1345

Db  1178 GCGGGCGCAGATTATCGATATCAACATGGACGAGGGATGTCGACGCCCGAAGCCGCGA 1237
             ||||||||||||||||||||||||||||||||||
Qy  1346 TGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGAATGCAAAGGTACCTTTGTGCA 1405

Db  1238 TGGTGCGTTTCCTCAACCTGATCGCCGGTGAGCCGTGAACATCGCCCGCGGATCATGA 1297
             || |||||||||||||||||||||||||||||||
Qy  1406 TCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCA 1465

Db  1298 TTGACTTCCCAAGTGGGAGGTCATCGCAAAAAAGGGCGTGAAGTGCATTCAGGTAAAGGCA 1357
             |||||| ||||||||||||||||||||||||||||||
Qy  1466 TTGTCAATAGCATTAGTCTGAAGGAGGAGGACGACTTCTTGAGAAGGCCAGGAAGA 1525

Db  1358 TCGTCAACTCTATCTGCATGGAAGAAGAGGGCGTTGATATCTTTATCCACCACGGAAGATGG 1417
             |||| |||||||||||||||||||||||||||||||
Qy  1526 TTAAAAGTATGGAGCTGTCTATGGTGGTCATGCTGTTTGATGAGAAGAAGACAGGCAACAG 1585

Db  1418 TCCGCGCTACGGTGGCCGGTGGTGAGCCTTTGACCGGTGGGCCAGGCGGATA 1477
             ||||| ||||||||||||||||||||
Qy  1586 AAACAGACACAAAAATCAGAGTGTGCACCCGGCCTACCATCGTCGTGATGAAAACTGG 1645

Db  1478 CCCGGAGCGTAAAATTGAGATATGCCGCGGTGTGGTGATGCCTTTGACCGGTGGGATTG 1537
             |||||||||||||||||||||||||||||
Qy  1646 GCTTTAATCCAAATGACATTATTTTTGACCCTAATAATCCTAACCATTGGACTGGAATGG 1705

Db  1538 GCTTCCCGCCGAAGCATTATCTTTGACCCCGAATATCTTCCGCGTCGCGGGGATTG 1597
             ||||||||||||||||||||||||||||||
Qy  1706 AGGAACACAACTTGTATGCCATTAATTATTTATCCATGCAACAAAAAGTCATTAAAGAAACAT 1765

Db  1598 AAGAGCACAACAACTATGCCCAGGACTTTATCGGCCATGTGAAGACATCAAGCGCAAGC 1657
             |||||||||||||||||||||||||||||||
Qy  1766 TACCTGAGCCAGAATAAGTGAGGTCTTTCCAACTTGTCCTTCCGGAGGATGG 1825

Db  1658 TGCCCGCACGCGCGTGATCTCCGGCGGGCGTGTCAAATCGGATGAGGCTGGTAACG 1717
             ||| |||||||||||||||||||||||||
Qy  1826 AAGCCATTCGAGAAGAAGCAATGCATGGGCGTTTTCCTTTACCATGCAATCAAGTCTGGCATGG 1885

Db  1718 ACCCGGTGCGGAAGCCATCCACGCCGTGTTCTCTACTACGCCATGGCATGG 1777
             ||||||||||||||||||||||||||||
Qy  1886 ACATGGAGAGTAGTGAAGATCTCATCTGAATAAAGATGCTGAAACCTCCCTGTATGATGATGAGGAACTTC 1945

Db  1778 ACATGGGATCGTTAACGCGGCCCAGCTGACGATCTCCCTGCCGAGCTGC 1837
             |||||||||||||||||||||||||
Qy  1946 TGCAGTCTCGTGAAGATCTCATCTGGAATAAAGACCCTGAGCAAGCTCTTAC 2005

Db  1838 GCGAAGACGCGTAGAGGAGATACTGATTACGGAGGGAAGACGCCACCCACCCGACCTC 1897
             ||| |||||||||||||||||||||
Qy  2006 GTTATGCCAGAGACTCAAGGC------ACAGGAGGAAGAAAGTCATTCAGAGACTGATG 2056

Db  1898 ACCTGGCGGAGAAATATCGGCGAGCGCAAATCGGATGAGGCGGCAAACGTTCAGCAGGCCG 1957
             ||| ||||||||||||||||||||||||
Qy  2057 AGTGGACAAATGGCCCCTGTCGAAGAATGCCCTTGTGAAGGGCATTGAAA 2116

Db  1958 AGTGGCGGTTCCTGGGAACGTGGGGACTTACTCGCTCGAATACTCGCGTCAAAGCATCACCGG 2017
             ||| |||||||||||||||||||||||||
Qy  2117 AACATATTATTGAGGAGTACTGAGGAAGCCCAGGTTAAACCAAAAAAATATCCCCGGACCTC 2176
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Db  2018 AATTTATCGAGCTGCGATACCGAAGAGCGCGGCCAGCGGCAGA------------CCGCCCGA 2068
             |||||||||||||| |||||||||||||||||||
Qy  2177 TCAATATAATTGAAGGACCCCTGATGAATGGGTTGGTGATCTTTTTGAG 2236

Db  2069 TTGAGGTGATCGAAGGCCCGCTGATGGACGCATGAACGTGTTCGGCGGCGATCTGTTCGGTG 2128
             |||||||||||||||||||||||||||||
Qy  2237 CTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGTTATGAAGAAGGCTGTTG 2296

Db  2129 AGGGCAAAATGTTCCTGCGCAGCGGTGGTTAAATCCGGCCGCGATGATGGAAATCCGGTAG 2188
             |||||||||||||||||||||||||||||
Qy  2297 GCCACCTTATCCCTTTCATGGAAGAAAAAAGAAGAAGAAACCAGCAAAGAGAA------ 2356

Db  2189 CGTATCTTGAGCCCTACATCGAAGCCAGCAAAGAGAA------ 2226

Db  2227 ------GGTTCCAGCAACGCGCAAGAGTGTTATCGCGCTGCGCAGTGAGTCCACCCGTGAAGGGCGACGTGC 2275

Qy  2357 TAGAAGAAGAGACCCTTACCAGGCGCACCATCGTCGTCGGCCACTGTTAAGGCGACGTGC 2416

Db  2276 ACGACATCGGCAAGAACATCGTCGGCGGCAGTGCTTGCAGTGTAATAACTACGAAATTATCG 2335

Qy  2417 ACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCGTCGAATAATTTCCGAGTTATTG 2476

Db  2336 ACCTCGGCGTGATGGTCCCGGCGGACAAAATCCTCAGACCCGCGCGGAAGTGAACGCCG 2395

Qy  2477 ATTTAGGAGTCCATGACTCCATGTGATAAGATACTGAAAAGCTGCTTCCCTGGATGAAATGATTTTTGTTGCA 2536

Db  2396 ACCTGATTGGCCTCTCCGGCTTCGTGATAAGGCCAGGGCGCTGAAGCGGTGGCAA 2455

Qy  2537 ATATAATTGGCTCGTCAGGACTCATCATCACTCCCTTCCCTGGATGAAATGATTTTTGTTGCA 2596

Db  2456 AAGAGATGGAGCGGACACAGGGCTTCACCATTCCCGTATTGATTGGCGGCGCACCACCTCAA 2515

Qy  2597 AGGAAAATGGAGATTAGCTATTAAGGATTCCATTGTTGATTGTGATTGGCGGGCAACAG 2656

Db  2516 AAGCGCACACCGGCGGTGAAGATCGAGCAGAACTACACGCGGCCCGACGGTCTACGTGCAGA 2575

Qy  2657 AAACCCACACCAGTGAACAGCAGTAAAATAGCTCCGATGAGATGTTCCCAGCTGTTGATGAAAATCTAAAGCATGTCCTGG 2716

Db  2576 AGCGCCTCGGCGCGACACGGTGGGCGTAGTCTCTCCGGCTCCGGTCGTCTCCGACACCGTGCGCGACGATT 2635

Qy  2717 ACGCGTCCAAGAGTGTGTGGTGTTCCCAGCTGTTGATGAAAATCTAAAGCATGTCTAGATGAAAAACTAAAGGATGAAT 2776

Db  2636 TTGTGGGGCGGCGCACCCGCAAAGATGTACGAAACCGTTCGGCAATCGGCATCCAGCACGGCCGTAAGAGAGC 2695

Qy  2777 ACTTTGAGGAAAATCATGGAAGAATATGAAGATATTAGCACAGGACGACCATTATGAGTCTCTCA 2836

Db  2696 CGCGCACACCGGCGGCTGTTTCGCTTCAGGCGCGCGCCGACAACGATCTGGCCTTCGACTCGGT 2755

Qy  2837 AGGAGAGGAGATACTTAAGTCAAGCCAGAGAAAAAGTGCGTTTCCAAATGGATTCGC 2896

Db  2756 CCAGCTATACGGCCACCCGTGG----CACATCGTCTCGGGGCTGGAGGACGTGAGGCGCCA-- 2809

Qy  2897 TGTCTGAACCTCACCCAGTGAAGCCCCACGTTTATTGGGACCCCAGGTCTTTGAAGACTATG 2956

Db  2810 GCATCGGACGCGTCGCGTAACTACACTACGACTGCGAACGATATGATGAATCATACGGAGGCTTGG 2869

Qy  2957 ACCTGACGAAGCTGGTGGACTACACATTGACTGGAAGCCTTTCTTTGATGTCTGCAGCTCC 3016

Db  2870 CGGGCAAATATCCG------CCCATCCTGGAAGATGAGGTGGTTCGGCGAGG 2914

Qy  3017 GGGGCAAGTAGTACCCGAATCAGC------CGCATCCTGGAAGATGAGGTGGTTCGGCGAGG 3076

Db  2915 AGGCGGAGCGGCCTGTTTAAAGATGCCAACGACACCGTGCGCTGAGCCGCAGAGAAA 2974

Qy  3077 AGGCCAGGAAGTCTACAGATGATGCCCACAAATGCTGAACACTGATTAGTCAAAAGA 3136

Db  2975 CCCTCAACCCGCGGCGGCGTGTTGGTGGCCGTGTTCCGGGCGAACGTGGGCGACGCACATCG 3034

Qy  3137 AACTCCCGGCCCGGGCGTGGTTGGTTCTGCCGCCAGCACACAGAGTATCCAAGACGACATTC 3196

Db  3035 AAATTTATCGGCA------TGAAACCCGTACCCACCGTGCTGGCGGTCCGGTCTGCGGCCATCTGC 3088

Qy  3197 ACCTGTACGCAGAGGCTTGCTGCGTGCCCCAGGCTGCAGAGCCCATAGCCACTTTCTATGGGT 3256
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;   PRIOR APPLICATION NUMBER: 60/230,335
;   PRIOR APPLICATION FILING DATE: 2000-09-06
;   PRIOR APPLICATION NUMBER: 60/230,347
;   PRIOR APPLICATION FILING DATE: 2000-09-09
;   PRIOR APPLICATION NUMBER: 60/242,578
;   PRIOR APPLICATION FILING DATE: 2000-10-23
;   PRIOR APPLICATION NUMBER: 60/253,625
;   PRIOR APPLICATION FILING DATE: 2000-11-27
;   PRIOR APPLICATION NUMBER: 60/257,931
;   PRIOR APPLICATION FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: 60/267,636
;   PRIOR APPLICATION FILING DATE: 2001-02-09
;   PRIOR APPLICATION NUMBER: 60/269,308
;   PRIOR APPLICATION FILING DATE: 2001-02-16
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 78614
;   SOFTWARE: Patentin version 3.1
;
;   SEQ ID NO 32118
;   LENGTH: 3705
;   TYPE: DNA
;   ORGANISM: Pseudomonas putida
US-10-282-122A-32118

  Query Match            22.8%;   Score 894;  DB 7;  Length 3705;
  Best Local Similarity  55.2%;   Pred. No. 8.3e-259;
  Matches 2064;   Conservative   0;   Mismatches 1570;   Indels 108;   Gaps 12;

Qy    139 CTGCAGAAGAGGATTATGGTGCTGGATGGAGGGATGGGGACCATGATCCAGCGGGAGAAG 198
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Db     43 CTCAAAGAGCGCATCGATCCTGATCCGACGGCGACGGTACTGGTACTCCAAAGTACCGC 102

Qy    199 CTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATGCCAGCCGCTGAAAAGC 258
                 ||| || |   ||  |  || |    |  |   | || |  ||  |   ||||||
Db    103 CTCGAGGAACACGACTATCGTGGCACGGCGGTTTGCCGATTGGCCAAGCGCATGTGAAGGGT 162

Qy    259 AACAATGACATCATTTAAGTATAACTCAGCCTGATGTCATTTACCAAATCCATAAGGAATAC 318
                |||| |   ||   |  |||  |  ||| || |    |  |||  ||    | |  |||
Db    163 AACAACGACCTTTTGCTGCTCAGCCGATCGGACGTGATCGAGAAACAAATACTTTTAGCAGCA 222

Qy    319 TTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTCGAAACCCTTCAACGCGTGTTT 378
                 ||  |  |  ||| | ||  ||||  | |||  |  | || |   |  |  ||  |||
Db    223 CTGGATGCCGGTGCCGTTGCCGATATTGGCGATCGCCATGCACGACTAGTATTGCCCAA 282

Qy    379 GCTGACTATGGCCTTGAACACTTGGCTACGGCGGATGAACATGTGCTTCTGCGGGAGTGGCC 438
                ||||  ||||| | ||| || || | | ||| ||   |    | | | |  ||||  ||
Db    283 GCCGACTACGGCATGGCCATGGAGTGCGCTGGTTTACGAGTTGAACGTCGAAGGCGCATCGCT 342

Qy    439 AGAAAAGCTGCCGAGGAGGAGGTAACTCTCCAGA---CAGGAATTAAGAGGTTTGTGGCAGGG 495
                  |||| |||  || ||| |||  |  | | |||      || ||   |  || | || ||
Db    343 CGCCAGGTTGCCGATGCCAAGACCCCGGACAAGCCCGGACAAGCAAGCGCCGCTTCGTTGCCGCGC 402

Qy    496 GCTCTGGGTCCGACTAATAAGACACTCTTGTGCCCATCTGTGGAAAGGCCCGGATTAT 555
                || |  || | |  | |  || ||  | ||  ||| |  ||  ||   ||  || ||
Db    403 GTGCTCGGCCCTACCAGCCGAACCTGCTCGATTTCCCCGGAGGTCAACGACCCAGGGTTT 462

Qy    556 AGGAACATCACATTTGATGAGCTTGTTGGAAGCATACCAAGAGCAAGAGACTTCTG 615
                ||||| | |   |||    |  | | |  || |   | || ||   |  || | ||
Db    463 CGCAACGTCACCTTCGACGAGTTGGTGAGAAAACTACATCGAGGCTGATCCCGGCCTGATC 522

Qy    616 GATGGGCGGGTTGATGATGCTTCATTGACTTACTCATTGAAACATCATTTTGATACTGCCAAGGCA 675
                | |||   ||   ||| | | |    |  |  | |    |  | || |     |   |||| ||
Db    523 GAAGGCGGCGGCGCCGGCCGCAGCCTCAACGCCCTCAACACCCTGACACACCTCAACGCCAAGGGG 582

Qy    676 GCCTTGTTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCGGCCGATATCTTTATT 735
                |  |  | ||| | ||||  | |  | | || || | ||  | |  ||  | | | ||
Db    583 GCGATCTTCGCCGTGCAGCAAGTGTTCGAGGACGACACGCGTCGCGATCATGATC 642

Qy    736 TCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTTCCGGACAGACAGGAGGGATTT 795
                | |||  | ||| ||||||  || ||    | |  ||| |  | ||   | |  |
Db    643 TCCGGCACCATCACCGACGCCTCCGGTCGTACCCTGTCGGGGCCAGACCGAAGCGTTC 702

Qy    796 GTCATCAGCGTGTCATCGAGACCACTCTGCATTGGATTGAATTTAAATTGTGTTTGGGTGCA 855
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Db
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RESULT 8
US-10-282-122A-32118

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;  Sequence 32118, Application US/10282122A
;  Publication No. US20040029129A1
;  GENERAL INFORMATION:
;    APPLICANT: Wang, Liangsu
;    APPLICANT: Zamudio, Carlos
;    APPLICANT: Malone, Cheryl
;    APPLICANT: Haselbeck, Robert
;    APPLICANT: Ohlsen, Karl
;    APPLICANT: Zyskind, Judith
;    APPLICANT: Wall, Daniel
;    APPLICANT: Trawick, John
;    APPLICANT: Carr, Grant
;    APPLICANT: Yamamoto, Robert
;    APPLICANT: Forsyth, R.
;    APPLICANT: Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR APPLICATION FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR APPLICATION FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR APPLICATION FILING DATE: 2000-05-26
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Qy  1936 AAGGAACTTCTGCAGCTCTGTGTGAAGATCTCATCTGGAATAAAGACCCTGAGCGCCACTGAG 1995
         ||||| |||||||| ||||| ||||| || ||||| |||  ||  ||||||  || |||||
Db  1837 GCCCAGCTGCGTGAAAAGGTCGAGGACGTGGTACTCAACCGCACCCCGCATGGCACCGAT 1896

Qy  1996 AAGCTCTTACGTTATGCCGAGACT---CAAGGCACAGGAGGCGGGAAGAAAGTCATTCAGACT 2052
         ||| ||| ||| |||||||||||    ||||||||||| || |||||||| || |||
Db  1897 GCACTGCTGGCCATCGCCGACGACTACACAAGGGTGGCCGCGAAGAAGTGGAAAAC 1956

Qy  2053 GATGAGTGGAGAAACATGGCCGTCTGCGAAGAACCGCCTTGAGTATGCCCTTGTGAAGGGCATT 2112
         ||| ||||| || |||| ||||| |||||||| ||||||||||||||| || |||||||||||
Db  1957 GAAGAGTGGCGCGTCGCTGCGTCGGTGGGAAAAACGCCTCGGAGCACGCGTCGTCAAGGGCATC 2016

Qy  2113 GAAAAACATATTATTGACGGATACTGAGGAAGCCAGGTTAAACCAAAAAAAAATATCCCGA 2172
         ||||| ||| ||| ||||| ||||||||||  ||             |||||||||||||
Db  2017 ACCGCGTTCATCGTCGTGAAGACACCGAAG--------CATGCCGCCAGTGCGCGCGC 2067

Qy  2173 CCTCTCAATATAATTGAAGGACCCCTGATGAATGGAAATTGTTGGTGATCTTTTT 2232
         ||||| ||| |||| |||||| ||| ||||||||| |||  ||||| ||| ||
Db  2068 CCCATCGAAGTGATCGAGAGGCCGCATGAACGGCATGGTGTCGGCGGACCTGTTC 2127

Qy  2233 GGAGCTGAAAAATGTTTCTACCTCAGTTATAAAGTCAGCCGGGTATGAGAAGGCT 2292
         |||| |||| |  |||| ||  ||||| ||| || |||||  | || ||||| ||
Db  2128 GGCGCGGGTAAAATGTTCCTGCGCCAGGTGGTCAGTGGTCGGCGTGCATGAAACAGGCC 2187

Qy  2293 GTTGGCCACCTACCTTGTGTGTTGCCAAAGTG 2352
         |||| |||| ||  | |||||  ||||| |
Db  2188 GTTGCTCACCTGATCCGTTCATCGAGCCGAAAAAGGCGACA------ 2230

Qy  2353 ACAGTAGAGAGAAGCACCCTTACCAGGGCACACGTGTCTGCGCACTGTTAAAGGCGAC 2412
                                    ||||||||||| |||| |||| || || |||||||
Db  2231 ----------------AGCCGGAAGCCAAGGGCAAGGTGCCAAGATCCTGATGGCCAGGAAAGGCGAC 2277

Qy  2413 GTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCGTGCAATAATTTCCGAGTT 2472
         ||||| || |||||||||| ||| | |||||| |||| ||  | |||  |||||| ||| |
Db  2278 GTGCACGACATCGGCAAGAACATTGTCGGCGTCGTGGTCGTGTAACGGATACGACATC 2337

Qy  2473 ATTGATTTAGGAGTCATGACTCCATGTGTATAGATAGTCGCTCTTGACCACAAA 2532
         |||||||| ||||| |||||||||||| | |  |||||||||| | ||||||||
Db  2338 GTCGACCTTGGGCGTGATGGTACCGGCGGAGATCCTGATTACCCCGTCGGTGCAAAGCGAAGAAG 2397

Qy  2533 GCAGATATAATTGGCCTGTCAGGATTCTTGGAGAAG 2592
         |||| ||| |||||||||||| ||| || || ||||
Db  2398 TGCGACATCATCGGCCTGTCGCCGTCGTCGATGATCGACGAGGAAATGGTCCACGTT 2457

Qy  2593 GCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGAGGAGCAACCACT 2652
         ||||| |||| |||| ||||||||  ||||| || |  ||| ||| || |||| ||||
Db  2458 GCCCGGGAAATGCAGCGGCCAGGCTTCGAACTGCCGCGTGATCGGTGGCGCCACC 2517

Qy  2653 TCAAAAACCCACACAGCAGTGAAATAGCTCCCGAGATACAG---TGCACCTGTAATCCAT 2709
         |||| ||| ||||| |||||  |||  |||||||| |||||   |||||||||| |||| |
Db  2518 TCCAAGGCGCACACTGCAGTCGAGATCGAGCCCCAGTACCGAGCAACGACGCGTCATCTAC 2577

Qy  2710 GTCCTGACGCGTCCAAGAGTGTGGTCGGCCGGTGTTCCCAGCTGTTAGATGAAAATCTAAAG 2769
         |||||||||||||| |||||| ||||| ||||||||| || |||||||| || |||| ||||
Db  2578 GTCACCGACGCTTCGCGGCGCGATCTCGGCGGGCCACCCAGTTGCTGTCCAAAGAACTCAAG 2637

Qy  2770 GATGAATACTTTGAGGAAATCATGGAGAAATCAGGACCATTATGAG 2829
         ||| || |||  ||| |||| || |||||||  || |||||| |||
Db  2638 CCAGGCTTCGTCGAGAAGATCGAGAATACGCTGCGTGAGCTGTACCGCCAAC 2697

Qy  2830 TCTCTCAAGGAGGAGCGCGTCACAACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATG 2889
         || || ||||||| || ||| |||| || |||| |  ||||| || ||| ||  |||| ||||
Db  2698 CGCAGGGCCGACGCTTCGCACCCCGCCAGCTACGGCGCCGCGGAAGCCGAGTAC 2757

Qy  2890 GATTGGCTGTCTGAACCTCACCCAGCCATTCGAAGAAGCCATCGCATGGGCGTTTATTGGAC 2949
         |||| || || |||| |  ||| |||| |   |||||  | || |||||  ||| ||| ||
Db  2758 GACTG---GCCGGCTACCAGCCGATCCACACGCAACCGCTCTCAGGTGGCGTCAAGGGTCTGGAG 2814

Qy  2950 GACTATGACCTGGCAGAAGCTGTGGTGGACTACATTGATGGTATGATGATATCCAT 3009
         |||| |||||||| || ||  ||| |||| ||  | |||  |||| |||| ||
Db  2815 GACATCGATTTGCGACCCTGCCACCCGGCCGAGTAGCTGGACGCGCGTTCTTCATCTCCTGG 2874
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Db   703 TGGAACTTCGGTGCTCACGCCAAGCCCATTCCGTGGCCTGAACTGCGCCCTCGGCGCGCC 762
         || |||||||   ||| ||||||||||||  ||||||||||||  | || ||||||||
Qy   856 GCTGAGATGAGACCTTTTATTGAAAATAATTGAAAATGTACAACAGCCTATGTCCTCTGT 915
         | ||||  ||  | || ||  |||| |||  ||||| |||| |||| ||  |||||||||
Db   763 AAGGAACTTGCGGTATTTGGAAGAGCTGGCCAAGGCCTGGCCACCCCAGTGTCCGCC 822

Qy   916 TATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGAAACGCCTTCTATGATG 975
         |  || |||||||  || || |||||  ||||||||| ||||| | ||| |||| ||
Db   823 CACCCCAAGCCGGAACGCTGCCGAACCGGAACCCCGCCAAACCCCGCCGAGATG 882

Qy   976 GCCAAGCACCTAAAGATTTGCTATGATGGCTTGGTCAATATAGTTGGAGGATGCTGT 1035
         || || || ||||  | || ||| | |||| |||| |||||| |||| ||  ||||
Db   883 GCCGCGCGGTGGTCGAAGAATTCGGCGGCCAGGCTTCCTCAACATCATTGGGCCGCTGCTGC 942

Qy  1036 GGGTCAACACCAGATCATATCAGGGGAAATTGCTGAAGCTGTGAAAAAATTGTAAGCCTAGA 1095
         |||| || ||||| || || ||||| ||| | || ||||| ||  ||| |||  |||||
Db   943 GGCACCACCGCGGGGCACATGCCAAGCCGGGGCGCCAAGTACAAGCCGCCGGCGCGC 1002

Qy  1096 GTTCCACCTGCTCTGTTTGAAGGACATATGTTACTGTCTGGTTCTTGAGCCCTTCAGG 1155
         |||||| ||||   ||| || |||| |   ||||| ||  | ||| |||||| |||||
Db  1003 GAGATCCCGGAAATGCCAAGGCCTGCC-----GCCTGTCGGCGGCCGTTCACC 1056

Qy  1156 ATTGGACCGTACACCAACTTGTTAACATTGGAGAGGCGCTGTAATGTGTCAGGATCAAGG 1215
         ||||| || || |||||| | ||| |  ||||||||||  | |||||  || ||| |||
Db  1057 ATCGACCGCGTCGTTCGTCAACCTGATGGCCACAATCACCGGTTCCGGCC 1116

Qy  1216 AAGTTTGCTAAACTCATCATGCGCAGGAAACTATGAAGAGCCTTGTGTTGCCAAAGTG 1275
         ||||| |||| |||| ||  | |||||  |||| ||| ||||| | ||||||| |
Db  1117 AAGTTCGCCAGCTGATCCGCGAAGAACTATACCGAAGCTCGCGAAGTCGCCCTGCAG 1176

Qy  1276 CAGGTGGAAAATGGGAGCCCAGTGTTGGATGTCAACATGATGGCATGCTAGATGGT 1335
         |||| || | ||||| ||||||||| |  | ||  |||| ||| ||||  |||||
Db  1177 CAGGTGAGGCGGCCGCCGCCAGTAATCAACATCAACATGGCGAAGGGATGCTCGACTCC 1236

Qy  1336 CCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCAGACATCGCAAGGTA 1395
         || || |||||  |||| |||   |||| |  |||  |||||||||| || || || ||
Db  1237 CAGGCGGCCATGGTCCGGTTCCTGCAACCTGATGCGCGGGTGAGCGTGAGCCGACGCGTA 1296

Qy  1396 CCTTTGTGCATCGACTCCTCCAATTTTGCGTGATTGAAAGTGCTGCCAA 1455
         || ||||||| | |||| | |||| |||  ||| ||||||  |||||||
Db  1297 CCGATCATGATGACTCGTCCAAGTCCGGGGCCGGCGTCGCCTCAAGTGCATCCAG 1356

Qy  1456 GGGAAGTGCATTGTCAATAGACATTATATCTGAGGAGGACGACTCTTGGAGAAG 1515
         |||| ||| || ||||  ||||| ||| ||  |||||||| || || ||||| |
Db  1357 GGCAAGGGCATGTCAACTCCATTTCCACCATGGTCGTGTGGTCGCCGGCTCAAGCACCAC 1416

Qy  1516 GCCAGGAAGAAGTTAAAAATGAAGTCCATGTGGCTATGGCCATGACGGAAG 1575
         |||| ||| ||  ||||| || ||  || |||  |||||| ||||  |||
Db  1417 GCCCGGCCTGTGCAAGGCCATGGCGCCGCTGGCCATCGCCGACGGAGTCGGC 1476

Qy  1576 CAGGCAACAGAAACAGACAACAACTCAGAGTGCACCCGGGCCTACCATCTGCTTGTG 1635
         ||||| || || ||| ||| ||   | ||| | |||||||||| ||  |  ||||||
Db  1477 CAGGCGCCTGGCGGCACAACACCGCGGGGCGCAAGATCGCGCAGCCGCAGCTGCTGGTC 1536

Qy  1636 AAAGAAACATTGGGCTTTAATCAATGACAGATTATTTTTTGACCCCTTAAATATCCTTCTTC 1695
         |||  || |||||| ||| ||  |||| | |||| || | |||||| | |||||||| | |
Db  1537 AACGAAGTGGGCTTCCCCGGTGAAGCGTGTGAGAGTTGGTCCCGGTCGTGGGGCCTGCC 1596

Qy  1696 ACTGGAATGGAGGAACAACTGGCCATTCGAAGAAGCATGGAAATGCAACAAAAAAGTCATT 1755
         || || ||| |||| | || || |||  || ||||| || ||| |||| || ||  |
Db  1597 ACCGGTATCGAAGAGCACAACACGCCGTCGACTTCATCGAGGCCGTGTGCCTATATC 1656

Qy  1756 AAAGAAACATTACCTGAGCCCAGAATAAGTCATGGAGGTCTTTCAACTTGTCCTTCCTTC 1815
         ||| ||| ||| || ||| | ||   |||| || |||| ||||| ||  ||||| | |||
Db  1657 CGCGACGACCTGCCCACGCCCCAGCCCTCAGCTCGGTGTGTCCAATGCGTCGGCTCGGTTC 1716

Qy  1816 CGAGGAATGGCAGCCATTCAGAGAAGCAATGCAATGCGGTTTCCTTTACCATGCAATCAAG 1875
         ||| ||||| |||||  |  ||| ||||| ||| |||   || || |  |||||  |||
Db  1717 CGTTGGCAACAACAGCCACCACCGGCGTGTGTCCGTGTTCCTGTATCGCGATCACGCGGCCAG 1776

Qy  1876 TCTGGCATGGACATGAGGATAGTAGTCAAATGCTGAATGCTGATGATGATATCCAT 1935
         ||| || || || ||| || | | |||||| | | |||||   ||||| || ||
Db  1777 AACGGGCCTGACCATGGTATCGTCAACGGCCGCCGAGGATCTCAACGGGCTGAGTTCTGG 1836
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Query Match   22.8%;   Score 892.2;   DB 7;   Length 3717;
Best Local Similarity   55.2%;   Pred. No. 2.9e-258;
Matches 2070;   Conservative   0;   Mismatches 1563;   Indels 120;   Gaps 12;

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Qy  138  TCTGCAGAAGAGGATTATGGTGTCTGGATGAGGATGGGGACCATGATCAGGCGGGAGA  197
              ||||| |||| |||||| ||| |||||||| | ||||||||||| |||||
Db   42  TCTGAAACAGAGAATCCTGATTCTGATGAGGATGGGGACCATGATCCAGAGCTACAG  101

Qy  198  GCTAAACGGAAGAACACTTCCGAGGTCAGGAATTAAAGATCATGCCGAAGG  257
              | | ||||| ||| || ||||||||| |||| || |||||| |||||
Db  102  GCTTGAGGAGAGAGACTATCGGGGCAAACGTTTTGCCGACTGGCAAGTGACGTCAAGGG  161

Qy  258  CAACAATGACATTTAAGTAATAACTCAGCCTGATGTCATTACCAAATCCATAAGGAATA  317
              |||||| || ||| |||| || ||||||| || |||||| ||| |||| |||||
Db  162  CAACAACGACCTGCTGATCCTGACCCGTCCCGACGTGACCGTCCATCGAGCAGCGGCGTA  221

Qy  318  CTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTAGCACTAGTATTGCCCA  377
              ||||| ||||||||| |||| |||||| |||| ||||||| |||||| ||||
Db  222  TCTGGATGCCGGTGCCGACCATCCTGAAACCACCTTCAACGCCACACAGTGTCCCA  281

Qy  378  AGCTGACTATGCCTTGAACACTTGGCTACCGATGAACATGTGCTCTGCAGGAGTGGC  437
              |||||||||||| || ||||||||||| ||||| || ||||||||
Db  282  GGCCGACTACGCCATGGAATCGATCGTCTACGAGCTGAACGTCGAAGGGCCCTCTGGC  341

Qy  438  CAGAAAAGCTGCCGAGGAGGAGTAACTCTCCAGA---CAGGAATTAAGAGGTTTGTGGCAGG  494
              ||||||| ||| || ||||||||| || ||||||        ||| |||| || ||||||
Db  342  CCGTAAGGTCGCAGACGGCCAAAACCCTGAAAACCCGGACAAACCCGGCTTCGTTGCTGG  401

Qy  495  GGCTCTGGGTCCGACTAATAAGACACTCTCCATCTGTCCCCATCTGTGGAAAGGCCGGATTA  554
              |||| |||||||||| ||| ||||| ||| || ||| ||||||||
Db  402  CGTGCTCCGGCCCGACCAGCCGCACCTGGTCGCCGGACACGTCAACAACCCTGGCTA  461

Qy  555  TAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAAGCAGGCCAAAGGACTTCT  614
              |||| || |||||||||||||||| || |||| ||||||||||| ||||||||||||
Db  462  TCGGCAACGTTCACGTTCGACGAACTATACCGGCGGTGGAGAACTATACCGAGGCCACCAAAGGCCTGAT  521
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Qy 3010 CAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCAGAGATATTTAACGACAAAAACAGTA 3069
Db 2875 GACCTGGCCGGCAAGTTCCCGCGC--------ATCCTCACCGACGAGGTGGTT 2919

Qy 3070 GGTGGAGGAGGCCAGGAAGGTCTACGATGATGCCACAATATGCTGAACACTGATTAGT 3129
Db 2920 GGCGAGGCCGCCACGGCGCGGCTCGCCGCGGTATTCGGCCTTCGGCCGGC 2979

Qy 3130 CAAAGAAACTCCGGGCCCGGGGTGTGGTTCGGTTCTGGCCAGCACAGAGTATCCAAGAC 3189
Db 2980 GAGAAGCTGATCAGCGCGCTCGCGCGGGTATTCGGCCTTCGGCCGGC----------CAAC 3027

Qy 3190 GACATTCACCTGTACGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAGCCACTTTC 3249
Db 3028 CAGGTGGACGATGACGACATCGAAGTCTACGGCGAAGACGACGGCCAGGCACTGGCCACCCTG 3087

Qy 3250 TATGGGTTAAGGCAACAGCAGGCTCTGCCAGCCACGGAGCCATACTACTGCCTC 3309
Db 3088 CATCACCTGCCCAGCAGACCATCAAGCCGGACGGCA------AGCCCAACTGGTCGCTG 3141

Qy 3310 TCAGACTTCATCGTCCTCCCTTGCATTCGGCATTCGGCTGACTACTT---GGGCCTGTTTGCC 3366
Db 3142 GCCGACTTCGTCGCACCGAAAGACAGTGGCGTTACCGACTACGTAGGTGGTTTCATCACC 3201

Qy 3367 GTTGCCTGCTTTGGGGTTAGAAAGACTCGAGCAAGGCCTATGAGCATGATGGTGACGACTAC 3426
Db 3202 ACCGGCCGGCATCCGTGCCGAGGAAGTGCCGAGCTTACCGGAGCAAGGGCGACGACTAC 3261

Qy 3427 AGCAGCATCATGGTCAAGGCGCTGGGGGGACCGGCTGCGCAGAGAGCTC 3486
Db 3262 AGCTCGATCATGTCAAGGCACTGGCCGACCGGCCGCACCGGTGCCGAGCGGTGACATGGCTG 3321

Qy 3487 CATGAAAGAGTTCGCCGAGAACTGTGTGGGCCTACTGTGGCAGCAGCTGGACGTCGCA 3546
Db 3322 CACGAGCAGTGCGTGCGTAAAGACACTGGGCTATGCCCCGGACTGGACCAACGAG 3381

Qy 3547 GACCTGCGAGGTTGCGGTACAGAGGGCGCTGCGGCATCCGCCCGGCTCCTGGCTACCCCAGCCC 3606
Db 3382 GGCTGATCAAGGAACAGTAGCGCGGCGCATCCGCGGCATCCCGCCCTGCCTGCTGCCGGCGTTATCCGGCCTGCCCC 3441

Qy 3607 GACCACACCGGAGAAGCTCACCATGTGAGACTTCGAGACTCCAGCAGCATC---------GAG 3651
Db 3442 GACCACACTGAAAAGGAAGAAACTCTTCCGCCTGCTGCTGCTGATGGCACCGCCATCCGTGAAACC 3501

Db 3502 CAGTCTACAGGCATTAGGTTAACAGAGATCATTAGCAATGCACTTCGCGATGTTCCCGGCGGCGGGTCAGC 3561

Qy 3712 GGCCTCTACTTCTCAATTTGAGTCCAAATATTTTCTGTGTGGGAAGATTTTCCAAGGAT 3771
Db 3562 GGGCCGAGCGGGGTGTAGCAGGGTATTTTGGCCGTAGGCGGGCGAAGTAGTGCTGGGGTCAGC 3621

Qy 3772 CAGGTTGAGGATTATGCATTGAGGAAGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTT 3831
Db 3622 GGCCTCTACTTCGCCCCACCCGGAGTGGGAAGTAGTCTTGGCTGGCTGCAAGAAGCAAGGAC 3621

Db 3772 CAGATCGAGCGTTACAGCGCAAGGCCACGCAAAGGCCAGGATATCAGCGTGGATGGGGTATGACA 3831

Qy 3832 GGACCCATTTGGGATATGATA 3853
Db 3682 GCGCCTAACCTGGGGTATGACA 3703

RESULT 9
US-10-282-122A-33284
; Sequence 33284, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

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Qy    615 GGATGCGCGGGGTTGATATCTTTACTTCATTGAGTACTATTTTTGATACTGCCAAGGC      674
              ||||| |||||    |||| | |  || |||||||      |     ||||||| ||
Db    522 CGAGGGCGGCGGGTTCGGGGCGTGTGTTCGAGGAGTTGAACTGCCTATCTTTAT          581

Qy    675 AGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGGCCTATCTTTAT     734
              ||||||  ||||| || | || |||||||  || || ||||| ||||   ||||
Db    582 GGGCGATTTTCGCCGTGTGTCAGGGCGTGTTCGAAGAGTTGGGTTTTGAACTGCCTATCATGAT  641

Qy    735 TTCAGGACGATCGTTGATAAAGTGGGCGACTCTTTCCGACAGACAGGAGAGGATT         794
             ||||| | || ||  |||| |||  | || || |||||||||||| ||||  ||
Db    642 TTCCGGCGACCACCATCACCGCCTCCGGTCGGGTTCGGGCCAGACTACCGAAGCGTT       701

Qy    795 TGTCATCAGCCTGTCCATGAGCAACCACTCTGCATTGATTAAATTGTGCTTTGGGTGC      854
              ||||||||| |||||||||  ||| | ||||||||| |||  ||||||||  ||||
Db    702 CTGGAACTCGATCAGCATGGGCATGGCATCGTCCGTTCGCCGGCCTGAACTGCGCCCTGGGTGC  761

Qy    855 AGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAAATGTACAACAGCCTATGTCCTCTG     914
              |||||  ||||| ||| | ||| |||||| |  |||| ||| ||||||||||||  ||||
Db    762 CAGTGAACTGCGGCCCTTACCTGGCCAAGAAGCTGGCCAACAAGGCCAACACTACTGTGTCTGC  821

Qy    915 TTATCCCAATGCAGGTCTTCCCACAACCTTTGGTGACTATGATGAAACGCCTTCTATGAT     974
              | ||||||||| ||||  |||||||||  ||||||| |||  |||| |||  ||||||
Db    822 GCACCCCAACGCGGGCCTGCCCGAGTACGACGAACTGCCCGAGCTGCCGCAGAC         881

Qy    975 GGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTGGTCAATAATAGTTGGAGGATGCTG    1034
             |||||||||  |||||||| ||| |||||||  ||| | ||||  |||||||||||||||
Db    882 TGCGGAAGATCATCGAAGAATTCGTCAAAGGCGTTTCCTGAACATTGTCGGCGCGTGCTG       941

Qy   1035 TGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATGTGAAGCCTAG    1094
              ||| ||||||||| | | ||   ||||||||| ||||||||| |||||||||||| ||
Db    942 CGGCCACCACCTGAGCACTGCGGCAGTGTCGGCCAGCAGTGTCTTGGTTATGCACCCCG     1001

Qy   1095 AGTTCCACCTGCCACTGCTTTTGAACGGACATGTTACTCGTCTGGTCTCTAGAGCCCTTCAG   1154
              || |||||||||  |||  ||||||||||| | | ||| | || ||||||||||||
Db   1002 TGAAATTCCAGACACATCCCAAAGCCTGCC------GCCTGTGGGCCTTGAACCGTTCAC     1055

Qy   1155 GATTGGACCGTACACCAACAACTTTGTTAACATTGGAGAGCGCTGTAATGTTGCAGGATCAAG   1214
              ||||||||| |||||||||||||||||||| ||||||||||| |||||||||||||||| ||
Db   1056 CATCGATCGGCCAGTCGCTGCTGTCGTCAACGTCGGCGGAGCGCCACCAACATCACCGGCTCCGC  1115

Qy   1215 GAAGTTTGCTAAACTCATCATGGCACAGAAACTATGAAGAAGCCTTGTCGTGTGTGCCAAAGT   1274
              ||||||||| ||||| |||||  ||| |||| ||| |||||||| | | | | | ||||||
Db   1116 CCGCTTTGCCCCCGATCCGTGCCGGAGGCGCTGCGAAGCGGTCGCCCCCTGCA          1175

Qy   1275 GCAGGTGGAAATGGGGAGCCCAGGTGTTGGATGTCAACATGATGGCATGCTAGGATGG       1334
              |||||||||||||  ||||  ||| |||| |  ||||||||||  ||| ||| |||
Db   1176 ACAGGTCGAAGCCGGTGTCCCAGTGATCGACACATCAAGGATGCTCACTC            1235

Qy   1335 TCCAAGTGCAATGACCAGATTTTGCAACTTAAATTGCTTCCGAGCCAGACATCGCAAAGGT    1394
              ||||||||||| |||||  ||||| ||| |||||||||| |||||||||||| ||||||
Db   1236 GAAGAAGGCCATGGTCACCCTCCTCAACCTGATCGGAGCGCCGGAGATCTCTCGCGCT      1295

Qy   1395 ACCTTTGTGCATCGACTCCTCCAAATTTGCTGTGATTGAAAGTGCTGCCA               1454
              |||| |||||||| ||||| |||||  || |  || ||||||  |||| ||
Db   1296 GCCGATCATGATGACTGACTCCTCCAAGTGGCATCGGTCTCAAGTGCATTCA            1355

Qy   1455 AGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACTTCTTGGAGAA     1514
              |||||||||||||| || |||| |||||||||||||||||||||||||||||  ||||
Db   1356 GGGCAAGGCCATCATCGGCTCGATCGAGAAGGAAGGAGGCGTCGAGCAGCAGTTCCATGT  1415

Qy   1515 GGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGTCATGGTCATTGATGAAGAAGG    1574
              ||||||||||||  | |||||| || |||| |||||||| | ||| ||||||||||||
Db   1416 CGCTCGCCGTGCACCGGCTTCCCGCGCCTCGTCGTCCCAGGCCTACATCTGCGTT         1475

Qy   1575 TTCAAAAACCCCACACAGCAGTTAAAAATAGTCCGGCCTACCATCTGCTTGT             1634
              ||||||| |||||||| | | |||||||| || |  |||||||||||  |||
Db   1476 CTCCAAGGCGACACCGAGGCGCAAGCGGCTCGTCAAGCGGCATTCTGT              1535

Qy   1635 GAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCTTAATCCTAACCATTGG      1694
              ||||||  ||  |||  |  ||||||| ||| |||||| || || ||||||||||||
Db   1536 CAACGAAGTGGCTTCCCCGGCCTCGGAAGGAAGAAATCTGCAAGCGGCTCAAGGAACATTGC  1595
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Qy   1695 GACTGGAATGGAGGAACACAACTTGTATGCATTAATTTTATCCATGCAACAAAAGTCAT     1754
              ||||| || ||  ||||||| | |||| || || | || |||| |||||||| ||||
Db   1596 CACCGGTATCGAAGAGCACAACAATTACGCCCTGGACTTCATCAACGCCTGTGTGCCTACAT  1655

Qy   1755 TAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGTTCTTTCCAACTTGTTCTTCCTT      1814
              || |||| ||| ||||| ||||| ||  |||| || ||| |||||||||| | ||||
Db   1656 CCGCGATGAACTGCCCACGCGCGTGACCCGTGTGCAACGTGTCGTTCTCGTT           1715

Qy   1815 CCGAGGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTCCTTTACCATGCAATCAA     1874
              ||| |||||| | ||||||||| | |||| | |||||||||| ||||| ||| |||| ||
Db   1716 CCGCGGCAACAACCCGGTACGCGAAGCCATTCACTCGGTGTTCCTCGTGTTCCACGCGGATCCG  1775

Qy   1875 GTCTGGCATGGACATGGAGATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCA    1934
              ||| || ||||| || ||||| || ||||  || ||| || | ||| || ||  || ||
Db   1776 CAATGGCCTGAGCATGGGCATCGTCAATGGCATGGGCAGCTGGAAATCTACGACCAGATCCC  1835

Qy   1935 TAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGAGAATAAAGACCCTGAGGCCACTGA    1994
              || ||||||||||  ||  || ||| ||| | | ||||||||| |||||||||| | ||
Db   1836 GGCCGAGCTGCGCGACTGTGTCGACAAGCGTGTCAACCGTAATCCCGAAGGCACCGA      1895

Qy   1995 GAAGTCTTACGTTATGC---CCAGACTCAAGGCACAGGAGGGGAAGAAGTCATTCAGAC     2051
              ||  || | | ||| |   ||| | | || ||||||| |||| | |||| ||| || ||
Db   1896 GGCGTTGCTGCTGCCATTGCCGACAAGTACAGAGGCGATGGCAGCGCGTCAAGGAGCTGAAAC  1955

Qy   2052 TGATGAGTGGAGAAATGCCCTGTCTGAAGACGACGCCTTGTGAGGGCAT              2111
              | ||  || |  ||||||   || ||||  ||||| | ||| |||| |||| |||||| ||
Db   1956 CGAAGAATGGGCCGAGCTGGCCGGCCTGCCTCAACCAGCCGCCCTGGCTGGTCGTCAAGGGCAT  2015

Qy   2112 TGAAAAACATATTATTGAGGATGACTACTGAGGAGCCCCAGGTTAAACCAAAAAAATATCCCG   2171
              |||||| || ||  | || |||||  || |   |||||| ||||  |   | |
Db   2016 CACTACCCACATCGTCGCAGGACCACACCGGAAGAGAGTTCGGGCTCGGC------TTCACCCG  2066

Qy   2172 ACCTCTCAATATAATTGAAGGACCCCGTGATGAATTGTTGGTGATCTTT             2231
              |   | ||||| ||||||  ||||  ||| |  | | ||| ||||| |||
Db   2067 GCCTATCGAGTGATCGAAGTCGAAGGCCCGTGATCGATGTCGGTGTCGGTGACCTGTT       2126

Qy   2232 TGGAGCTGGAAAAATGTTTCTACCTCCAGGTTATAAAGTCAGCCCGGGTTATGAAGAAGGC    2291
              ||| |  |||  ||||||| ||||  |||| || | || | |  ||||| | ||||||||
Db   2127 CGGCGCGGGCAAGATGTTTCTGCCGCCAGGTGGTGAAGCTGACGGGTGATGAAACAGGCAT  2186

Qy   2292 TGTTGGCCACTTGTCCGTGTGTAAAATCATGAAGAAGACCTTGTGTGTTCGCCAAAGT     2351
              | |  ||| |  | ||| | | || |   |||||||||  || | | ||| | |
Db   2187 GGTGCGCGCACCCTTATTCTCCGTTCATCGTTCATCGAGCCGAAAAAGAGGCGGACA        2230

Qy   2352 GCAGGTGGAAATGGGGAGCCCAGGTGTTGGATGTCAACATGATGGCATGCTAGGATGG      2411
              |||  | || | |   |||| ||| | |||| || ||||||| ||| ||  |||| |||
Db   2231 --------------AGCCCGAGCCAAGGGCCAGCAAGATCCTCATGGCTCACTGGACGTCAAGGGCCA  2276

Qy   2412 CGTGCACGACATAGGCAAGAACATAGTTGGAGTGCTTCCTTGGCTGCAATAATTTCCGAGT    2471
              |||| | | || |  || |||||| || || || | | ||| || || | || |||| |
Db   2277 CGTTCACGACATCGGCAAGAACATCGTCGGCGTGTGTAACGGCGTGTAACGGGCCATGACAT  2336

Qy   2472 TATTGATTTAGGAGTCATGACTCCATGTGAAGCTGGTTAAAGTGCTGCCA             2531
              | | |||| | |||| ||| || ||| | ||||| | |||| | | ||| ||||||||||
Db   2337 CGTCGATCTGGGTGTGATGGTGCCTGCCGGAGGATCCTCAGGTGTCGCGCCCGGCGAGAA   2396

Qy   2532 AGCAGATATAATTGGCTGTCAGGACTCATCATCACTCCTTCCCTGATGAAATGATTTTTGT   2591
              ||| ||| || || ||||||| |||||| || ||| || |||||| ||| ||| || |||
Db   2397 GTGCGACATCATCGGCCTGTCCGGCGTCGATCACTCGGTGTCACGGCCGCGAAATGTGCATGT  2456

Qy   2592 TGCCAAGGAAATGGAGATTAGCTATAAGGATCTGTTTTGATGAAGAAGG              2651
              ||| ||| |||||| | |  |  |||| || ||| |  ||||||||| |||||||||| ||
Db   2457 TGCCCGTGAAATGCAGGCCTCCCGGTAGTAGCTGCCTTCCTGGACGGGGGCGGCGGACCAC  2516

Qy   2652 TTCAAAAACCCCACACAGCAGTTAAAAATAGTCCGGCCTGTAATCCA            2708
              || | || || ||||||| |  || ||  |   |  |   |||||| ||||||||
Db   2517 CTCCAAGGCGCCACGCGGTCAAGATCGGGCTAAATACAGCAACGATGCAGTGATCTA        2576

Qy   2709 TGTCCTGACGCGGTCCAAGAGTGTGGTGTTCCAGTCGGTGTTGTAGTGAAAATCTAAA     2768
              ||  || |||||| || |||| ||| |||  ||||||||||||| |||||| ||||||
Db   2577 CGTCACCGAGCGCTCCCAGCGGGGGGTCCCCAGTGTCGTGCTGCTGTGTCGGAAGAGCTGAA  2636

Qy   2769 GGATGAATACTTTGGAGGAAATCATGGAAGAATATGAAGAATATTAGCAGGACCATTATGA   2828
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Db   3681 CGAACGCTGGCTGGCACCCAACCTTGGCTACGA 3713

RESULT 10
US-10-282-122A-20596
; Sequence 20596, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20596
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-282-122A-20596

Query Match   22.6%; Score 883.8; DB 7; Length 3684;
Best Local Similarity   54.4%; Pred. No. 1e-255;
Matches 2043; Conservative   0; Mismatches 1612; Indels 102; Gaps 9;

Qy   120 GGATGAGATCAATGCCATTCTGCAGAGAGGATTATGGTGCTCGATGGAGGGATGGGGAC 179
          ||| ||||||| ||||||||||||||||||| ||||| ||||||||||||||||||||
Db   15 GGAACAACTGCGTGCGCAGTAAATGAACGTATTCTCGGTCGCTGGCTGGTATGGGCAC 74

Qy   180 CATGATCCAGCGAGCGGGAGAAGCTAAACGAAGAGAACACTTCCGAGGTCAGGAATTTAAAGATCA 239
          ||||||||||||| ||| |||||||||||| ||| ||||||||| |||| ||||||||||||||||
Db   75 CATGATCCAGAGTTATCGACTGGAAGCGAAGCTGACGATTTTCGTGGTGAACGCTTGCCGACTG 134

Qy   240 TGCCAGGCCGCGTCGAAAGGCAACAATGACATTTTAAGTAATAAACTCAGCCTGATGTCATTTA 299
          || |||||||| | |||||||||| | |||||||| ||||||||||||||||| ||||||||||
Db   135 GCCATGCGACCTCAAAGGCAACAACGACCTGGTACTCAGTAAACCGGAAGTGATCGC 194

Qy   300 CCAAATCCATAAGGAATACTTGCTGGGGGCAGAATCATGGAAACAAATACTTTTAG 359
          ||||||||||||||||| |||||||| || |||||| |||| ||||||||||||||
Db   195 CGCTATCCACAACGCCTACTTTGAAGCGCGGCGGCGGGATATCATCGAAACAACCTTCAA 254

Db   2637 ACCGGGCGGTTCATTGAAGGAGGAGGAGATACTTACCCTTGAGTACGTCGAAGTCAAGCCAGAAAAAGTGGTTTCCAAAT 2696
          |||| ||||||||| ||| ||| |||||| |||| ||||| |||||| |||||||||| ||||||||||||||||
Qy   2829 GTCTCTTCAAGGAGGAGGAGATACTTACCCTTAGTCAAGCAGCCAGAAAAAGTGGTTTCCAAAGT 2888

Db   2697 GCGCGAGTGCAACGGCACCGAGCGCCTGAGCTATGGCGGCGTGGCGAAAAAGCCGAAGTT 2756
          ||| ||||| |||||||||||| |||||||||||||| |||||||||||||||||||||
Qy   2889 GGATTGGCTGTCTGAACCTCACCAGTGAAGCCCAGTTTATTGGGACCCAGGTCTTTGA 2948

Db   2757 CGACTGGGAAAGTTACAC---CCCTGCCAAGCCGACCTTCACTGGCACCCGGTTCTCGCA 2813
          ||||||||||||||| | || || |||||| |||||||||||||| |||||| |||
Qy   2949 AGACTATGACCTGCAGAAGCTGGTGAGAAGCTGGTGGAAGCCTTTCTTGATGTCTG 3008

Db   2814 GGACACATCGAACGTGCTGGCTGACTACATCGACTACATATTTCCCAAGATATTTAACGACAAAAACAGT 2873
          |||| || |||| | |||||||||| |||||||| | || |||||||||||||||||||||| |||
Qy   3009 GCAGCTCCGGGCAAGTACCCGAATCGACGAGGCTTCCCAAGATATTTAACGACAAAAACAGT 3068

Db   2874 GGACCTGGCCGGTAAATACCCGCGC----------ATCCTGACCGACGAAGTGGT 2918
          |||||||| |||| ||||| ||| |||||||||||||||||||
Qy   3069 AGGTGAGAGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACACTGATTAG 3128

Db   2919 TGGCGAAGCTGCCACTGCGCCCGGGGGTGGTTGGGTTCTGGCCAGCACAGAGTATCCAAGA 2978
          ||||||| |||||| | ||||| || ||| |||| |||||||||||| |||||||||||
Qy   3129 TCAAAAGAAACTCCGGGGCCCCGGGGGTGGTTGGGTTCTGGCCAGCACAGAGTATCCAAGA 3188

Db   2979 TGAAAAACTGATCAGCGGCGCGCGGCCGTATTCGGCTTCGGCCGACCAACCAACAGATCAACGA 3038
          |||||||||||| ||| ||| || ||||||| ||||||||| | |||||| ||||||||||
Qy   3189 CGACATTCACCTGTACGCAGAGCTGTCTGTGCCCCAGGCTGCGAGAGGCCCATAGCCACTTT 3248

Db   3039 TGACGATC----------TTGGAGGTCTATGGCGAAGACGGCAAGCCGCTGGCGAAACT 3086
          |||||||| |||||| ||| ||||||||||| |||||||| |||| |||
Qy   3249 CTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCAACGAGCCATACTACTGCCT 3308

Db   3087 GCATCACCTGCCGCCAGCAGACCATCAAGCCTGACGGCA------AACCGAATTTCTCGCT 3140
          | ||||| | |||| ||| ||||| |||| | |||| | ||||||||||||||||
Qy   3309 CTCAGACTTCATCGCTCCTTGCATTCATTCTGACTACCT---GGGCCCTGTTTGC 3365

Db   3141 GGCAGACTTCGTTGCGCCCAAGGACAGCGGCCTGACCGAGGCTGAGCGAAGTGAGGAGCCTATGAGGATGATGGTGACGACTA 3200
          |||| ||||||| ||| |||||||||||||| |||||| ||||||||||||||| ||||||||||||||||||||||||||||
Qy   3366 CGTTGCCTGCTTTGGGGTGGTAGAAGAGCTGAGCAAGGCCTATGAGCAAGTGATGTGGTGACGACTA 3425

Db   3201 CCCGGCCAGGCATTGGCGCCGAGGAAGTGGCCAAGGCTTATCAGGACAACACGGACGACTA 3260
          |||||| ||||||| ||||||||| |||||||||||||||| || |||||| |||| ||||
Qy   3426 CAGCAGCATCATCAGTCAAGGCGGCTCGGGGGACCCGGCCTTGCAGAAGAGT 3485

Db   3261 CAACTCGATCATGGTCAAGGCCTTGGCCGACCGTTCCTGCCGCCGGAATGGCT 3320
          ||| |||| |||| |||||||||| ||||||| ||||| ||||||| |||
Qy   3486 CCATGAAAGAGTTCGCCGAGAACTTCTGGAGGCTACTGTGGCAGCAGTCTGAGCAGTTCGGC 3545

Db   3321 GCACCAACAGGTGCGCAAGGATAACTGGGGTTACGCGAAAGACGAAGCGCTGGACAACGA 3380
          |||||||||||| |||||||| ||||||| ||||| ||||| ||| |||||||||||||
Qy   3546 AGACCTGGAAGGTTGCGTACAAGGCGTACAAGGGCATCCGCCGCTCCTGGCTACCCCAGCC 3605

Db   3381 AGACCTGGAAGGTTGCGATCAGGCCGGTCAAGGAGCAGTACAATGGCATTCCGCCTCGGCTATCCGCGGTCGCC 3440
          ||||||||||||||||||| |||||||||||||||||||||||||||||||| || ||| |||||||
Qy   3606 CGAACCACCGAGCGAAGCTCACCATGT-------------GGAGACT 3638

Db   3441 TGACCATACCGAAAGGGCACCCTGTTCGCCCCTTCGCCCGCTCGACCCCGCTGCCGGAAGGCACGCC 3500
          |||||||| ||||| ||| |||| || || |||||||| ||||||||||||||||||||||||||
Qy   3639 CGCAGAGCAATGCGAGCCAGTCTCACAGGCCATTAGGTTAACAGCAGAATCATTAGCACCGTATGGGGCAC 3698

Db   3501 CGAGCACACGCCGGGCAAAAGCGGAGTGTTCCTGACCGAGCACTACGCCATGTTCCCCGGC 3560
          |||| ||| |||||| |||||| |||| || |||||||||| || || |||| ||||||
Qy   3699 TTCAGCAGTCTCAGGCCCTACTTCTCCATTTGAAGTCCAAATATTTGCTGTGGGGAA 3758

Db   3561 GGCGGCAGTGGCGGCGGCGATCAGCGCGGTGATTATCGCTCATCCTCAGCGCGTACTTTGCAGTCGCA 3620
          ||||| |||||||| ||| ||||| | |||||||||| || || | ||| ||| ||||| ||
Qy   3759 GATTTCCAAGGATCAGGTTGAGGTTGAGGAATATGCATTGAGGAAGAACAGATATCTGTGGCTGAGGT 3818

Db   3621 GGTCGACAAGGATCAGGTCGAAAGCTACACAGCAGATACTCGTGGTGCTGAGGT 3680
          |||||| ||||||||||| |||||||| || |||||||| |||| ||| ||
Qy   3819 TGAGAAATGGCTTGGACCCCATTTGGACCATTTGGGATGA 3851

Db   3681 ...

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Qy   1329 AGTCTGAAGTGTATCCAGGGCAAAGGCCATTGTTAACTCTATCTCGATGCTGCTATGGTGGTCAT 1388
          |||  |  ||| |||| || ||||||  || || |||||  ||||||  |||||| |||
Db   1497 GGACGACTTCTTGGGAGGAGGCCAGGAGGTAACTCTCCAGACAGGAAT 1556

Qy   1389 CGATGCCTTTATCCATCACGCGGAAATTGTTGCGTCGCTACGGTGCGGCAGTGGTGGTAAT 1448
          |  |  | ||| || |||| |||   ||| || || |||| || | |||| |||| ||
Db   1557 GGCTTTTGATGAAGAAGCACAGGCCAACAGGACGGCAACGCAAAATCAGAGATCGCGATC 1616

Qy   1449 GGCCTTTGACGAACAGGACAGGACCGATACTCGGCACGGGAAAATCAGAGATTGCCGGTCG 1508
          ||||| |||  |||| |||  |||| |  | |||  ||||| |  | ||||||  || || ||
Db   1617 GGCCTACCATCGTCTTGTGTGAAGATGAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCC 1676

Qy   1509 GGGGTACAAAATCCTCACCGGCGTTGGCTTCCCGCCAGAGAAGATCATCTTCGACGA 1568
          |||||||||||||  ||||| |  ||| |||||| |||||| ||||||| ||||
Db   1677 TAATATCCTAACCATTGGACTGGAATGGAGGAGAACACAACTTGTATGCCATTAATTTTAT 1736

Qy   1569 AAACATCTTCGCGGTTGCGAACTGCCTTTATCCTGATTGAAACCGTTTTTCGA 1628
          |||| | | | ||  || ||| |||  | || |||   ||||| ||||| ||
Db   1737 CCATGCAACAAAGTCATTAAAGAACATTACCTGGAGCCAGAATAAGTGGACCAGAGGAGGTCTTTC 1796

Qy   1629 CGGCGCGTGGAAGACATCAAACGGGAATGCGCCACTGATATGGGGATCATGGTTCCGGGCGCGTATC 1688
          ||||| |||| || ||||  |||| |||| | ||| |||||||| ||| ||| | |||||| |
Db   1797 CAACTTGTCCTTCTCCGGAGGAATGAAGCAATGCATGGCCATTCACCGGGTTTT 1856

Qy   1689 TAACGTTGCTTTTGCGTATTTGCGTGAAGAACGGAGTTTGCGAAGCCTGGGCGT 1748
          |  |||| || | | |||   ||  |  ||| ||||| ||||| ||||| | ||
Db   1857 CCTTTACCATGCAATCAAGTCTGGCATGGCAGATAGTGAATGCTGGAAACCTCCC 1916

Qy   1749 CCTCTACTACGGTATTGCCACTCATCGCGCCGAAGCTCTGACCTTTGGCCT 1808
          || |  | |||  ||| | |   ||||| || |||| ||||| |||| ||
Db   1917 TGTGTATGATGATATCCATAAGAACTTCTGCAGCTCTGTGAGATCTCATCTGGAATAA 1976

Qy   1809 GAATTACGACGACCTACCCGCTGAACTGCGCGACGCGGTGAAGATGTGATTCTTAATCG 1868
          |  |||  | |  |  |    |||||  | |||  ||| |||| ||  |   || ||| |
Db   1977 AGACCCTGAGGCCACTGAGAAGTCTCTACGTTATGCCCAGACTCATATGA--------AC 2027

Qy   1869 TCCGGCAATGGCATGGCACCGAGCGTTCACTGACGGCGTTACTGAGGCAGCAAATATCCGGCAACAAAC 1928
          ||| || |  |  |||| |||||||| |||| |  || || ||  | ||||| |||||| || ||||||
Db   2028 AGGAGGAAGAGAAAGTCATTCAGACTGAGTGAGTGGAAAAAATGTTCTACCTCAGTTATAAA 2087

Qy   1929 CGACGACACCGGCCAACGCGCCAGCGGCGGAGTGGCGCGTCGTGGGAAGTGAATAAACGTCT 1988
          |||| |||||| |||| |||||||| |||||| | || ||| ||||||| ||||| ||||||
Db   2088 TGAGTATGCCCTTGGAAGGGGCATTGGAAAAACATATTATTGAGGAAGTAGTACTGAGGAAGCCAG 2147

Qy   1989 GGAATACTCGCTGGTCAAAGGCATTACCGAGTTATCGCAGCAGGATACCGAAGAGC---- 2045
          |||||| | | |||  ||||| | |   | | |||| | ||||||| |||| ||||
Db   2148 GTTAAACCAAAAAAAATATCCCGACCTCTCAATATAATTGAAGGACAATATATTGAAGTCG 2207

Qy   2046 -----CGCCGCAGCAGGTCACCGGGAAATTGCCCGCTAGCCTGCCGT-----TTGTC 2099
          |||||||||||| |  |||| |||||| ||  | |||| || || ||||| |
Db   2208 CCGCCAGCAGGCTACCGGTACGGCGCCCGTTGATGGTGAAGTGGTCCGG 2267

Qy   2100 CGGCCCTGGAGCGCGTGAACATTGGCGAAGATAGCCTGTTTGTGTGCGAAGCGCGGTCAA 2159
          || |||||||| | |||||||| ||||||||| ||| | | |||| |||||||  ||||
Db   2268 AATGAAAATTGTTGTGATCTTTTTGGAGCTGATAGTGGAAAAAATGTTCTACCTCAGTTATAAA 2327

Qy   2160 GTCAGCGCCGGGGTATGAAGAAGCTGTTGGCCACTGTTGGCACCTATCCCTTCATGGAAAAGAAGC 2218
          ||||||||  | ||||| || | | ||| |||||   | ||||| ||    | ||||   || |
Db   2328 AGAAGAAACCAGAGTGCTTAACGACGCCACAGTAGAAGAGGAGCCACCAT 2387

Qy   2219 -----AAGAGCAGGGGCAAAACCAACGGCAAGAT 2246
          |||||  |||| | | ||||| |  || |||||
Db   2388 CGTGCTGCCACTGTTAAAGGCGACAGTGAGTAGT 2447

Qy   2247 GGTGATCCGCCACCGTCGAAGGGGACGTCCACGATGGTTCCTGCGAAGATAAACATCGTTGGTCGTGT 2306
          || | |||| ||| || ||||||||  ||| || | | |  || |||  |||||| ||||||||| ||
Db   2448 CCTTGGCTGCAATAATTTCCGAGTTATTGATGATTAGGAGTCATCATGTGATAGAT 2507

Qy   2307 GCTGCAATGTAACAACTACGAAATTGTCGGATCTTCGGGCGTTATCGTGCTGCTTCAGGACTTGA 2366
          ||| || ||| ||| | || || ||| |||||| |  ||||| | | ||  |||  |||||| ||
Db   2508 ACTGAAAGCTGCTTGACCCAGAAGCAGCAGAATATAATTGGCCTTGCCTCTCAGGACTCACTCC 2567
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Qy    360 CAGCACTAGTAGTTGCCCAAGCTGACTATGGCCTTGAACACTTGGCTACCGATGACAT 419
          ||    | |  |||  |||||||    || ||||  |  |||  || ||  |||||||
Db    255 CTCCACGACCATTGCGATGGCGGATTACCAGATGGAATCCCTGTCGGCGGAAATCAACTT 314

Qy    420 GTGCTCTGCAGAGTGCCCAGA---AAAGCTGCGAGGAGGTAACTCTCCAGACAGGAAT 476
          | || | |||| || |   || |||||  | |||  | || || | ||  | | ||||
Db    315 TGCGGGCGGCGAAACTGCGCGAGCTTGTGCTGCAGGGGCTCTGGCGCACGGACCGGACC 374

Qy    477 TAAGAGGTTTGTGTGGCAGGGGCTCTGGGCTCGACTAATAAGACACTCTCTGTGTCCCCATC 536
          |   |  | | ||  |||   ||  |||| |  ||||  ||  || |  |  | | ||| |
Db    375 ACCGGCGCTACGTTGCCGCGGTGTTCTCGGCCCGACCAACCGGCCGTCTATTTCTCCGGA 434

Qy    537 TGTGGAAGGGCCGGATTATAGGAACATCACATTGATGAGCTTGTTGAAGCATACCAAGA 596
          | |||||  | || || |||| || || | || |||||| | || |||| ||| || ||
Db    435 GGGGTACAAAATCCTCACCGGCGTTGGCTTCCCGCCAGAGAAGATCATCTTCGACGA 494

Qy    597 GCAGGGCCAAAGGACTTCGGAGACTTCTGGCGGGGGGTTGATATCTTACTCATTGAAACTATTTTTGA 656
          |||| ||||||| ||| | ||| | | || | |||| | ||||| | || || ||||| |||||  ||
Db    495 GTCCACCAAAGCGCTGGTGGAGGGTGGCGGGATCTGATTGAAACCGTTTTTCGA 554

Qy    657 TACTGCCAAATGCCAAGGCAGCCTTGTTTGCACTCCAAATCTTTTGAGGAGAAATATGC 716
          ||| ||||| ||| |||||||  | ||||| |    || |||| | ||||| || |||
Db    555 CACCCTTAACGCCAAAGCGGGGTATTTGCGTGAAGAACGGAGTTTGCGAAGCCTGGGCGT 614

Qy    717 TCCCCCGGCCTATCTTTATTTCAGGGACGATCGTTGATTAAAAGTGGGCGGACTCTTTCCGG 776
          | |   || || | |  | | |||| || | ||||| | |  | || ||| || |  ||||
Db    615 TGAGCTGCCGATTATGATCTTCCGGGTCGCTGGCGCACCATCACCGACGCGCTCTCTCGCGG 674

Qy    777 ACAGACAGGAGGAGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTTCTGCATTGGATT 836
          ||||||||| |  |  ||| |||| ||||  | || | |||||| || ||||| || | |
Db    675 GCAGACCACCGAAGCATTTTTACAACTCATTGCGCGCCGAAGCTCTGACCTTTGGCCT 734

Qy    837 AAATTGTGCTTTTGGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGAAAAATGTAC 896
          |  ||||||   ||| |||| || | |   || ||   | |||| |||||| | |||| ||
Db    735 GAACTGTGCGCTGGGCGGGCGCCCCAGTGCGCGCGCCAGCGTGCGCAGGATTGC 794

Qy    897 AACAGCCTATGTCCTGTTTATTCCCAATGCAGGTGTCTTCCCAACACCTTTGGTGACTATGA 956
          || |||| | ||| | | |   || || || || | || ||||| || |||||||| |||||
Db    795 GGAATGCTACGTCACCGCGCTACGCGCGGGCTACCCAACGCCCTTTGGTGAGTACGA 854

Qy    957 TGAAACGCCTTCAGAGCCTTCTCAGGATTGGCAGGGGCTCTAAAGCACCTGGATGATGGCCTAAAAGGATTTGCTCAAGTGTCAA 1016
          |||| |||| | || | |  | ||| | |||  |||||| ||||| ||  | |||||| || | |||| || ||  ||| | |||
Db    855 TCTCGACGCCGACACGGCCAAACAGATACGTGGATGGGCGCAAGCGCGGTTTTTCTCAA 914

Qy   1017 TATAGTTGGAGGATGCGTGGGTCAACACCAGATCATATCCAGGGAAATTGCTGAAGCTGT 1076
          || ||| || || ||||| || | |||||| ||| | | |||| |||||||||| | ||
Db    915 TATCGTCGCGGCGGTTGCCGCTGCTGCGGTGGCACCGGCCAACAATGGGGCGATGAGTCGCAGT 974

Qy   1077 GAAAAATTGTAAGCCTAGAGTTCCACCTGCTGCTTTGAAGGACATATGTTACTGTC 1136
          |||| || | ||||| |  | | |  ||||| |  ||| ||| |   | |  || |
Db    975 AGAAGGGATTAGGCGGCGCCGCAAATGCGCCGAAATTGCCCGCTAGCCTGCCGT-----TTGTC 1028

Qy   1137 TGGTCTCTAGAGCCTTCAGGATTGACCCGGCCTTCTCAGGATTGGTTAACATTGGAGAGGCGCTG 1196
          | | ||| ||||| | |||||||| || |||| || | ||| || ||||||||||||||| ||
Db   1029 CGGCCCTGGAGCGCGTGAACATTGGCGAAGATAGCCTGTTTGTGTGCGAAGCGCGGTCAACGCAC 1088

Qy   1197 TAATGTTGCAGGATCAAGGAAGTTGTCAACTCATGTCTAAACTCATGGCAGGAAACTATGAAGAGC 1256
          |  |||| | || || |||||||| | || || ||    |   |||| | ||| | | ||||| |
Db   1089 CAACGTCACCGGTTCCGCTAAGTTCAAGGCCCTGGGAAATGTGGAAGAGAGAGAAATCAGCGAGGC 1148

Qy   1257 CTTGTGTGTTGCCAAAGTCGCAGGTGGAAATGGGAGCCCAGTGTTGGGATGTCAACATGGA 1316
          | || || | ||  ||||| |  | || |  || |  ||  |||| |||||||||||||||
Db   1149 GCTGGATGTCGGGCTGCGCGTGGCGAAGATAGCGCGCGTGGCCATTATCGATATCAACATGGA 1208

Qy   1317 TGATGGCCATGGTCTAGGATGGTTGCCAAGTGATCCTCAAGTTTGCTTCCGA 1376
          || |||  | || | | ||||| |||| || ||  |  || ||| ||||  |
Db   1209 TGAAGGGGATGCTTCGATGCCCGAAGCGCGATGGTGTGCGGTTTTTCTCCAATCTGATTGA 1268

Qy   1377 GCCAGACATCCGCAAAGTACCTTTGTTGTGTCATCGTGTTGCTGATTGAAGC 1436
          |||||  |||| || ||  | ||| | ||   |||  |  | ||  ||||| |
Db   1269 ACCGGATATCCGCTGCCGATTATGATCTTCCAATCTCAAATGGACGTCATTGGAAAAAT 1328

Qy   1437 TGGGTTAAAGTGCTGCCAAGGAAGTCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGA 1496
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Db   2367 TCTCCGTACCGCTAAAGAAGTGAATGCTGATCTGATTGGCCTTTCGGGGCTTATCACGCC 2426
Qy   2568 TTCCCTTGGATGAAAATGATTTTTGTTGCCAAGAAATGAGAGATTAGCTATAAGGATTCC 2627
Db   2427 GTCGCTGGACCAGATGGTTAACGTGGCGAAAGAAGATGGAGCGTCAGGGCTTCACTATTCC 2486
Qy   2628 ATTGTTGATTGAGGAGGAGCAACACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAG 2687
Db   2487 GTTACTGATTGGCGGCGGACGACCACCTCAAAAGCGGCGGTGAAAATCGAGCAGAA 2546
Qy   2688 ATACAGTGCACCTGTATCCATGTCTCTGGACGGTCCAAGAGTGTGTGGTGTGTTCCCA 2747
Db   2547 CTACAGCGGGCCCGACGGTGTATGTGCAGAAATGGCCTCGCGTACCGTTGGTGTGGCGGGC 2606
Qy   2748 GCTGTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAAGA 2807
Db   2607 GCTGCTTTCCGATACCCAGCGTGATGATTTTGTCGCTGTGACCGCAAGAGTACCGAAAAC 2666
Qy   2808 TATTAGACAGGACCATTATGAGTCTCTCAAGAGAGGAGATACTTACCCTTAAGTCAAGC 2867
Db   2667 CGTACGTATTCAGCACGGGCGCAAGAAACGCGCCACCACGGTCACGCTCGAAGCGGC 2726
Qy   2868 CAGAAAAAGTGGTTTCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTT 2927
Db   2727 GCGCGATAACGATTTTCGCTTTTGACTGGCAGGCTTACACGCGCCCGTGGCGCCACCGTCT 2786
Qy   2928 TATTTGGGACCCCAGGTCTTTGAAGACTTGCGAAGCTGGTGGACTACATTGACTG 2987
Db   2787 CGGCCGTTGCAGGAAGTC-----GAAGCCAGCATCGAAAACGTGCGTAATTACATCGACTG 2840
Qy   2988 GAAGCCTTTCTTTGATGTCTCCGGCAGCTTCCGGCAAGTCACCCGAATCGAGGCTTCCCAA 3047
Db   2841 GACACCGTTCTTTATGACCTGGTCGCTGCGGGAGTATCCG--------CG 2885
Qy   3048 GATATTTAACGACAAAACAGTAGGTGAGAGGCCCAGGAAGGTCTACGATGATGCCCACAA 3107
Db   2886 CATTCTGAAGATGAAGTGGTGGCGTTGAGGCGCAGCGGCGTGTTTAAAGACGCCACACGA 2945
Qy   3108 TATGCTGAACACACTGATTAGTCAAAAGAAAACTCCGGGCGTGTGGTTGGTTCTG 3167
Db   2946 CATGCTGGATAAATTAAGCGCCGAGAAAACGCTGAATCCGCGTGGCGTGGTGGGCCTGTT 3005
Qy   3168 GCCAGCACAGAGTATCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGCGTGTGCCCAGGC 3227
Db   3006 CCCGGCAAAACGTGTGTGGGATGCATTTGAAATCTACCGTGACGAACGCGTACCATG- 3064
Qy   3228 TGCAGAGGCCCATAGCCACTTTCTATGGGTTAAGGCAACAGAGCGTGAGAAGGACTCTGCCAG 3287
Db   3065 --------------TGATCAACGTCAGCCACTTCATCGTCCCCCTTTGCATTCTGGCATTCTGGTGTGA 3107
Qy   3288 CACGGAGCCATACTACTGCCCTCCAGACTTCATCGTCCCCCTTTGCATTCTGGCATTCTGGTGA 3347
Db   3108 AGGCTTCGCTAACTACTGTCTCGCTGACTTCGTTGCGCCGAAGCTTTTCTGGTAAAGCAGA 3167
Qy   3348 CTACCTGGGCCTGTTGCCGTTGCCTGCGTTTGGGGTAGAAGAG---CTGAGCAAGGCCTA 3404
Db   3168 TTACATCGGCGCATTTGCCGTGACTTGGGGCTGGGAAGAGGAGAACGCACTGGCTGGCTT 3227
Qy   3405 TGAGGATGATGGTGACGACTACAGACAGCAGCCATCATGGTCAAGGCGCTGGGGGCTGGC 3464
Db   3228 TGAAGGCGCAGCGACGATGATTACAACAAAATCATGGTGAAAGCGCCTTGCCGACCGTTTAGC 3287
Qy   3465 AGAGGCCTTTGCAGAAGCTCCATGAAGAAGAGTTCGCCGAAGAGTTCGTGGGCCTACTGTGG 3524
Db   3288 CGAAGCCTTTGCGGAGTATCTCCATGAGCGTGTGCGTAAAGTCTACTGGGCTATGCGCC 3347
Qy   3525 CAGTGAGCAGCTGCGACGTCGCAGACCTCGCAGACGTTGCCGGTACAAGGGCATCCCCGGC 3584
Db   3348 GAACGAGAACCTCAGCAACCAACGAGCTGATCCGCGGAAAACTACCAGGGCCATCCGCGGC 3407
Qy   3585 TCCTGGCTACCCCAGCCAGCCGACCACCACCAGCTCACCATGTGGAGACTCGCAGA 3644
Db   3408 ACCGGGCGCTATCCGCCCCTGCCCCGGAACATACGGAAAAAAGCCACCATCTCGGGAGCTGCTGA 3467
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Qy   3645 CATCGAGCAGTCTTACAGGCATTAGGTTAACAGAATCATTAGCAATGCGCACCTGCTTCAGC 3704
Db   3468 AGTGGAAAAACACTGGCATGAAACTCACAGAATCTTTCGCCATGTGGCCCGGTGCATC 3527
Qy   3705 AGTCTCAGGCCCTCTACTTCTCCAATTTGAAGTCCAAATATTTGCTGTGGGAGAGATTTC 3764
Db   3528 GGTTTCGGTTGGTACTTCAGCCACCCGGACAGCAAGTACTACGCTGTAGCACAAATTCA 3587
Qy   3765 CAAGGATCAGGTTGAGGATTATGCATTGAGCGAAGAACATATCTGTGGCTGAGGTTGAGA 3824
Db   3588 GCGCGATCAGGTTGAAGATTATGCCCCGCGTAAAGGTATGAGCGTTACCGAAGTTGAGCG 3647
Qy   3825 ATGGCTTGGACCCATTTTGGGATATGATACACAGACTAA 3861
Db   3648 CTGGCTGCGCACCGAATCTGGGGTATGACGCGGACTGA 3684
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RESULT 11
US-10-282-122A-40847
; Sequence 40847, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40847
; LENGTH: 3681
; TYPE: DNA
; ORGANISM: Vibrio cholerae
US-10-282-122A-40847

  Query Match             22.5%;  Score 883.2;  DB 7;  Length 3681;
  Best Local Similarity   54.7%;  Pred. No. 1.6e-255;
  Matches 2032;  Conservative 0;  Mismatches 1583;  Indels 99;  Gaps 10;

Qy   140 TGCAGAAGAGGATTATGGTTGCTCGGATGTCGAGGGGGGATGGGGACCATGATCCAGCGGGGAGAAGC 199
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Db    1112 GTTTTAAGCGTTTAATTAAAGAGAGCAATACGAGAAGCGTCGATGTGGCGGCGTGAGC 1171
           |||||||||||||||||||  || |||||||||||||||||||||||||||||||||||
Db      38 TGAAACAACGTATCCTACTACTGATTGATGGTGTGGTACCATGATGAGTTATATAAGT 97

Qy    1277 AGGTGGAAATGGGACCCAGGTGTTGGATCAATCATTGCCAGGCGCTGAAAGGCA 1336
           |||||||   |||   |||| |||||||||||| ||||||||||||||||||||
Qy     200 TAAACGAAGAACACTTCCGAGCTCAGGAATTAAAGATCATGCCAGGCGCTGAAAGGCA 259

Db    1172 AAGTCGAAAACGGCGCGCAGATTTGCACGATTTGTGATTGGCACTGTGTTGGACGCCG 1231
           |||  | || ||  |||||||| ||||||||||||||||||||||||| ||||||
Db      98 TACAAGAGGAAGACTATCGCGGTGCACGATTTGTCGATTGGCACTGTGATTGAAAGGAA 157

Qy    1337 CAAGTGCAATGACCAGATTTGCAACTAATTGCTTCCGAGCCAGACATCGCAAAGTTAC 1396
           ||||||||||||||| |||||||||||||||||| | ||||||||||||||||
Qy     260 ACAATGACATTTAAGTATAAACTCAGCCTGATGTCATTACCAAATCCATAAGGAATACT 319

Db    1232 AGGCGTGTATGGTGCGCTTTTGAATCATCATGCGCCTCTGAACCAGAAATATCCAAAGTC 1291
           | || ||||||| ||  ||| ||||||||||||||||||| |||||||  ||||
Db     158 ATAACGACCTCTTAGTGCTTCAGCCGCAAATATTATTAAAGATTCACTCCGCTTACC 217

Qy    1397 CTTTGTGCATCGACTCCTCCAATTTGCTGTCGTGATTGAAGCGTCGGTTAAAGTGCTGCCAAG 1456
           ||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||
Qy     320 TGCTGGCTGGGGCAGATCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCCAAG 379

Db    1292 CGGTGATGGTCGACTCCTCTAAATGGGAAGTCATTGAAGCGGCGGTCTGAAATGCATTCAGG 1351
           || | ||||| ||||||| ||||||  |  ||| ||||| ||||||||||||||
Db     218 TTGAAGCGGGGGCGGATATTCTTGAGACCAACAACCACCTTAACTCAACCACGATTGCCATGG 277

Qy    1457 GGAAGTGCATTGCAATAGCATTAGTCTGAAGGAGGAGGACGACTTCTTGGAGAAGG 1516
           ||| ||||||||||||  |||| ||| ||||| |||||||||||||||||||
Qy     380 CTGACTATGGCCTTGAACACTTGGCTACCGGATGAACATGTCTGCAGGAGTGGCCA 439

Db    1352 GTAAAGGCATCGTCAACTCTATCTCTCAAGAAGGGAAAAGAGAAGAGTTTATTGCCCAAG 1411
           ||| | |||| | |||| |||||  | ||   ||
Db     278 CAGACTATGCAATGCACTCTGAAATTAACTTTCGCCGCGGCCTAAGCTTGCAC 337

Qy    1517 CCAGGAAGATTAAAAGTATGGAGCTGCTATGGTGGTCATGGCTTTTGATGAAGAAGGAC 1576
           |||||||| |||||| | |||||||||||||||||| ||||||||||||||||
Qy     440 GAAAAGCTGCCGAGGAGGTAA---CTCTCCAGACAGGAATTAAGAGGGTTTGTGGCAGGGG 496

Db    1412 CCAAATTGGTGCGCCGCGTGATTGTGATTGGCATTTGAGCGAGTGGGGC 1471
           ||  |  | |||||| ||| || ||| ||||| ||  |||||
Db     338 GTGAAGTGCGCGGATGAGTGAGCGCGTCAAGATCTCGGCCACCGTGGCTGGTG 397

Qy    1577 AGGCAACAGAAACAGACACAAAATCAGAGTGTGCACCCGGGCTACCATCTGCTTGTGA 1636
           |||||||| ||  |||| ||||||||||||||| |||||| ||||||||||
Qy     497 CTCTGGGTCCGACTAATAGAGACACTCTCTGTCCCCATCTGTGGAAAGGCCGGATTATA 556

Db    1472 AAGCCGGATACCCGTGAGCGCAATTAGAGATCTGTTCGTCGGGCTTACCATATTTGGTCG 1531
           | ||||| |||||||| || |  | |||||| || || ||||||| |||
Db     398 TGCTTGGGCCAACCAACCGTATTCGCGGATGTGAACGATCCAGGATTTC 457

Qy    1637 AAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATATCCTAACCATTGGGA 1696
           ||| |||||| ||| |||||| ||||| || | || || |||
Qy     557 GGAACTCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCCAAAGACTTCTGG 616

Db    1532 ATGAGGTGGGCTTCCCACCCGGAAGATCTTTTTGACCCGGACATCTTTGCGTTGGCA 1591
           ||| || | ||||||   | |||| || |||||| ||| || ||
Db     458 GTAACGTCACTTTTGATGGGCGTTGTGGGGCTTGTTGAAGCCTATTCGCGACGCGCCGCTTCA 517

Qy    1697 CTGGAATGGAGAACACACAACTTGTATGCCATAATTTATCCATGCAACAAAAGTCATTA 1756
           |||| | |||||| ||||| || ||||||| ||| |||||||| ||||| ||||
Qy     617 ATGGGCGGGGTTGATATCTTGTACTACTGAAACTATTTTTGATACTGCCAAGCAG 676

Db    1592 CCGGAATTGATGAGCACAATAACTACGGCATTCATTAATGCAGTCAGTGGCGGCGACATTA 1651
           |||| | | || ||| || ||| || ||||| |||| || |||| ||| ||
Db     518 AAGGTGGCAGCGGATCTGATCCTCATTGAAAGCGATCCTCGATTACACTTAACGGCAAAGCCTT 577

Qy    1757 AAGAAAACATTACCACCTGGAGCCAGAATAAGCGAGGTCTTCTTCCAACTTGTCTCCTCC 1816
           ||| ||| ||  ||  | || | || || |  |||||| |||| ||||||||
Qy     677 CCTTGTTGCACTCCAAAAATCTTTTGAGGAGAAATATGCTCCCCGCCCTATCTTTATTT 736

Db    1652 AGCGTGAGCTGCCGCATGGCGATGCATTGCTGATTTCTCGGCGGGTGTTTCTAACGTTCCTTCTTTCC 1711
           |||| || || || ||||| | || ||  | ||  |||
Db     578 GTGCGTTTGCGGTCGGATAGCGTCGATAGGCTGGAGAAGCTGAAGAGT 637

Qy    1817 GAGGAATGGAAGCCATTCGAGAAGCAATGCAATCGTGAGGGGTTTTCCTTTACCATGCAATCAAGT 1876
           |||| |||||||||| |||||||||| | ||  ||||  || ||||
Qy     737 CAGGGACGATCGTCGTTGATAAAGTGGGCGGCGACTCTTTCCGGACGAGGAGGATTTG 796

Db    1712 GCGGCAACAACTATGTGCGTGAAGCGGATCCATGCCATGTCTGTGAAAAATCTACTGCTTCAAAC 1771
           | ||||| |||| | | || |||||| |||  |||| || |||
Db     638 CCGGCACGATTACCGACGTCCTGGGGCAACTCTGTCAGGAGGACAACGGAAGCTTTCT 697

Qy    1877 CTGGCATGGACAGTGGAGATAGTGAATGCTGAAAACCTCCCGTGTATGATGAATCATCATA 1936
           |||||||||| || || || |  |||||| ||  || |||
Qy     797 TCATCAGCGTGTCATGGAGAACCACTCTGCTTGGTGTCAGTTTGGGTGCAG 856

Db    1772 ACGGGCATGGACATGGGGGATTGTCAACGCAGCGGCAGCTTGAAATCTACGATAACGTTCCGC 1831
           | |||||||| ||||||  || ||||  ||||||| ||| |||
Db     698 ACAACGCCTTGCGCATGTACGGCGATTTCGTTGGCTTGGCGTTAGGTCCTG 757

Qy    1937 AGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATCTCGAGGCCCACTGAGA 1996
           ||||||| | ||||| ||||  | |||| ||||||| | |||||||| |||
Qy     857 CTGAGATGAGACCTTTATTGAAATAATGGAAAAATGCACACAGTCCTCTGTT 916

Db    1832 TGAAACTGCGTGAGGCAGTGGAAGATGTGATCCTCAATGCAGCGAGGCACGGAAA 1891
           ||| || |||| | || | ||||| |  |||||| |  |||||
Db     758 ATGAGCTGCGCGCAGTAGCTGGAAGAGCTGGCATTTCACGCATGTCTCCCGCGC 817

Qy    1997 AGCTCTTACGTTATGCCCAGACTCAAGGCACA-------GGAGGAGAAAGTCATTC 2047
           ||| || |  ||| |||| || | |||  |||        || |||||| |||
Qy     917 ATCCCAATGCAGGTCTTCCCAAACACCTTGGCTGGACTATGAGATGGAAACGGCCTTCTATGATGG 976

Db    1892 GACTGCTTGGAGATCGCCGAAGCCGTATCGCGAAACAGTGTTGTGGTAAAGACGGATGCTT 1951
           | || | | ||| || |   ||| |||   |  ||| |  | | ||
Db     818 ACCCAAATGCCCAACTGCGCCAATGCGTTGGTGAATACGGATCTCTCGCCCAGGAAATGG 877

Qy    2048 AGACTGATGAGTGGACATGGGAGAAATGCGTGAGTATGCCCTTGAGTGAGCACGTGAAGG 2107
           |||||||||| || | |||||||| ||||||   | ||||||||
Qy     977 AGACTCACCTGCCACTGCTTTTGGTCATGATGCTTGGTTCAATAGTGTTGGTGTG 1036

Db    1952 CTGCATTAGAGTTGGCGGCCATGGCAGCACGCTTTGTTAGTCAAGG 2011
           ||| ||| || | |||||| |||| ||| ||| |||||||
Db     878 CTGCATGGTAAGCTTGGTTTTTGAATTTGGTCGGTGCTGCTGTG 937

Qy    2108 GCATTGAAAAACATATTATTGACGAAGTTAAGCGTGTAAAAATTGTTGGTGATC 2167
           |||||| |||| | | |||| | |||||| | ||||||||| |||||||
Qy    1037 GGTCAACACCAGATCATATCCCAAACACCTTGGCTGACTATGAAAGCCTTCTATGATGG 1096

Db    2012 GATCACCGAATTTATCGTCCAAGAAGCCGTCGAGGGTGTAAAACCAAGGG 2066
           |||| || || || ||||| ||||| | || || | |||||||
Db     938 GAACTACACCTGCACCTGAGCATATCGCCGCCATTGCCAAAGCCGTCGAGGGTGTAAAACCAAGGG 997

Qy    2168 CCCGACCTCTCAATATAATTGAAAGACCCCTGATGAATGGTGATC 2227
           |||| || | ||| |||| ||||| | ||| |||||||
Qy    1097 TTTCCACCTGCCACTGCTTTTGGAAGGACATATGTCTCGTCTAGAGCCCTTCAGG 1156

Db    2067 ----ACCACTGGAAGTGATTGAAGGGGCCGCTGGTGAACGTTCGGTGACT 2122
           |||||||| | || | |||||||| || | || |||
Db     998 CTCTGC-----CAGATCTGAAATGAGCGTCTCTCCGGGTTTAGAGCCGCTCAATA 1051

Qy    2228 TTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTTCAGGAGAAGA 2287
           ||| || |||| |||||| ||||| ||||||| | || |||  ||||||
Qy    1157 TTGGACCGTACACCAACTTTGTTAACATTGAAGAGCGCGTGTAATGTTGCAGGATCAAGGA 1216

Db    2123 TGTTCGGGGAAGGGAAAATGTTCCTACCGCAAGTCGTAAAATCAGTGTCTCATGAAAAC 2182
           | || || | |||  |||  || ||| | | | | |  ||| | || |||
Db    1052 TTGGTCCTGAAACCTTGTTTGTTTAACGTGGGGGCGAACGTACTAACGTCACCGGTTCTCGCGC 1111

Qy    2288 AGGCTGTTGGGCCACCTTATCCCTTTCATGGAGAGAAACTATGAAGAGAAGGAAGAAACCAGAGTGCTTA 2347
           ||| || ||| ||||| |||  | |||||  | |||||| |  |||  | || |||||
Qy    1217 AGTTTGTGCTAAACTCATCATGCAGGAAGCTATGACAGAGAAGAAGGCCTTGTCGTGTTGGTTCTCGC 1276

Db    2183 AAGCCGGTTGCGTATCTTCAGCCTTTCATTAATGCGCAAAAAGTGGTAGCA-------- 2233
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Qy 2348 ACGGCACAGTAGAAGAAGAGACCCTTACCAGGGCGACCATCGTGCTGGCCACTGTTAAAG 2407
Db 2234 ------------------CTTCAAATGGTAAGATTTTGCTGTCGGACACCGTAAAAG 2269

Qy 2408 GCGACGTGCACGACATAGGCCAAGAACATAGTTGGAGAGTAGTCGTCGTGGCGCAATAATTCC 2467
Db 2270 GCGATGTGCATGACATTGGTAAGACAACATTGTTGGGTGCGCAGTGTAATAACTTCG 2329

Qy 2468 GAGTTATTGATTTAGGAGTCATGATGATAGATACTGCTCTTGACC 2527
Db 2330 AGATCATCGATCTTGGTGTGATGGCCTTGCGCAGATCCTCAAAGTCGCACGCGGAGC 2389

Qy 2528 ACAAAGCAGATATAATTGGCCTGTCGCAGACTCATCACTCCTTCCCTGGATGAAATGATTT 2587
Db 2390 AAAATGTCGATATCATCGGTCTCTCTGGCGTTATCACGCCGTCTTTGGATGAGATGGTAC 2449

Qy 2588 TTGTTGCCAAGGAAAATGAGAGATTAGCTATAAGGAGTTCCATTGTTGTTGATTGGAGGAGCAA 2647
Db 2450 ACGTGGCGAAAGAAGATGGAGCGCACAAGGGTTTGAACTGCCACCTTTGATTGGTGGGGCAA 2509

Qy 2648 CCACTTCAAAAACCCACACAGAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCC 2707
Db 2510 CAACGTCTAAAGCGCATACTGCCGGTGAAGATTGAACAGAATTATCATGCGCGTAGTGT 2569

Qy 2708 ATGTCCTGGACGGCGTCCAAGAGTGTGTGGTGTGTCCCAGCTGTTAGATGAAAATCTAA 2767
Db 2570 ACGTGAATAACCGGTCGCGCGCGGTAGGGTGTGCACATCATTATTGTCTGATGAACAGC 2629

Qy 2768 AGGATGAATACTTTGAGGAAAATCATGAGGAAATCATGAGGATGAAGATATTAGACAGGACCATTATG 2827
Db 2630 GCCCCCGGATTATTGACGTTTGGATCTCGAACGTTTATGAGCGCACGCGTGATCAGCATGCTC 2689

Qy 2828 AGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAGAAAAAGTGTTTTCCAAA 2887
Db 2690 GTAAAACGCCCAAATCGCGCCCAGTCAGCTTAGAGCAGGCACGTGTAATAAAGCGGCGC 2749

Qy 2888 TGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCTTATTGGACCCCAGGTCTTTG 2947
Db 2750 TGGATTGGCAAATTACACGCCCGCCCG---CTTCCTGCGAAACCGGGTGTGCATGTGTTTG 2806

Qy 2948 AAGACTATGACCTGCAGAAGCTGGTGACTACTACCATTGACTGAGAAGCCTTCTTTGATGTCT 3007
Db 2807 AAAACATTGCGTTAGCCACACTACGTCCTTATATCGAGTTGACGCCCTTTTTTATGACTT 2866

Qy 3008 GGCAGCTCCGGGGCAAGTCACCCGAATCGAGCGCTTCCCCAAGATATTTAACGACAAAACAG 3067
Db 2867 GGTCGCTTATGGGCAAATA-----------CCCTGCCATTTTGGAGCATGAAGAGG 2911

Qy 3068 TAGGTGAGAGGGCCAGGAAGGTCTACAGATGACGCCCACAAATATGCTGAACACACTGATTA 3127
Db 2912 TCGGTGAAGAGGGCAAACGTCTGTTTCATGAATGCCAATGCCTTACTTGATAAAGTAGAGC 2971

Qy 3128 GTCAAAAGAAGAAACTCCGGGGCCCGGGCGGTGTGGTTGGTTCGTGGCGTGCACAGAGTATCCAAG 3187
Db 2972 GAGAAGGACTACTGAAAGCCAGTGTATGTGCACTGTGTCCAGCAGCCAGCCGCTGGGCG 3031

Qy 3188 ACGACATTCACCTGTACGCGAGAGGCTGCTGCGTGTCGTGTCGTGCCCCAGGCTGCGAGAGCCCACTT 3247
Db 3032 ATGACATTGAGCGTGTACAGTGCTGATGTGAATCGCGCGCA-------TGTGC 3082

Qy 3248 TCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCAGGACCCCATACTACTGCC 3307
Db 3083 TGTACAACTTGCGTCAGCAGACTGAGAA--------ACCGAAAGGGGCCAACTACTGTT 3133

Qy 3308 TCTCAGACTTCATCGTCCTCCCTTGCATTCTGGCATCCGAGTGTCGGCCTGTTTGCCG 3367
Db 3134 TGTTCGGACTATGTTGCTCGCCGGCTAAACGTGCGTGAATTGGGATTGGCGCGTTTGCAG, 3193

Qy 3368 T---TGCCTGCTTTGGGGTAGAGAGAGCTGAGACAGCAAGGCCTATGAGGATGGTGACGACT 3424
Db 3194 TAACTGGTGGCATTGGTGAGCCAGCGCCTTGGCCATGATGCTTATAAAGCTCAGGGTGATGATT 3253

Qy 3425 ACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCAGAAGAGC 3484
Db 3254 ACAATGCGATCATGATCATCCAAGCGGGTAGCCGGCTTGTTTGCGGAAGCCTTTGCGGAAATATC 3313

Qy 3485 TCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCGAGTCGACGTCG 3544
Db 3314 TGCATGAAAAGTGCGTAAAGACAGATTTGGGGTTATGCGGATGAAAATCTCTCCAATG 3373

Qy 3545 CAGACCTGCGAAGGTTGGCGGTACAAGGGCATCCGCCTCCTGGCTGCCTACCCCAGCCAGC 3604
Db 3374 ATGACCTGATCCGTGAGCGTTATCAGGGCATTCGAGGGTATCCGCGGTGTC 3433

Qy 3605 CCGACCACACCGAGGAAGCTCACCATGTGGAGACTCGCAGACATCGAGCAGTCTACAGGCA 3664
Db 3434 CTGAGCCATACCGAGGAAAGCGACTTTGTGGCAGATGCTAAATGTCGAAGGACCATAGGTA 3493

Qy 3665 TTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACTTCT 3724
Db 3494 TGTCACTGACCACAAGCTATGCGATGTGCCGGGCGCTTCGGGTATCCGGTTGGTATTTCT 3553

Qy 3725 CCAATTTGAAGTCCAAATATATTTGCTGTGGGAGAGATTTCCAAGGATCAGGTTGAGGATT 3784
Db 3554 CGCATCCCGATTCTCGCTATTTTGCGGTAGCCGAGATCCAACCAGATCAACTGCACAGCT 3613

Qy 3785 ATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAAATGGCTTGGACCCA 3838
Db 3614 ACCGTGAGCGCTAAAAGGTTGGCGTTTGGAAGAAGCTGAAAAGTGGCTAGCGCCTA 3667

RESULT 12
US-10-282-122A-39570
; Sequence 39570, Application US/10282122A
; Publication No. US2004002912A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 39570
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Salmonella typhi
US-10-282-122A-39570

Query Match      22.1%;    Score 867.2;   DB 7;    Length 3684;
Best Local Similarity 54.4%;  Pred. No. 1.1e-250;
Matches 2028;   Conservative 0;   Mismatches 1598;   Indels 102;   Gaps  10;

Qy    149  GGATTATGGTGCGGATGAGGGACGCCCATGATCCAGCGGCGGAAGCTAAACGAAG   208
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Db     44  GTATTCTGGTGCTGACGCGGCGTATGGCACCATGATCACGAGCTATCGTCTACATGAAG   103

Qy    209  AACACTTCCGAGGTCAGGAATTTAAAGATCATGCCAGGCCCTGAAAGGCAACAATGACA   268
               ||  ||||| ||||  ||||  ||  ||    ||||||  |||||||||||||||
Db    104  AAGATTTCCGCGGAGGAGCGCTTGCCGACTAGCGCCCTGCCGACCTGAAAGGCAACAATGACC   163

Qy    269  TTTTAAGTATAACTCAGCCTGATGTCATTTACCAAATCCATAAGGAATACTTGCTGGCTG   328
              |||||   || |||  ||| || |||  ||  ||||| |||||  |||||||| |||||
Db    164  TGCTGGTCCTCAGCAAGCCGGAGTGCGCGCTATCCACAACGCCTACTTTGAGGCTG   223

Qy    329  GGGCAGATATCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCCAAGCTGACTATG   388
                ||||| ||| |||||||  ||||  |||| |||||| ||| ||||||| |||| ||
Db    224  GCGCGGATATCATCGAACAAACCAACACCTTAACTGCCGATAGTGCCGATTACC   283

Qy    389  GCCTTGAACACTTGGCCTACCGGATGAACATGTCTCTGCAGGAGTGGCCAGAAAAGCTG   448
              ||||||||||||| || |   || ||||| |||  ||| |||| || || |||||| ||
Db    284  GGATGGAATCCCTGTCGGCGGAAATTAACTATGCGCGGCGCCAAACTGGCGCGGCCTGCG   343

Qy    449  CCGGAGGAGTAACTCTCCAGA---CAGGAATTAAGAGGTTTGTGGCAGGGGCTCTGGGTC   505
              ||||| || ||    || ||     |||||  ||||||||||| |||| ||  ||||| |
Db    344  CCGATGAATGGACGGGCGAACACCAGAAAAACCACGCTTTGTTGCGGGCGTGCTTGGTC   403

Qy    506  CGATTAATAAGACACTTCTGTGTCCCCATCTGTGTGAAAGGCCGGATTATAGGAACAATCA   565
             ||   ||||  ||  ||||||||| ||||||| | |||||||||||| || |||||||||
Db    404  CAACTAACCGCACGGCCTCCATTTCGGCCGACGTCAACGACCCGGCGTTTCGTAATATCA   463

Qy    566  CATTTGATGAGCTTGTGTGAAGCATACCAAGAGCAGGCAAAGGACTTCTGGATGGCGGGG   625
               ||| ||||||| |||||| |||||| | ||||| || ||| ||||||  ||||| ||||
Db    464  CCTTCGATCAGCTGGTGGCGGCCTACCGTGGCGGCGAATCCGCAAAGCGCTGGTCGGAAGGCGCGGG   523

Qy    626  TTGATATCTTACTCATTGAAACTATTTTTGATACTGCCAATGCCAAGGCAGCCCTTGTTTG   685
             |||| |  || ||||| ||||| || |||| ||| |||||| |||||| |||||| || ||
Db    524  CGGACCCTGATCGGATTGAAAACTGTCGCGACACCCTCACGCCCAAAGCGGCGGGTGTTTTG   583

Qy    686  CACTCCAAAATCTTTTGAGGAGAAAATGTCCCCCGCCTATCTTTATTCAGGGACGA   745
              || | ||||||||| |||| |||| ||| |||||||| || |   ||| ||| |||
Db    584  CGGTGAAAGAGAGTTTGAAGCGCTGAGCGGCGTTGATCTGCCGATCATGATTCCGGCCACCA   643

Qy    746  TCGTTGATAAAGTGGGCGGACTCTTCCGGACAGACAGGAGAGGGATTTGTCATCAGCGG   805
             ||| || |||||| ||    |||| || ||||||| || || | ||| || |||| ||
Db    644  TCACCGACGCCTCTGGCCGTACGGCTTTCCGGCCGAAGCCTTTTATAACTCGC   703

Qy    806  TGTCTCATGGAGAACCACTCTGCATTGGATTAAAATTGTGCTTTGGGTGCAGCTGAGATGA   865
             ||  |||| || || || || || |  |  |||||||||||  || ||||| ||| |||
Db    704  TGCGCCCACGCCAGGCGGCGCTCACTTTGTCCTTAACTGCCGGCGCTGGGGCCAGAGTGAACTGC   763

Qy    866  GACCTTTTATTGAAAATAATTGAAAAATGTACAAACAGCTTGGTCCTCTGTATCCCAATG   925
             || ||||| || ||| |||| ||| || ||  |   |||| |   |||| |||||||| ||
Db    764  GCCAGTACGTCCAGGAACTGTCGCGGATTGCGCGGAATGCTACGTCACCCGGCACCCGAACG   823

Qy    926  CAGGTCTTCCCACAACACCTTGGTGACTATGATGAAACGCCTTCTATGATGGCCAAGACC   985
              |||  |||||| |||||| || |  || ||||| | ||  || | ||| ||||||  |||
Db    824  CCGGGCCGTGCGGAACGCTTTCGGCGAGTCGAGTACGCCCTTGTGAAGGGCATTGAAA   883

Qy    986  TAAAGGATTTTGCTATGGATGGCTTGGTCAATATAGTTGGTCATATATTGAGGATGCTCAAAC   1045
               || |||| ||| | |||  ||||| ||  | || | |  |||| |   |||||| |||||
Db    884  TTCGGAATGGCGGAAGCGGCGGTTGGGCTTCCTGGTGGTGTAGTACTGACCG   943

Qy   1046  CAGATCATATCAGGGAAAT GCTGAAGCTGTGAAGAAATTGTAAGCCTAGAGTTCCACCTG   1105
                || |  || |||||||  ||| ||||||  |||  ||  |   ||||||| ||| ||
Db    944  CCGAGCGCATATTGCGGCGATGAGCCGCCGGTTGCCGCGCCGGTTTGTCGCCCAGCTGCCGG   1003

Qy   1106  CCACTGCTTTTGAAGGACATATGTTACTGCTGGTCTGGTCAGAGCCCTTCAGGATTGGACCGT   1165
               | |||| |||| ||| |   |   | ||||||||||||| | ||    ||||||||||||
Db   1004  ATATCCCGGTGGCCTGCC------GCCTTTCCGGCCGGAGGCCGGACTAACGTTGCAGGATCAAGGAGTTGACG   1057

Qy   1166  ACACCACTTGTTAACATTGGAGAGCGCTGTAATGTTGCAGGATCAACATTGGTGCTA   1225
               | |  |||  ||| || ||||  |  ||   || |||| || |||||||| ||||
Db   1058  ATAGCCTGTTTGTCAACGTCGGCGAACGTACTAACGTCACCGGCTCGGCCAATTTAAAC   1117

Qy   1226  AACTCATCATGCCAGGAAACTATGAAGAAGCCTTGTTGTGTCGTGCAAAGTGCAGGTGGAAA   1285
                ||||| || | |   ||  |    ||  |||| ||  | | |  |||||||||| || ||
Db   1118  GCTTGATCAAGAAGAGAAATACAGCGAAGCCAAGCCGTGGATGTCGGGCCGTCAGCAGTCGAAA   1177

Qy   1286  TGGGAGCCCAGGTGTTGCAACTAAAGATGATGATGAGCATGCTAGATGGTCCAAGTGCAA   1345
               | || ||||   | || || |||||||| |  |||| ||  | || |  |||||  || ||
Db   1178  GCGGGCGCAGATTATTGATATCAATATGGATGAGGGGGATGTCGACGCCGAGGCCGGCGA   1237

Qy   1346  TGACCAGATTTTGCAACTTAATTGCTTCCGAGCCAGACATCGCAAAGTACCTTTGTTGCA   1405
               ||  || |||||| |||||||| |||| || |||| ||||  | |||| |||||  ||
Db   1238  TGGTGCGTTTCCTGGCCGGTGCCGGTGCGGTGACGGACATGTTCCGGGTTACCACCAATCATGA   1297

Qy   1406  TCGACTCCTCCAATTTTGCTGTGATTGAAAGTGCTGCGCCAAGGGAAGTGCA   1465
             |||| |||| ||| || || | | ||||  |  || |||||||| |||||  ||
Db   1298  TTGACTCCTCCAAATGGGAGGTTTATCCGAAAAGGGCTGAAGTGCATTCAGGGGTAAAGGCA   1357

Qy   1466  TTGTCAATAGCATTAGTCTGAAGGAAGGAGGACAGACTTCTTGGAGAGGCCAGGAAGA   1525
               |||| ||| |||  |||||||| ||||  || ||  ||  || || || || |||||||
Db   1358  TCGTCAACTCTTATTTCGATGAAAGAAGAGAGGCGGTGGAAGCCCTTGTTATTCATGCTCCGGAAGTTGC   1417

Qy   1526  TTAAAAAGTATGGAGCTGCTATGGTGGTCATGGGTCTTTGAAGAGAGAAGAGCAACAG   1585
                |  ||||||||| |||| || |||||||| || | || || || ||  |||||||||
Db   1418  TACGTCGCTACGGCGCCGGCCAGTCGGTGGTGTGTGGGGCCGGACCCGGCAGGCCGACA   1477

Qy   1586  AAACAGACACACAAAATCAGAGTGTCGCACCCGCGCGCTTGTGAAAAAACTGG   1645
             ||  | ||| | ||||  ||    |||||| || |||| || || || ||||||
Db   1478  CCCCGGACGTAAAATCAGATTGGCGCGGCGGAATATCTTCGCGGCAATATCGGCGGTTTCGAAGAGGTAG   1537

Qy   1646  GCTTTAATCCAAATGACATTATTTTGACCTAACCATTGGGACTGGAATGG   1705
             ||||||  ||||| || |  ||  || |||| |||||| | | || |||||
Db   1538  GCTTTCCGCCGAAGACATCATCTTCGCCACCCGAATATCTTCGCCGTCGCCACCGGTATTG   1597

Qy   1706  AGGAACAACAACTTGTATGCCATTAATTTATCATGCAACAAAAGTCATTAAAGAAACAT   1765
                || || || ||||| ||| | |||  ||||||| || ||||||| |||||||| ||
Db   1598  AAGAGCAACAACTACGCCAGGACTTTATCGCGCCGTTGTGTGCAATATCAAAGCGCGAGC   1657

Qy   1766  TACCTGGAGCCAGAAGTGGAGGCTCTTTTATTCAGGGACGA   1825
             |||||| ||||| |||| || ||||   | || ||| ||||
Db   1658  TGCCGCACGCGGTGATCCTCGGCGGTGTCAACGTGTCCTTCTCGTTTCGCGGCAACG   1717

Qy   1826  AAGCCATTGAGAAGCAATGCATGGGGGATTTGTCATCAGCGG   1885
              || ||||| |||||||| |||||  || ||||| ||| ||||
Db   1718  ACCCGGTACGTGAGGCTATCCACGCGGGTATTCCTCACTACGCCATCCGCAACGCCATGG   1777

Qy   1886  ACATGGAGATAGTGAATGCTGAAACCTCCCTGTTGTAGTGCAGCTGAGATGA   1945
             |||||| || |  || || |||  | ||| || | || | | |||||| |||
Db   1778  ACATGGGCATCGTCAACGCGTCCAACGGCCCGGGCGATTTATGACACCTGCTGCTGGTG   1837

Qy   1946  TGCAGCTCGTGTGAAGATCTCATCTGGAATAAAGACCCGTGAGCCACTGAGAAGCTCTTAC   2005
              | ||| |||| |||| ||||| || | || ||||| || |||  | | ||||||  ||||
Db   1838  GCGATGCAGTTGAAGATGTCATTCTTAACCGTCGCGATGACCGCACCGAGGCGTTTGCTGG   1897

Qy   2006  GTTATGCCCAGACTCAAGGCACCAAGGCACACAGGAGGAAGAGTCATT---------CAGACTGATG   2056
                | |||| ||| |||    |  || |  ||| || ||| || || ||||         ||| || ||
Db   1898  ATTTGGCGGGAGAAATATCGCGGCGCAAAACCGAGGCTGCCAGTGCCAGCAGGCGGAAACG   1957

Qy   2057  AGTGGAGAAATGCCCCTGTGAAGAACAGCCTTGTGAGTATGCCCTTGTGAAGGGCATTGAAA   2116
             || || ||||| ||||| ||||||  ||   || | | | |||| ||   |||| |  |||
Db   1958  AATGGGAGCTGGGACGTCACGCCTCTCAACGCGTCTCGAATACTGACCGGTGGTAAAGGCATTACCG   2017

Qy   2117  AACATATTATTGAGGATTACTGAGGAGCAGGTTAAACCAAAAAATATCCCGACCTC   2176
                |   ||  || || |   | || || ||  ||        || |||   |||||
Db   2018  AGTTTATCGAACAGGATACCGAAGAGCC--------CGTCAGCAGGCCGGACATCCAGAGCTGCCGG   2068
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Qy   2177  TCAATATAATTGAAGGACCCCTGATGAATGAAGAATTGTTGGTGATCTTTTTGGAG  2236
           |||||||  | |||||||||||| || |||||||  |||||| |||  ||||||||
Db   2069  TTGAGGTGATTGAAGGGCCGCTGATGACGGAGGGCCATGAACGTGGTCGGCGACCTGTCGTTCGGCGCG  2128

Qy   2237  CTGGAAAAATGTTTCTACCTCAGGTATAAAGTCAGCCCGGGTTATGAAGAAGGCTGTTG  2296
           |||      ||||   |||||||||  |||||||||||||||||
Db   2129  AAGGGAAAAATGTTCCTGCGCGATGGCTGCGTGGTGAAATCCGCTCGCGTGATGAAACAAGCGTGG  2188

Qy   2297  GCCACCTTATCCCTTTCATGGAAAGAAGAAGAGAAACCAGAGTGCTTAACGGCACAG  2356
           ||||
Db   2189  CCTACCTGGAGCCGTTTTATTGAAGCCAGCAAAGAAAA--------------  2226

Qy   2357  TAGAAGAAGAGACCCTTACCAGGGCACCATCGTCGGCCACTGTTAAAGGGACGTGC  2416
           ||||||||  |||  ||||||||||| ||||
Db   2227  -------GGCTCCAGCAACGGCAAGATGGTGATTGCCACCGTGCCACCGTGAAGGGCGGATGTGC  2275

Qy   2417  ACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCCGAGTTATTG  2476
           ||||||| ||||||||||  ||  ||  || ||||  ||||
Db   2276  ACGACATTGGCAAGAACATTGTCTCGCGTGCGTGGTGCTGCTGGAGAGCTGTCTCTTGATGA  2335

Qy   2477  ATTTAGGAGTCATGACTCCGTCATGTGATAAGAATCGAAAGCTGCTCTTGACCACAAAGCAG  2536
           |||  |||||||||||  | ||| |||  |||
Db   2336  ATCTTTGGCGTGATGGTGCCAGCGGAGAAAATCCTCAGACGGCGTGAAGTGAATGCCG  2395

Qy   2537  ATATAATTGGCCTGTCAGGACTTCATCACTCCTTCCCTGGATGAAATGATTTTTGTTGCCA  2596
           ||||  || |||||  ||  |||   |||||
Db   2396  ATCTGAATTGGTCTTTCCGGGCTTATCACCCCGCTCGGACGAAAATGTCAACGTGGCGCA  2455

Qy   2597  AGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAA  2656
           |||||||||||||||||||| |||||||
Db   2456  AAGAGATGGAGCGTCAGGGCTTTACTATCCGAGCGGCGGCGCCAACCACTTCGA  2515

Qy   2657  AAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTACGTCCGAGATACAGTAC  2716
           ||||||||||||||  |||||||| |||| |||||| || ||
Db   2516  AAGCGCATACACGGCGGGTGAAAATCGAGCAGAACTACAGCGGTCACGGTCACGTCAGA  2575

Qy   2717  ACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTAGATGAAAATCTAAAGGATGAAT  2776
           |||  |||| ||||||||||||||||||||||    |||
Db   2576  ATGCTTCGCGTACCGGTGGTGTGGTGGGCGTACTCTCCGACACCCCAGCGTGATGACT  2635

Qy   2777  ACTTTGAGGAAATCATGACAGAGAATATGAAGAATAGACAGGACCCATTATGAGTCTCTCA  2836
           ||||  ||||| |||||| |||||||||| |||| |||
Db   2636  TTGTCGCCCGTACCGGCAAAGAGTACGCGAAACCGTGCTATTCAGCACGCCCAAAAAAC  2695

Qy   2837  AGGAGAGAGAGATACTTACCCCTTAAGTCAAGCCAGAAAAAGTGGTTCCAAATGGATTGGC  2896
           |||||||||  |||  ||||   |||||  || ||| || | |||||||| | |||||||||
Db   2696  CCGCACGCCGGGCGCGCCGGTCACGCTGGAAGCCGCGGCGCGGATAATGATCTGGCATTTGATTGGG  2755

Qy   2897  TGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCCAGGTCTTGAAGACTATG  2956
           || |||   ||||||| |||||||| ||| |||||||||  |||||||| ||||||
Db   2756  AACGCTACACCCCGCCGTAGCCGTCTCGGGCGTGCAGGAGGT----GGAAGCCA  2809

Qy   2957  ACCTGCAGAAGCTGGTGACTACATTGACTGAAGCCTTTCTTCTGATGTCTGGCAGCTCC  3016
           || |||| ||||  || ||
Db   2810  GCATCAGAAACGCTGCGCAACTACATCGACTGGACGCGCCGTTCTTTATGACCTGCTGCTGG  2869

Qy   3017  GGGGCAGTACCCGAACTCGAGCGTTCCCAAGCAATATTTAACGACAAAACAGAGGTGGAG  3076
           |||   ||||
Db   2870  CCGGCAAATACCCG--------------CGCATTCTGGAAGATGAGGTGGTTGGGCGTTG  2914

Qy   3077  AGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACACTGATTAGTCAAAAGA  3136
           |||||  || ||   ||  ||| |||| |||||  || | ||||||
Db   2915  AGGCCGCGAGCGTCTGTCTTAAAGACGGCCAATGATATCGGATAAACTGACGCGCCGAGAAAC  2974

Qy   3137  AACTCCCGGGCCCCGGGCGTGGGTTGCTGGTTCTGGCCAGCACAGAGTATCCAAGACGACATTC  3196
           ||     |||   |||   ||||||| |||||||||||
Db   2975  TGTTGAATCCGCGCTGGCGGTGGCGGCCTGTTCCCGGCGGAACCGTGTCGGGTGACGACATCG  3034

Qy   3197  ACCTGTACGACAGGCTGCTGTCGTGCCCCAGGCTGCAGAGCCCCATAGCCACTTTCTATGGGT  3256
           ||  | | |||      ||  ||
Db   3035  AAATCTATCGCGACGAAACCCGTACTCATGTTCTGACGGTCA-------GCCACCACC  3085

Qy   3257  TAAGGCAACAGGCTGAGAAGGACTCTGCCAGCAGGACTCTGCCGACGACGGAGCCCATACTACTGCCTCTCAGACT  3316
           ||||
Db   3086  TGCCAGCAGACCGAGACCGAGAAAGTTGGTTTGCTA--------ACTACTGCTCGGCGGATT  3136

Qy   3317  TCATCGCTCCCTTGCATTCTGGCATCCGTCGGCATTGAGCAGTGAC  3375
           |  ||    ||||||| |||||||||||
Db   3137  TTGTCGCGGCCGAAACTGAGCGGCAAAGCGGACTACATCGTGCTTCGCGGTGGTGACCGCGCG  3196

Qy   3376  --TTTGGGTAGAAGACTGAGCGAGTGACGCCTATGGAGCAAGGCC  3433
           ||||||||||||||  ||  | || || |||||||||||||||||||
Db   3197  GTCTGAAGGAGGATGCGCTGGCCGACGCCTTCGAAGCCGCTTGGAAGTTTCGAAGAAGAGTTCCATGAAA  3256

Qy   3434  TCATGGTCAAGGCCTGGGGGAGCCGGGCTGGCAGGACGTGGGGAGAGAGCTCCATGAAA  3493
           |||||| |||| |||  |||||||| |||||  || |||||| | ||||| |||| | |||
Db   3257  TCATGGTGAAAGCGATTGCCAACCGGTCTGGCGGAAGCGTTTGCCGAGTATCTGCATGAGC  3316

Qy   3494  GAGTTCGCCGAGAACTGTGTGGGCCTACTGTGGCAGCAGTGACGCTGCAGACCTGC  3553
           ||||||  |||||| || | ||||  || |||||| |||||  ||||||||||
Db   3317  GTGTACGTAAGGTTACTGGGGATATGCGCCCGGGCCTGGGTACCACCCGACCACCA  3376

Qy   3554  GAAGGTTGCGGTACAAGGCATCCGCCCGGCTCCTGCTACCCCAGCCAGCCACCA  3613
           ||||     ||    ||||    |||||||||||||||||| | ||  |||  ||
Db   3377  TCCGGGAAAACTACCAGGGGATTCGCCCGGCCGGGGTTATCCTCGCTGCTGGAACATA  3436

Qy   3614  CCGAGAAGCTCACCATGTGGAGACTCGCAGACATGCAGCGTCTACAGGCATTAGGTAA  3673
           || || |||    |||||||  |||||||| ||||||  ||  ||| ||||||||
Db   3437  CCGAAAAAGGCACTATCTGGCAGTACTGGATGTGAAAAACACACCGGATGAAGCTCA  3496

Qy   3674  CAGAATCATTAGACAATGCAATGGCACCTGCTTCAGCTGGCGCCTTCAGCCATCCTG  3733
           ||  ||  | |||   ||  ||| |   ||| ||| ||   |||||| ||||
Db   3497  CCGAATCTTCGGCCATGGCCATGGCGGGCGTTGGTGGTACTTCAGCCATCCTG  3556

Qy   3734  AGTCCAAATATTTGCTGTGTGGGAGAAGATTTCAAGGATCAGGTTGAGGATTATGCATTGA  3793
           || | ||  ||| |||||  | | || |||  ||    | |||  || || |||  || |
Db   3557  AGAGCAAATACTTCGCGTGTAGCCGATCCAACGCGATCAGGTGACAGATTATGCTTTCC  3616

Qy   3794  GGAAGAACATATCTGTGGCTGGAGGTTGAGAAATGGCTTGGAAATATGGGGATATGATA  3853
           || |  |||||| | |  |  || ||  ||||| || |||  |||||||||||
Db   3617  GTAAAGGAATGAGCGTTGAGCGGTGAGCTTGGGCTGCGGCGCCGAACCTGGGTTACGATG  3676

Qy   3854  CAGACTAA  3861
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RESULT 13
US-10-282-122A-24011
; Sequence 24011, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, Liangsu
;   APPLICANT: Zamudio, Carlos
;   APPLICANT: Malone, Cheryl
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Kari
;   APPLICANT: Zyskind, Judith
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John
;   APPLICANT: Carr, Grant
;   APPLICANT: Yamamoto, Robert
;   APPLICANT: Forsyth, R.
;   APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR APPLICATION FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06

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;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24011
;  LENGTH: 3681
;  TYPE: DNA
;  ORGANISM: Klebsiella pneumoniae
US-10-282-122A-24011

Query Match             21.9%;  Score 859;  DB 7;  Length 3681;
Best Local Similarity   54.4%;  Pred. No. 3 4e-248;
Matches 2028;  Conservative  0;  Mismatches 1595;  Indels 102;  Gaps  11;
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Qy      149 GGATTATGGTGCTGGATGGGAGCTGGATGGGGACCCATGATCCAGCGGGAGAAGCTAAACGAAG 208
                | |||||||| || || ||||||||| |||||||||  |  |||||||
Db       44 GTATTCTGGTTCTGATGGGGGCATGGGCATGGGCACCCATGATCATCGTCTGAGTGAGC 103

Qy      209 AACACTTCCGAGGTCAGGAATTTAAAGATCATGCCAGGCCGCTGAAAGGCAACAATGACA 268
                 | |||||  ||| ||||  ||| ||||
Db      104 AGGACTTTCGCGGTGAGCCTTGCTACTGGCCGTGCCGTGCGAACCTGAAAGGCAACAACGACC 163

Qy      269 TTTTAAGTATAACTCAGCCTGATGTCATTTACCAAATCCATAAGGAAATACTTGCTGGCTG 328
                | |||  |||
Db      164 TGCTGGTGCTCAGCAAACCCGAAGTGATCCCGGAGATCCACGACGCTATTTCGAGGCCG 223

Qy      329 GGGCAGCAGATATCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCCAGTCGACTATG 388
                |||||| ||||| | |   ||  ||
Db      224 GCGCCGGATATCATTGAGACACCTTTAACTCACGACCATCGCGATGGCGGATTACC 283

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                |||||||| |||||| ||||    |  || ||
Db      284 AGATGGAATCCCGTCGGCCGAGATCAACTTGCCGGCCGAGAGCTGGCCCGCGGGCCAGCG 343

Qy      446 CTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGAGGTTTGTGCAGGGGCTCTTGGGTC 505
                |||||| ||||  ||  | ||| ||| | |
Db      344 CCGACGCCTGGACGCCCGCACGCCGGGAAAAACCGGCCTATGTTCGGCGGGGCTGCTTGGCC 403

Qy      506 CGACTAATAAGACACTTCTCTGTGTCCCCATCTGTGGAAAGGCCGGATTATAGGAACAATCA 565
                |  ||  |||| |||| | |||||
Db      404 CGACCAACCGCACCGCCTCTATCTCGCCTGATGTGAACGATCCGGGCGTTCCGTAATATTA 463

Qy      566 CATTTGATGAGCTTGTTGAACAGCATACCAAGAGCAGGCCAAAGACTTCTGATGGCGGGG 625
                ||||||| |   ||| ||  ||
Db      464 CCTTTGACCAGCTGGTGGTCCGCCTATCGCGGAATCCACCCGGGCGCGTGGTGAAGGCGGGCG 523

Qy      626 TTGATATCTTACTCATTGAAACTATTTTTGATACTGCCAAGGCCAGCCTTGTTTG 685
                ||  | |  ||  ||  ||
Db      524 TGGATCTGATCGAATGAAACGTGTTTGACACCCGTGACCGCTAAAGCCGCCATCTATG 583

Qy      686 CACTCCAAAATCTTTTTGAGGAGAAAATGCTCCCCGGCCTATCTTATTCAGGGACGA 745
                 ||| |||| | |  | ||  |
Db      584 CGGTGAAAGAGGAGGCTGGAGGCGTTAGGCGTTGACCTGGCGTTGACCTGTTCCGGGACCA 643

Qy      746 TCGTTGATAAAGTGGGCGGACTCTTTCCGGACAGACAGAGGATTTGTCATCAGCG 805
                | |||  ||| || |    |   |
Db      644 TTACCGATGCCTCTCGGCCGCACGCGCTTTCCGGACAGACAGAGCCTTTTATAACTCGC 703

Qy      806 TGTCTTCATGGAGCAACCACTCTGCATTGGATTTAAATTTGTGCTTTGGGTGCAGCTGAGATGA 865
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Db      704 TGCGTCACGCCGAAGCCTTATCGTTTGGTTCTGAACTGGACGGGCGCCGGGCCGGGACGAGGAGCTGC 763
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Qy      866 GACCTTTTATTGAACATTGGAGAGCGCTATGTCCTCTGTTATCCCAATG 925
                || ||   || | |  ||    |  |||
Db      764 GGCAGTACGTCCAGGAGCTCCAGGAGCGTGCGCCATTGCCGAATGCTACGTCGCCGAACGACG 823

Qy      926 CAGGTCTTCCCACACCTTTGTGACTATGATGAAACGCCTTCTATGATGGCCAAGCACC 985
                  |||||  |||||||| | ||
Db      824 CCGGCCTGCCCAACGCTTTCGGCGAATACGATCTGGACGCCGCAGACCATGGCGACGCAAA 883

Qy      986 TAAAGGATTTGCTATGGATGGCTTGGTCAATATAGTTGGAGGATGCTGTGGGTCAACAC 1045
                ||    ||| |||   ||  || || |  |  || |  |
Db      884 TTCCGGAATGGGCGGCGGAGCCGGTTTCCTCAATATCGTCGGCGGCTGCTGCGCGGTACCACCC 943

Qy     1046 CAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCCACTG 1105
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Db      944 CCGGAGCATATCCGCCATGAGCCGGGCGGTAGCGGCGCTCGCGCCGCGTCAGTTGCCGG 1003

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Db     1004 AAATTGCGGTGGCCTGCGC------CTCGCCGGCCTGGAGCCGTTGAATATCGGCGACG 1057

Qy     1166 ACACCAACTTGTTAACATTGGAGAGCGCTGTAATGTTGCAGGATCAAGGAAGTTTGCTA 1225
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Qy     1226 AACTCATCATGGCAGCAAACTATGAAGAGAGCCTTGTGTGTTGCCAAAGTGCAGGTGAAA 1285
                ||||| ||||| |   || ||  ||     |||  || | || || ||  |||| ||||
Db     1118 GGCTGATTAAAGAAGAGAGATTCACAGCGGAGGCCGGGCGTTGCGCGTCAGCAGGTGGAA 1177

Qy     1286 TGGGAGCCCAGGTGTTGGATGTCAACATGGCATGCATGCTAGTAGTGTCCAAGTGCAA 1345
                | ||    |||| | ||  | | |  | ||
Db     1178 GCGGCGCCAGATTATCGTATCAACATGGACGAGGGGATGCTCGACGCGAAGCGGCGA 1237

Qy     1346 TGACCAGATTTTGCAACTAAATTGCTTCCGAGCCAGCATCGCAAAGTACCTTTGTGCA 1405
                ||  |  ||   |||   ||  || ||| ||
Db     1238 TGGTGCGTTTCCTTAACCTGATTGCCCGGCCGAGCGAGCCCGTCGCCACGCCTATTTCGAGGCCG 1297

Qy     1406 TCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCA 1465
                | ||||  |||||  |  | |   | ||  ||
Db     1298 TTGACTCCTCCAAGTGGAAGTCATTGAAAAGGCCTGAAATGTATTCAGGGCAAAGGCA 1357

Qy     1466 TTGTCAATAGCATTAGTCTGAAGGAAGGCACTTCTTGGAGAAGGCCAGGAAGA 1525
                ||||||| | ||  |   || |||  |
Db     1358 TCGTTAACTCGATTTCGATGAAGAAAGAGGGCGTCGAATCCTTTATCCACCATGCGAAACTCG 1417

Qy     1526 TTAAAAGTATGGAGCTGCTATGGTGTCATGGTCTTTGATGAAGAAGGACAGGCAACAG 1585
                ||  | |  ||  |  | ||   ||   ||
Db     1418 TTCGCCGCTACCGCGCCGGTTGTGCAGGTGGTGGTCTCAGGCCGACA 1477

Qy     1586 AAACAGACACAAAAAATCAGAGTGTGCACCCGGCTGTGACTCGCTTGTGAAAAAACTGG 1645
                ||  ||||||| |    | ||||
Db     1478 CCCGGCGACGTAAAATTGAGATTTGCGTCGGCGGCCTACCGCTTACAAAATCCTGAGAGAGGTCG 1537

Qy     1646 GCTTTAATCCAAATGACATTATTTTTGACCCTAATATCCTAACCATTGGGACTGGATGG 1705
                ||| |  ||    | || | ||
Db     1538 GCTTTCCCGCGGAAGATACCAATATCTTTGCGCATCACTACTACGGCATGG 1597

Qy     1706 AGGAACAACTTGTATGCCATTAATTTTATCCATGCAACAAAGTCATTAAAGAAACAT 1765
                 |||| |  ||   |  ||  ||| |  |  |||
Db     1598 AAGAGACATAACAACTACGCACAGGACTTTATCGGCGAAGACATCAAACGCGAGAGC 1657

Qy     1766 TACCTGGAGCCAGAATAAGTGGAGTCTTTCCAACTTGTCCTTCTCCGAGGAATGG 1825
                 | ||| |  || |||  ||||| |  |  | ||
Db     1658 TGCCGCATGCGAATCTCCGCGGGGTCTCCAACGGTTAATCTCCTTCTCCGCGGTAATG 1717

Qy     1826 AAGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTTACCATGCAATCAAGTCTGGCATGG 1885
                ||||  | |  ||   ||
Db     1718 ACCCGGTACGTGAGGGCGATCCACGCGGATTCCTACTACCGGATCCGCAACGCGCATGG 1777

Qy     1886 ACATGAGAGTAGTGAATGCTGTGAAACCTCCCGTGTGTATGATAATCCATAAGGAACTTC 1945
                ||||| | |  | ||| || |  ||   | | |||
Db     1778 ACATGGGGATCGTCACGCCCGTCAGCTGCCATCATGATGAACGTCCCGGGCGCGAGCTGC 1837

Qy     1946 TGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCCTGAGGCCACTGAGAAGCTCTTAC 2005
                ||||| || |  ||| ||    ||||| |  |
Db     1946 TGCGTCACGCCGAAGCCTTATCGTTTGGTTCTGAACTGGACGGGCGCCGGGCCGGGACGAGGAGCTGC 1946
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Qy 1838 GCGACGCGGTCGAAGACGTGATCCTCAACCGCGCGATGACAGTACCGAACGGTTACTTG 1897
Db

Qy 2006 GTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAGTCATTCAGACTGAT-------G 2056
Db 1898 AGCTGGCGGGAAAAATATCGCGGGACGCAGCAGACGGCGGCGAATGCCCAGCAGGCGG 1957

Qy 2057 AGTGGAGAAATGGCCCTGTCGAAGAACGCGCCTTGAGTATGCCCTTGTGAAGGCATTGAAA 2116
Db 1958 AGTGGGCCACCTGGGAAGTGAAAAAACGCCTCGAATATTCGCTGGTTAAGGGCATTACCG 2017

Qy 2117 AACATATTATTGACGATTACTGAGGAAGCCAGGTTAAACATTAAACCAAAAAAAATATCCCGACCTC 2176
Db 2018 AATTTATCGAACAGGACACCGAAGAGAGC-------GCGTCAGCAGGCCGCCGCCCGA 2068

Qy 2177 TCAATATAATTGAAGAGACCCCTGATGAATGGAATGAAAATTGTTGGTGATCTTTTTGGAG 2236
Db 2069 TTGAGGTCATTGAAGGGCCGCGCTGATGGACGCGGCATGCGGCCGGATCTGTTCGGCGG 2128

Qy 2237 CTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGTTATGAGAGGCGTGTTG 2296
Db 2129 AAGGCAAAATGTTCCTGCGCAGGTGGTGAAATCCGCCGGTGTAATGAAACAGGCCGTGG 2188

Qy 2297 GCCACCTTATCCCTTTCATGGAAAAAAGAAGAGAAACCAGAGTGCTTAACGGCACAG 2356
Db 2189 CCTACCTTGAGCCGTTTATTGAAGCCAGTA-------- 2218

Qy 2357 TAGAAGAAGAGACCCCTTACCAGGGCACCATCGTGTCGGCCACTGTTAAAGGCGACGTGC 2416
Db 2219 ---AAGAGCAGGGCTCCAGTAACGGCAAAATGGTGATTGCCACGGTAAAAGGCGACGTTC 2275

Qy 2417 ACGACATAGGCAAGAACATAGTTGAGTAGTCCTTGGCTGCAATATTTCCGAGTTATTG 2476
Db 2276 ATGACATTGGCAAAAACATCGTCGGGCGTGGTGCTGCGTCGCAGTGCAATAACTACGGAAATCATCG 2335

Qy 2477 ATTTAGGAGTCATGCATGTGATGATAAGATACTGAAAGCTGTCTTGACCACCAAAGCAG 2536
Db 2336 ATCTTCGGCGTGATGGTCCCGGCGGATAAAATTCTCAAAAACGGCCAAAGAGGTAAACGGCGG 2395

Qy 2537 ATATAATTGGCCTGTCAGGACTCATCATCCTCCTTCCCGGATGAAATGATTTTGTTGTCCA 2596
Db 2396 ATCTAATTGGTCTTCTTCCGGCTGATTACCCCCATCGCTGGACCAGATGGTTAATGTGGCGA 2455

Qy 2597 AGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAA 2656
Db 2456 AAGAGATGGAGCGGCCCAGGCGCTTTACCATCCCCGCTGCTGATAGGCGGCGGCGACCACCTCGA 2515

Qy 2657 AAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCCACCTGTAATCCATCATGCCTCTGG 2716
Db 2516 AAGCGCATAACGGCGGGTGAAAATCGAGCAGAACTACAGCGCCCCACCGTTTACGTACAGA 2575

Qy 2717 ACGGGTCCAAGAGTGGTGTGTGTTCCCAGCTGTTTGATGATGAGATCTAAAGGATGAAT 2776
Db 2576 ACGCCCTCGCGGCACCGTCGGTGTCGTGCTTCTCGCGGACCAGCCGCCGACCAGT 2635

Qy 2777 ACTTTGAGGAAATCATGCAAGAAATATGAAGATATTGAGACAGGACCCATTATGAGTCTCTCA 2836
Db 2636 TTGTGCGCCCGGCACGCGCAAAGTGATCCGGCCCAAATGGGCGTATCCGCATCGGGGTAAAAAAC 2695

Qy 2837 AGGAGAGGAGAGAGATACTTACCCTTAAGTCAAGCCAGCCAGAGAATAGTCGTTTCCAAATGGATTGGC 2896
Db 2696 CGGCGTACGCGCCGGTGACCCGGTCTATTGCCGCGGAAGCCCCACGTTATTGGGACCCAGTCTCTGG 2755

Qy 2897 TGTCTGAACCTGACCTCACCCGGCGCCGGTGG----CTCATCGTCTCGGGAGTACAGACGGTGAAGCCAGT 2956
Db 2756 AGAGCTACACGCCGCCGGTGGACTGGACCATTGACTGACGCCGTTCTTCATGACCTGGTCGCTGG 2811

Qy 2957 ACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCCTTTCTTTGATGTGTCTGGCAGCTCC 3016
Db 2812 ATC--GAGACTCTGCGCAACTACATCGACTGGACGCCGTTCTTCATGACCTGGTCGCTGTGG 2869

Qy 3017 GGGGCAAGTACCCGAATCGAATCGAGGCTTCCCCAAGATATTAACGACAAAAACAGTAGGTGGAG 3076

Db 2870 CGGGTAAATATCCG-----------CGCATTCTGGAAGATGAAGATGTGGTAGGGGAAG 2914

Qy 3077 AGGCCACGGAAGGTTCTACGATGATGCCCACAATATGCGTGAACACACTGATTAGTCAAAAGA 3136
Db 2915 AGGCGCAGCGCGCCTGTTCAAAGACGTAACGAGCTGCTGGATAAGCTTAGCGCAGAGAAAA 2974

Qy 3137 AACTCCCGGGCCCGGGTGTGGTTCTGGCACAGAGTATCCAAGACGACATTC 3196
Db 2975 CCCTGAACCCGCGCGCGGGTCGGTCGTTCCCGGCCAACCGCGTGGGCGACGATATTG 3034

Qy 3197 ACCTGTACGCAGAGCGTGCTGTGTGCCCAGGCTGCAGAGCTGCAGAGGCCCATAGCCACTTTCTATGGGT 3256
Db 3035 AAATCTATCGCGGATGAAACCCGCACCCACG-----TGCTGACGGTGAGCCATCATC 3085

Qy 3257 TAAGGCAACAGAGGACTCTGAGAAGGAACTGCTGCCAGCACGGAGCCATACTACTGCCTCTCAGACT 3316
Db 3086 TGCGGCCAGCAGACGGAGCAGAAGGTTGGCTTGCCA--------ACTACTGTCTCGCCGATT 3136

Qy 3317 TCATCGCTGCCCTTGCATTCTGGCATCCGGACTACCTGGCCTGTTGCCGTTGCCTGCT 3376
Db 3137 TTGTCGGCCGGAAGCTGAGCGGCAAGGCGGCAATCGCGGCCGTCGCCGTGACCGGCG 3196

Qy 3377 TTGGGGTAGAGA---GCTGAGGCAAGGCCTATGAGATGATGAGGTGACGACTACAGCAGCA 3433
Db 3197 GCCTGGAAGAGGAGGACGCGCTGGCGACGCCTATGAGGCCAGCATGATGACTATAACAAGA 3256

Qy 3434 TCATGGTTCAAGGGCGTCGGGGGACCGGCTGGCAGTGTTGCAGAGAGAGCTCCATGAAA 3493
Db 3257 TCATGATTAAAGCCATGCGCCTGGCGCCTGGGAGGCCTTTGCCGGTATCTGCATGAGA 3316

Qy 3494 GAGTTCGCGCAGAACTGTGGGCCTACTGTGGGCAGTGGACGTGCAGACCTGC 3553
Db 3317 AAGTGCGCAAGGTTTACTGGGATATGCCGGCCAATGCGGCGTTCAGCAATGAGGAGCTTA 3376

Qy 3554 GAAGGTTGCGGTACAAGGGCATCGGGGCTCCTGCGTACCCCGGCCAGCCGACCACCA 3613
Db 3377 TTCGCGGAAACTACCAGGGGATCCGACACGGCGCGGGGATATCCGGCGTCCGGGAGCACA 3436

Qy 3614 CCGAGAAGCTCCACCATGTGGCTGAGAGACTCGAGCAGTCGGCATCGAGCGGCATGATTAGGTTAA 3673
Db 3437 CCGAAAAGGGGACCATCTGGACGACTGGAGCTACTGGGACGTCGAAGCGCATGAAGCTCA 3496

Qy 3674 CAGAATCATTAGGACAATGCAAATGGCACCTGCTTCAGCGTCAGTCGTTCTCCAATTTGA 3733
Db 3497 CCGAGTCTTTGCGCCATGTGGCCAGGCGCCATCGGTTCCGGCTGGTACTTCAGCCATCCGG 3556

Qy 3734 AGTCCAAATATTTTGCTGTGCGGGGAAGATTTCAAGGATCAGGTTGAGGATTATGCATTGA 3793
Db 3557 ACAGTAAGTACTTCGGCGTGCCGGTCAGATCAGGCGGATCAGGTTCGAAGATTACGGCGTGC 3616

Qy 3794 GGAAGAACATATCGTCGGCTGAGGTTGAGAAATGGCTTGACCCCATTTTGGGATATGATA 3853
Db 3617 GTAAAGGAATAGACGCCGGCGGAGGTCGCAGCGCGCTGGTTAGCGCCTATGCTATGATG 3676

Qy 3854 CAGAC 3858
Db 3677 CGGAC 3681

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;  APPLICANT: Yamamoto, Robert
;  APPLICANT: Forsyth, R.
;  APPLICANT: Xu, H.
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;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 38912
;  LENGTH: 3771
;  TYPE: DNA
;  ORGANISM: Salmonella typhimurium
US-10-282-122A-38912

Query Match             21.9%;  Score 857.6;  DB 7;  Length 3771;
Best Local Similarity   54.2%;  Pred. No. 9.2e-248;
Matches 2022;  Conservative    0;  Mismatches 1604;  Indels 102;  Gaps  10;

Qy    149 GGATTATGGTCCTGGATGAGGGGATGGGGACCATGATCCAGCGGGAGAAGCTAAACGAAG 208
              |||| ||| ||||  ||||| | ||||||||| ||  |||||||||||||||
Db    131 GTATTCTCGGTGCTGACACGGCGTATGGGCACTATGATCCAGAGAGCTATCGTCTACATGGAAG 190

Qy    209 AACACTTCCGAGGTCAGGAATTAAAGATCATCATGCCAGGCCGCTGAAAGGCAACAATGACA 268
              |||||||| ||||  |  |||||||||  ||||||
Db    191 AAGATTTCCGCGGGGACGCGTTTGCCGACTGGCCCTGCCCTCGCCGAAAGGCAACAATGACC 250

Qy    269 TTTTAAGTATAACTCAGCCTGATGTCATTTACCAAATCCATAAGGAATACTTGCTGGCTG 328
                |    |  ||| | |||| ||||||||
Db    251 TGCTGGTCCTCAGCAAGCCGGAGGTGATCGCCGCTATCGACAACACGCGCTACTTTGAGGCTG 310

Qy    329 GGGCAGATATCATCGAAACAAATACTTTTAGCAGCACTAGTATTGCCCCAAGCTGACTATG 388
              |||  ||| |   ||| |||||||||
Db    311 GCGCGGATATCATCGAAACACACCTTAACTCGACAACACCTTAACTGCGATGGCGGATTACC 370

Qy    389 GCCTTGAACACTTGGGCTACCGGATGAACAATGTGCTCTCGCAGGAGTGGCCAGAAAAGCTG 448
                 ||||||   |     |  | ||| |
Db    371 GGATGGAATCCCTGTCCGGCGGAGGTGATCGCGCTATCCGCAAAACTAACTAATGCGGCGG 430

Qy    449 CCGAGGAGGTAACTCTCCAGA---CAGGAATTAAGAGGTTTGTGGCCAGGGGGCTCTGGGTC 505
              |||       ||||||          |||| | ||
Db    431 CCGATGAATGGACGGCGCGACCCGACGGCGGAAAAAACCACGCTTTGTTGTCGGGGCGTTGGTC 490

Qy    506 CGACTAATAAGAGACACTTCTGTCCCCATCTGTGGAAAGGCCGGATTATAGGAACATCA 565
              |||   | | | ||||  ||||||||| |||
Db    491 CAACTAACCGCCACGGCCCTCCATTTCGCCGACGTCAACGACCCCGGCGTTTCGTAATATCA 550

Qy    566 CATTTGATGAGCTTGTTGAAGCATACCAAGAACAGGACCAAAGGACTTCTGATGGCGGGGG 625
                 |    | |  || |||  | ||||||||| | | |||||
Db    551 CCTTCGATCAGCTGGTTGGCGGCCTACCACCAAAAGCGCTGGTGGTGAAGGTGGGCG 610

Qy    626 TTGATATCTTACTCATTGAAACTATTTTTGATACTGCCAATGCCAAGGCAGCGCCTGTTTG 685
              |||  |||  | ||||||  | | |||||||
Db    611 CAGATCCTGATTCGATTGAGACGCCGTTTTTGACACCCTGAATGCGGCCTATCTTTATTCAGGACGA 670

Qy    686 CACTCCAAAATCTTTTGAGGAGAAAATATGCTCCGGGCCCTATCTTTATTCAGGTGAAA 745
              |||    ||| |||||||||||  |||||||||
Db    671 CCGTGAAAGAAGAGTTTGAAGCGCTGGGCGTTGAACCTGGCGTTGACCTCATCGATTCCGCCACCA 730

Qy    746 TCGTTGATAAAAGTGGGCGGACTCTTCCGGACAGAGAGGATTGTCATCAGCG 805
              |  ||||   |||| ||| || || ||    |  | |||||||
Db    731 TCACCGACGCGCTCTGGCCGTACGCCTTTCCGGCCAGTAACGGCTTTATAACTCGC 790

Qy    806 TGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGTGCTTTGGGTGCAGCTGAGATGA 865
              | |   | || |  |||| || |  ||  || |||||||| |
Db    791 TGCGCCACGCGAGGCGCTCACTTTGGCCTTAACTGGCCACTGGGGCCAGATGAACTGC 850

Qy    866 GACCTTTTATTGAAATAGTCACAACAGCCTATGTCCTCTGTTATCCCCAATG 925
              | ||||| |||||| |  |  |    |||||| |||||  |||||| || |
Db    851 GCCAGTACGTCCAGGAACTGTCGCGGATTGCCGAATCGTACGTCACCCGGAACG 910

Qy    926 CAGGTCTTCCCAACACCTTTGTGACTATGATGATGAAACGCCTTCTATGATGGCCAAGCACC 985
              ||||| || ||||  |  |||| | ||| ||
Db    911 CCGGCCTGCCGAACGCTTTCGGCCTGAGTATGACCTCGACGCCGACACCATGGGCGAAACAGA 970

Qy    986 TAAAGGATTTGCTATGGATGGCTTGGTCAATATAGTTGGAGGATGCGTGTGGGTCAACAC 1045
              | |  |  |||| || | ||||| || |  |
Db    971 TTTCGGAATGGCGGAAGCGGCTTCCGATAATGCGTGGCCGGTTGCGCGCGCCACCACGCGC 1030

Qy   1046 CAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATTGTAAGCTAGAGTTCCACCTG 1105
              |   |||||  ||    ||||||| || || |   |  | ||||
Db   1031 CGGAGCATATTGCGGCGATGAGCCGCCGTTTGCCTGCGTTGCCGTCCAGCTGCCGCCGG 1090

Qy   1106 CCACTGCTTTGAAGGACATATGTTACTGTCTGGTCTAGAGCCCTTCAGGATTGGACCGT 1165
                              |||||| |  |||||||
Db   1091 ATATCCCGGTCGCCTGCC------GCCTTTCCGGCCTGGAGCCGCTGGAACATGGCGACG 1144

Qy   1166 ACACCAACTTGTTAACATTGGAGAGCGCTGTAATGTTCGAGGATCAAGGAAGTTTGCTA 1225
              | | | | |  | | || | ||||| ||
Db   1145 ATAGCCTGTTTGTGAACGCTGCGGCGAACGCTACTAACGTCACCGGCTCGGCCAAATTTAAAC 1204

Qy   1226 AACTCATCATGCGCAGAAACTATGAGAAGAAGCCTTGTGTGTTGCCAAAGTGCAGGTGAAA 1285
                  |||   |||| ||| |  ||||| || ||
Db   1205 GGCTGATCAAGAGAGAAAATCACGCCGAAGGCCTGGATGTCGCGCCGTCAGCAGGTAGAAA 1264

Qy   1286 TGGGAGCCCAGTGTGTTGGATGTCAACAACATGATGATGGCATGTCAAGTGGTCCAAGTGCAA 1345
              |  |    |||| | | || || |  | ||
Db   1265 GCGGGCGCGCAGATTATTGATATCAATATGGAGGGATGAGCGGGATGTCGACGCGCAAGCGCCGA 1324

Qy   1346 TGACCAGATTTTGCAACTTAATTGCTTCCGAGCAACAATACTTGCTGGCTG 1405
              | |  ||  ||   ||   | ||||||| |||
Db   1325 TGGTGCGTTTCCTCAGCCTGATTGCCCGTGTACCAATCATGA 1384

Qy   1406 TCGACTCCTCCAATTTTGCTGTGATTGAAGTTGCTGCCAAGGGAAGTGCA 1465
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Db   1385 TCGACTCCTCCAAATGGAGGTTATCGAAAAAGGGCTGAAGTTAAAGGCA 1444

Qy   1466 TTGTCAATAGCATTAGTCTGAAGGAAGGAGGACGACTTCTTGGAGAAGGCCAGGAAGA 1525
              | |   ||   |   |  || ||||| | | || | |||||
Db   1445 TCGTCAACTCTATTTCGATGAAAGAGAGAGGCGGTGGAAGCCTTTATTCATCGTCGAAGCTTC 1504

Qy   1526 TTAAAAGTATGGAGCTGCTATGGTGTCATGGTCATGGGGCTCAGGGGCTCTGGGTC 1585
              |  |||| |  |||| | |  || |||| ||||||
Db   1505 TGCCGTCCACGGCGCGGCAGTGGTGGGTGCGGATGAGCAGGGGCAGGGCCGATA 1564

Qy   1586 AAACAGCACAAAAATCAGAGTGTGCACCCGGGCTACCATCTGCTTGTGAAAAAACTGG 1645
                |||| | |||| |  |    ||||  |||  ||||
Db   1565 CCCGGCGCGGTAAAATCGAAAATGCGGGCTTCCCGGGATTATTTTGGTATGGTTGTAATATCA 1624

Qy   1646 GCTTTAATCCAAATGACATTATTTTTGACCCTAACCATTGGGACTGGAATGG 1705
                 |||  |    ||  || | || ||||||
Db   1625 GTTTCCCGGCGAAGCATCTTCTTGGCTGGAATGCGCTGGTGGGGCGGTATTGG 1684

Qy   1706 TTGATATCTTACTCATTGAAAACTATTTTTGATATCGCCAATGCCAAGGCAGCGCCTGTTTG 1765
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Db   1706 AGGAACACAACTTGTATGCCATTAATTTATCCATGCAACAACAAAGTCATTAAGAAACAT 1765
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Db   1685 AAGAGCACAACAACTACGCGCAGGACTTTATCGGCGTTGCGAAGACATCAAACGCGAGC   1744

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Qy   1826 AAGCCATTCGAGAAGCAATGCATGGGGTTTCCTTTACCATGCAATCAAGTCTGGCATGG    1885
               |||||||  || |  || ||   ||| ||||| ||||  ||||||| ||| |||| ||
Db   1805 ACCCGGTACGTGAGGCTATCCACGCGCGTATTCCTCTACTACGACCGGTATGG         1864

Qy   1886 ACATGAGATAGTGAATGCTGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTC    1945
               |||| ||  ||||| || |||   ||||| |||||||  || |   ||| |||| |
Db   1865 ACATGGGCATCGTCAACGTCTCAACGCTGGCTATCTACGACACCTGCCCGCCGAGCTGC    1924

Qy   1946 TGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGAAGCTCTTAC  2005
               || | | ||| |||||| |  |||| |||| || ||  ||||||| ||| | | |
Db   1925 GCGATGCGGTTGAAGATGTCATTCTTAACCGTCGCGATGACGGCACTGAGCGTTTGCTGG  1984

Qy   2006 GTTATGCCAGACTCAAGGCACAGAGGGAAGAAAGTCATT------CAGACTGATG        2056
               || |||  || ||||| ||  ||   || |||| |     |  |||||| ||
Db   1985 ATTTGGCGGAGAAAATACCGGCGCAGCAAAACCGACGAGCTGCCAACGCCCCAGCAGCGG 2044

Qy   2057 AGTGGAGAAATGGTTTCTACCTGCGAAGAACGGCCTTGAGTATGCCCTTGTTGAAGGGCATTGAAA  2116
               | |||| |||||  ||| || |   ||| |  |||| |||  ||  |||||| |||||| |||
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Qy   2117 AACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAATATCCCGACCTC     2176
               || ||||| | ||| ||| || |  || |||  ||  |     |||| |||  |||
Db   2105 AAATTTATCGACAGGATACCGAAGACCGAAGAGC------CCGTCAGCAGGCGCCGCCCGA  2155

Qy   2177 TCAATATAATTGAAGGACCCCTGATGAATGAAATTGTTGGTGATCTTTTTGGAG         2236
               |||| || || ||| | | | || |||| ||| | |||  | ||  |  |||
Db   2156 TTGAGGTGATTGAAGGCCGTTGATTGCCATCGACGACCTGTCGGCGACCTGTTTCGGCG    2215

Qy   2237 CTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTATGAAGAGGCTGTTG    2296
               ||||||||||| |||  || || | ||| || |  | |||| || ||| |||| |||
Db   2216 AAGGGAAAAATGTTCCTGCGCAGGTGGTGAAATCCGCTGCGCAGATGAAACAAGCCGTGG  2275

Qy   2297 GCCACCTTATCCCTTTCATGAAGAAAGAAGAGAGTGCTTAACGGCACAG            2356
               ||| ||| | |   || | ||||| | ||| || | |||  || |||
Db   2276 CCTACCTGGAGCCGTTATTGAAGCCAGCAAGAGAAA-----------------       2313

Qy   2357 TAGAAGAAGGACCCCTACCAGGGCACCATCGTCTGGCTGGCCACTGTTAAAGGCGACGTGC 2416
               || ||||| || |  || ||| |  ||  |  |  | ||  | || |||||| |  |||
Db   2314 ------GGCTCCAGCAACGGCAAGAGTGCATGGTGTCTCGGCATGATCGCCGATGTGC    2362

Qy   2417 ACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTCCGAGTTATTG   2476
               || ||  ||||||  || |||   ||| ||  || |||  ||| |  |||| |||| |
Db   2363 ACGATATTGGTAAAAATATCGTTGGCGTGGTGCTGTGCAATGTAACAACTACGAAATCGTTCG 2422

Qy   2477 ATTTAGGAGTCATGACTCCATGCTGATAAGAGACTGAAAGCTGTCTTTGACCACAAAGCAG  2536
               || |||||||| ||| ||||  | |  || |  |||  ||| ||| || || |||| |
Db   2423 ATCTTTGGCGTGATGGTGCCAGCGGCGGAGAAAATCTTCAGAATGGGAAGTGAAATGCCG  2482

Qy   2537 ATATAATTGGGTAAGAAGTGCGTGTTCCGGAGAATGATTTTTGTTGCCA            2596
               || | |||  |   ||||||| || ||| || |  ||| || || |||
Db   2483 ATCTGATCGGTTCTTGCCGACTCATCGATTACCCCGTCGCGTCGGTGATGGTGTCAGCCG 2542

Qy   2597 AGGAAATGGAGAGATTAGCTATAGAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAA 2656
               ||| | | ||| || || |  || | || ||  | |   || || |||| |||| ||
Db   2543 AAGAGATGGAGCGTCAGGCGTTTACTGATATCCCGCTACTGATCGGTTCATCGAGTCCTCGA 2602

Qy   2657 AAACCCACACAGCAGTGAGGTAAAATAGTTCCGCTACCTGTAATCCATGTCCTGG       2716
               ||| || || | ||||  || || |  ||| |  || | |||  ||| | |||
Db   2603 AAGCGCATACGGCGGTGAAAATCGAGAACGACTACACAGCGGTCTCACGTTACGTGCAGA  2662

Qy   2717 ACGGTCAAGAGTGTGGTGGTCGTGTTCCCAGCTGTTAGATGAAAATCTAAAGGATGAAT   2776
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Db   2663 ATGCTTCCGGTACCCGTGGCGTGGCGTGGCCGCCGCTACTCTCCGACACCCAGCGTGATGACT 2722

Qy   2777 ACTTTGAGGAAATCATGGAAGAGATATTAGACAGAACATTATGAGTCTCTCA          2836
               ||| ||||| || || |||| | || | || | ||  ||| || | | | ||
Db   2723 TTGTCGCCCGTACCCGGCGTTACCCGGTACCGGTGGCGTTGGCTCGCGCGCACGCCCCGCA   2776
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Db   2837 AGGAGAGAGATACTTACCCTTAAGTCAAGCCAGAAGAAAAGTGTTTCCAAATGGATTGGC   2896

Qy   2777 AAAAACCCGCACGCGCCGGTCACCCAGTGAAGCCCACCGTTATTGGGACCCAGGTCATATG 2836
               |||  ||| |||||| |||| || ||||||| |||||| | || ||||| | | |||
Db   2837 AATTGGGAACGCTACACCCCGCCGGTAGCCGTCTGGGCGTGCAGGAGGTGGAAGCCA    2896

Qy   2897 TGTCTGAACCTCACCCAGTGAAGCCCACCGTTATTGGGACCCAGGTCATATG         2956
               ||| |||||| ||| ||| ||||||||  |  |  ||| || |  |
Db   2897 ATTGGGAACGCTACACCCCGCCGGTAGCCGTCTGGGCGTGCAGGAGGTGGAAGCCA    2956

Qy   3017 GGGGCAAGTGACCGAATCGAGGCTTCCCAAGCATATTTAACGACAAAACAGTAGGTGGAG  3076
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Db   2957 CCGGCAAATACCG---------------CGCATTCTGAAGATGAGGATGAGGTGGCGTTG   3001

Qy   3077 AGGCCAGGAAGTCTACGATGATGCCCACAATATGCCACCAATGATAGTCTCGCATCAAAGA 3136
               |||| | |||| |||| ||| || | |||||| |||  | || | ||| |  ||| |||
Db   3002 AGGCGCAGCGTCGTGTTTAAAGACGAGATGATATGCTGGATAAACTGGATACTGAGCGGAAAC 3061

Qy   3137 AACTCCGGGCCCCGGGGTGTGGTTCGGCATCGGGTTCCCCGGCTATCCAAGACGACATTC   3196
               || || | | |||   |  |||| |   | |   |   |   ||  |||  |  |
Db   3062 TGTTGAATCCGGGCACTGAAACTGAGCGCGGATTATACTGGTGGTGTGTGGGTGACGACTCG 3121

Qy   3197 ACCTGTACGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAGCCACTTTCTATGGGT 3256
               || | ||| ||| | ||||  || |  | ||  | ||| || |  |       |||||
Db   3122 AAATCTATCGGACGAAACCCGTAAAACCCGTACTCATGTTCTGACCGTCA------GCCACCACC 3172

Qy   3257 TAAGGCAACAGCGTGAGAAGGACTCTGCCAGCACGGAGCCCCATACTACTGCCTCTCAGACT 3316
               | |||||| | ||||  | || | || |||  | ||    || |  | || || || | |
Db   3173 TGCGCCAGCGACCGAGAAGTCGGTTTGCCA----------ACTACTGCTCTGGCGGATT  3223

Qy   3317 TCATCGCTCCCTTGCATTCTCGGCATCCGTGACTACCTGGCCTGGTTGCCTGC-        3375
               ||| ||| | |  | || |   |||| |  ||  || || | || || ||  ||
Db   3224 TTGTCGGCGAACCTGAGCGGCAAAGCGGATTACATCGGTGGTAGCTGGTGGTGGACCGGCG 3283

Qy   3376 --TTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGACTACAGCAGCA 3433
                |  ||||||  ||| || ||||||| |  || ||||   | |  ||| || |||| |
Db   3284 GTCTGGAGGAGGATGGCGTGGCCGGACGGCCTTGGAAGGCGGCAACGACGACTATAACAAGA 3343

Qy   3434 TCATGGTCAAGGCGTTGGGGGCGGACACCGGCCTTGGCAGGAGGCCTTTGCAGAGAGCTCCATGAAA 3493
               ||||||| ||||| | ||| ||||  || |||  || ||   || | |  || |||| |||||
Db   3344 TCATGGTGAAAGCGATTGCCACGTTCGGAAGCGGTTCGCGGAATATCTGCATGAGC   3403

Qy   3494 GAGTTCGCGCAGAACTGTGTGGGCTATTGGGGCAGTGGACGTGCTCGCAGAGACCTGC    3553
               |||| || || ||  || ||| || ||| | |||| || ||  || | |||| ||
Db   3404 GTGTACGTGAAGGTTTACTGGATATGCGCCGGCGCCGGGCGCTAGCGAGTAACGCGAATTAA 3463

Qy   3554 GAAGGTTGGCGTACAAGGCATCCGCCTGGTACCCCAGCCCAGCCACCACA         3613
               || | | | ||||| || |  |  | || || |  | | | ||  ||  |
Db   3464 TCCCGGAAAACTACCAGGGGATTCGCCAGGCGGCGGGTTTATCCTGCCTGCTGGAACATA  3523

Qy   3614 CCAGAAGAAGCCATGTCAGGCATCGCCTGCTTCAGCAGGTGTCCTGCTTACAGGCATTGTGCCA 3673
               ||||| |||   | ||| || | ||  || | ||||||  || |  |   | || | ||||
Db   3524 CCGAAAAGGCACTATCTGGCAGCTACTGGATGTGCAGAAAAACACACCGGATGAAGCTCA  3583

Qy   3674 CAGAATCATTAGCAATGGCACCTGCTTGTTGATTGGAGGAGCAACCACTTCCAATTTGA  3733
               || ||||||  | ||||| ||| |  | | || |||| |||||  || | |||| | |
Db   3584 CCGAATCTTTGCGCTGTGCCATGTCGGTTGGCTGGGCCATCGTCCAAGGATCAGTTATGCATTGA 3643

Qy   3734 AGTCCAAATATTTTGCTGTGTGGGAAGAGATTTCAAGGATCAGGTGTTGAGATTATGCATTGA 3793
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Qy   3794 GGAAGAACATATCGTGTCGGTTGAGGTTGAGGTGGATGTTGAGCGTGATTTTGGGATAATGATA 3853
               ||| |||| || | | | ||||   |   | ||  | || ||| |  | ||| |||  |
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Qy   3854 CAGACTAA   3861
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RESULT 15
US-10-282-122A-41615
; Sequence 41615, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed -- See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41615
; LENGTH: 3696
; TYPE: DNA
; ORGANISM: Yersinia pestis
US-10-282-122A-41615

Query Match   21.8%; Score 854.4; DB 7; Length 3696;
Best Local Similarity   54.7%; Pred. No. 8.4e-247;
Matches 2042; Conservative   0; Mismatches 1591; Indels 103; Gaps   13;

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Qy   200 TAAACGAAGAACACTTCCAGAGTCAGGAATTTAAAGATCATGCCAGGCGCGTGAAAGGCA 259
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Db   110 TAGAAGAGGCAGATTACCGAGGCGCGCGTTTTGCTGACTGGGCAAGTGACCTAAAAGGTA 169

Qy   260 ACAATGACATTTTAAGTATAACTCAGCCTGATGTGTCATTACCAAAATCCATAAGGAATACT 319
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Db   170 ACAATGACCTCTTGGTGCTCTCCAAGCCAGAGTCATCACCGGCGATCCATAATGCCTACC 229

Qy   320 TGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCCAAG 379
          ||| |||| ||| ||| | | ||||| |||||||||||| || ||| |||||||
Db   230 TTGAAGCCGGTGCTGACATTCGAAACCATTCGAAACCAATACCTTTAACTCTACCTCCATTGCCGATGG 289

Qy   380 CTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACACTGTGCTCTGCAGGAGTGGCCA 439
          |||||| ||||| ||| | | || | |||||| ||||| ||| ||| || |||||||
Db   290 CGGACTATCAGATGGCTGCTCACTGTGCTCGGCTGAAATTAACTATGAAGCGCCGCCGTCTGCGCCC 349

Qy   440 GAAAAGCTGCCGAGGA--GGTAACTCTCCAGACAGGACACTCTGTGTCCCATCTGTGGAAAGCCGATTATA 496
             ||| ||||| ||| |||||||||||| | |||| | ||| |||||||||||||||||| |||
Db   350 GTATCTGTCGCCGATGAATGGAGCCCCGCACGCCAGAGAAAACCACGTTATGTTGCCGGGG 409

Qy   497 CTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGGAAAGCCGATTATA 556
          ||| || | |||||| ||| |||||| ||| || |||||||| |||| ||| |
Db   410 TGCTGGGGCCAACCAACCGTACTGCCTCCATCTCCCCTAAAGTTAATGACCCGGCGTTCC 469

Qy   557 GGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCCAAAGGACTTCTGG 616
          ||||| || |||| |||| |||| |||| | | ||| ||| |||| ||| || || ||
Db   470 GTAACGTCAGTTTTGATCAGTTGGTCGAGGCCTATCGTGAGTCTACCCCGCGCTGATTG 529

Qy   617 ATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTGCCAAGTGCCAAGGCAG 676
          | || ||||| | | |||| |||| ||||| | |||||||| ||| |||||||| ||
Db   530 AAGGGGGTGTGTTGATTAATTATTGATGAATCGAAACGGTCTTCGATACGGTTGAATGCGAAGGCCG 589

Qy   677 CCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAAATATGTCTCCCGGCTATCTTTATT 736
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Db   590 CGACCTTTGCGGTTGAAAGCGAATTCGAGTGTGATGGGGCGTGTTGGGGTGATGATT 649

Qy   737 CAGGGACGATCGTTGATAAAGTGGGGCGACTCTTCCGGACAGACAGGAGGAGGGAGGATTTG 796
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Db   650 CCGGCCACCATTACCGATGCCTCCGCGTACCGCTGTCGGTCAAACGACGGAAGCTTTTT 709

Qy   797 TCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGTGCTTTGGGTGCAG 856
          ||| | ||||| |||||||| || ||| || || ||||| || ||| ||||||| |||
Db   710 ATAACTCCTGCGCCCATGCAAGTCAAACCGCGTGTCGTTTGGTCTGAACTGGTCGTTGGGTGGGGCCG 769

Qy   857 CTGAGATGAGACCTTTTATTGAAAATGTTACACAGCCTATTTATGTGGTTGCAGTGCGC 916
          ||||| |||| || | | |||| |||| |||||| || |||||||||| |||||||||
Db   770 ATGAACTGCCCAATAGTGTGGAGTTATCGCGAATGCTTTTGGTGAATATGATCTCAGTGCGC 829

Qy   917 ATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGAAAGCCTTCTATGATGG 976
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Db   830 ACCCGAATGCCGGTTTGCCGAATGCTTTTGGTGAATATGATCTCGGAAGCCAAAGAGATGG 889

Qy   977 CCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAGTTGGAGGATGCGTGTG 1036
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Db   890 CTGAGCAGATTGGCAGTGGGCACGTGGGGCGATTTTTGAATATTGTCGGCGCGGTTGCTGCG 949

Qy   1037 GGTCAACACCAGATCATCAGGGAAATTGCTGAAGGTGTGAAAAATGTAAGCCTAGAG 1096
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Db   950 GTACCACACCCCGGCATATTGCCGGATGGTCAACGCTGTCGCGTGTGTGGGGTGCCTCCGCGC 1009

Qy   1097 TTCCACCTGCCTTTGAAGGACATATGTTACTGTCTGTCAATAGTGGAGAGCCCTTCAGGA 1156
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Db   1010 CGTTGCCTGATATTCCGGTTGCCTGGCCGCGTTTGG------CCGGCCTGGAGCCCACTGACTA 1063

Qy   1157 TTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCGTGTAATGTTGCAGGATCAAGGA 1216
          |||| ||| ||||| ||| | ||| |||||||||| | | ||| || || |||||||
Db   1064 TCGATGCCAATACCCTGTTTGTGAACGTCGGTGAACGCGGTGATGCGGTTCACGGGGTTCGGCAC 1123

Qy   1217 AGTTTGCTAAACTCATCATGCCAGAGAAACTATGAAGAACCTTGTGTTGTTGCCAAAGTGC 1276
          || | || ||| ||||| |||| ||| ||||| |||||||| ||||| |||| ||||
Db   1124 GCTTTAAACGGTGATAAAGAGAGAAGAGAAGTACGGCGAGGCGCGGTGGATGTTGCCGATGTT 1183

Qy   1277 AGGTGGAAATGGGAGGTCAGAGTTGTTGGATGTCAACATGGATGATGGCTAGATGGTC 1336
          || | |||||||| ||||||| || || || | ||||||| || | || |||| | ||
Db   1184 AGGTCGAAAGCGGCGCGGCGCAGATCATCGATCAACATCAACATGGATGGCATGGTTGTT 1243

Qy   1337 CAAGTGCAATGACCAGATTTTGCTGCAACTTAATTGCTTCCGAGCCAGACATCGCAAAGTAC 1396
          |||||| || | | |||||| | | | || | |||||| | ||| |||||| |
Db   1244 AAGCGGGCCATGGTGCGTTTCCTTAATCGATTGCCGCGGGGAGGGTTGCAGGGGTGCAGGGGTGC 1303

Qy   1397 CTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGCTGATTGGGTTGCCAAG 1456
          | | ||| | | |||||||| | | ||||| | || ||| || || |
Db   1304 CGATTATGATCACTCCTCCCAAGGTGGGGATGTGATTGATTTGAAATGTATTATTCAAG 1363

Qy   1457 GGAAGTGCATTGTCAATAGCATTAGTCGAAGAAGGAGGACGACTTCTTGGAGAGG 1516
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Db   1364 GCAAAGGCATCGTGAACTCCATTTCGATGAACAGTGTGCTCTGCGCAGGAGTGGCGTCCATCACG 1423

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Db   3501 GAAACTGACCGAATCCTACGCCATGTGGCCTGGGGCTTCGGTATCCGGGTTCGGTATTTCAG 3560
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Qy   3726 CAATTTGAAGTCCAAATATTTGCTGTGGGAAGATTTCCAAGGATCAGGTTGAGGGATTA 3785
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Db   3561 CCACCCAGACAGCAAATATTTTGCCGTAGCACAAATTCAGCGTGATCAGGTTGAGGATTA 3620

Qy   3786 TGCATTGAGGAGAACATATCGTGCTGAGGTTGAGGTTGAGAAATGGCTTGGACCCATTTGGG 3845
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Db   3621 TGCCGCCCGTAAAGGGATGCCCACTGCCGAAGTTGAACGCTGGCTAGCCCCTAATCTGGG 3680

Qy   3846 ATATGATACAGACTAA 3861
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Db   3681 TTACGATGCGGATTGA 3696
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Search completed: March 6, 2006, 19:35:54
Job time : 2013 secs

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              GenCore version 5.1.7
      Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    March  6, 2006, 19:02:53 ; Search time 698 Seconds
                                       (without alignments)
                        12309.956 Million cell updates/sec

Title:     US-10-607-712-1.
Perfect score: 3919
Sequence:  1 ggtcacctgtggagcacg.........ctcaaggaaatacaacctag 3919

Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 1.0

Searched:   7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters:      14437070

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA_New:*
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   2: /cgn2_6/ptcodata/2/pubpna/US06_NEW_PUB.seq:*
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   4: /cgn2_6/ptcodata/2/pubpna/PCT_NEW_PUB.seq:*
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   7: /cgn2_6/ptcodata/2/pubpna/US10_NEW_PUB.seq:*
   8: /cgn2_6/ptcodata/2/pubpna/US10_NEW_PUB.seq1:*
   9: /cgn2_6/ptcodata/2/pubpna/US11_NEW_PUB.seq1:*
  10: /cgn2_6/ptcodata/2/pubpna/US11_NEW_PUB.seq2:*
  11: /cgn2_6/ptcodata/2/pubpna/US11_NEW_PUB.seq3:*
  12: /cgn2_6/ptcodata/2/pubpna/US11_NEW_PUB.seq4:*
  13: /cgn2_6/ptcodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	883.8	22.6	3684	8	US-10-858-730-261	Sequence 261, App
2	141.4	3.6	1275	6	US-09-925-065A-727226	Sequence 727226,
c 3	135.8	3.5	494	9	US-11-116-881A-1611	Sequence 1611, Ap
4	112.8	2.9	2599	12	US-11-055-822-211	Sequence 211, App
5	112.8	2.9	2599	12	US-11-055-822-709	Sequence 709, App
6	112.8	2.9	3666	8	US-10-858-730-260	Sequence 260, App
7	112.4	2.9	2578	12	US-11-055-822-213	Sequence 213, App
8	112.4	2.9	2578	12	US-11-055-822-711	Sequence 711, App
c 9	101.4	2.6	616	8	US-09-925-065A-697175	Sequence 697175,
10	93.4	2.4	3477	8	US-10-858-730-141	Sequence 141, App
11	91.4	2.3	3513	8	US-10-858-730-142	Sequence 142, App
12	89.6	2.3	3621	8	US-10-858-730-144	Sequence 144, App
13	88.2	2.3	3579	8	US-10-858-730-143	Sequence 143, App
14	46.4	1.2	50	12	US-11-175-859-4373	Sequence 4373, Ap
c 15	43.2	1.1	616	6	US-09-925-065A-483679	Sequence 483679,
c 16	41	1.1	588	6	US-09-925-065A-39453	Sequence 39453, A
c 17	40.4	1.0	1877	6	US-09-925-065A-671655	Sequence 671655,
c 18	40	1.0	119036	8	US-10-995-561-13314	Sequence 13314, A
c 19	39.6	1.0	591	6	US-09-925-065A-408435	Sequence 408435,
c 20	39.6	1.0	731	6	US-09-925-065A-680394	Sequence 680394,
21	39.6	1.0	731	6	US-09-925-065A-680395	Sequence 680395,
22	39.6	1.0	160226	12	US-11-121-086-29	Sequence 29, Appl
c 23	39	1.0	611	6	US-09-925-065A-460077	Sequence 460077, Ap
c 24	39	1.0	1284	12	US-11-098-686-9926	Sequence 9926, Ap
25	39	1.0	1457619	12	US-11-098-686-8739	Sequence 8739, Ap
c 26	38.8	1.0	354	6	US-09-925-065A-125604	Sequence 125604,
27	38.8	1.0	1100	8	US-10-750-185-25373	Sequence 25373, A
c 28	38.2	1.0	179487	7	US-10-750-623-25373	Sequence 25373, App
c 29	37.6	1.0	591	6	US-10-330-773-664	Sequence 664, App
30	37.6	1.0	591	6	US-09-925-065A-281175	Sequence 281175,
31	37.6	1.0	21442	8	US-10-995-561-13469	Sequence 13469, A
c 32	37	0.9	499	6	US-09-925-065A-594374	Sequence 594374,
33	37	0.9	560	6	US-09-925-065A-215989	Sequence 215989,
c 34	37	0.9	591	6	US-09-925-065A-816505	Sequence 816505,
c 35	36.8	0.9	319608	12	US-11-145-703-1	Sequence 1, Appli
36	36.6	0.9	2475	12	US-11-136-527-3385	Sequence 3385, Ap
37	36.6	0.9	200	12	US-11-098-686-7768	Sequence 7768, Ap
c 38	36.6	0.9	499	6	US-09-925-065A-594373	Sequence 594373,
39	36.6	0.9	568	6	US-09-925-065A-428604	Sequence 428604,
c 40	36.6	0.9	571	6	US-09-925-065A-330747	Sequence 330747,
41	36.6	0.9	573	6	US-09-925-065A-598361	Sequence 598361,
42	36.6	0.9	602	6	US-09-925-065A-384546	Sequence 384546,
c 43	36.6	0.9	1273	8	US-10-750-185-41055	Sequence 41055, A
c 44	36.6	0.9	1273	8	US-10-750-623-41055	Sequence 41055, A
c 45	36.6	0.9	2141	6	US-09-925-065A-685376	Sequence 685376,

ALIGNMENTS

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RESULT 1
US-10-858-730-261
; Sequence 261, Application US/10858730
; Publication No. US2005025568A1
; GENERAL INFORMATION:
;  APPLICANT: Bailey, Richard B.
;  APPLICANT: Blomquist, Paul
;  APPLICANT: Doten, Reed
;  APPLICANT: Driggers, Edward M.
;  APPLICANT: Madden, Kevin T.
;  APPLICANT: O'Leary, Jessica
;  APPLICANT: O'Toole, George
;  APPLICANT: Trueheart, Joshua
;  APPLICANT: Walbridge, Michael J.
;  APPLICANT: Yorgey, Peter S.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
;  TITLE OF INVENTION: PRODUCTION
;  FILE REFERENCE: 14184-030001
;  CURRENT APPLICATION NUMBER: US/10/858,730
;  CURRENT FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/475,000
;  PRIOR FILING DATE: 2003-05-30
;  PRIOR APPLICATION NUMBER: US 60/551,860
;  PRIOR FILING DATE: 2004-03-10
;  NUMBER OF SEQ ID NOS: 364
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 261
;  LENGTH: 3684
;  TYPE: DNA
;  ORGANISM: Escherichia coli
US-10-858-730-261

Query Match             22.6%;  Score 883.8;  DB 8;  Length 3684;
Best Local Similarity   54.4%;  Pred. No. 2.2e-238;
Matches 2043;  Conservative    0;  Mismatches 1612;  Indels 102;  Gaps  9;

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              ||||||||||||  |||||   ||| |||||||||| ||||| || ||| |||||||||
Db     15 GGAACAACTGCGTGCGCAGTTAAATGAACGTATTCTGGTGTCTGGACGGCGGTATGGGCAC 74

Qy    180 CATGATCCAGCGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAATTAAAGATCA 239
              ||||||||||||| |||  ||| || ||||||| || |||| |  |||||| ||||
Db     75 CATGATCCAGAGTTATCGACTGAACGAACGAAGCCGATTTCGTGGTGAACCGTTTCCGACTG 134
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Qy   1317  TGATGGCATGCTAGATGGTCCAAGTGCAATGCACCAGATTTGCAACTTAATTGCTTCCGA  1376
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Db   1209  TGAAGGGATGCTCGATGCCGATGCGGCGGGCGGATGGTGGCGGTTGTCGATTGCCGGTGA  1268

Qy   1377  GCCAGACATCGCAAAAGTACCTTGTGCATCGACTCCTCCAATTTTGCGTGATTGAAGC    1436
           ||| ||  ||||   | ||  ||| | ||| |||| || |||| | ||| ||||||||
Db   1269  ACCGGATATCGCTCGCGTGCCGATTATCGATCGACTCCTCAAAATGGGACGTCATTGAAAA  1328

Qy   1437  TGGGTTAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCACATTAGTCTGAAGGAAGGAGA  1496
           || ||| ||||| ||| ||  | ||| |  | | || |  ||| | |  |||| | |||
Db   1329  AGTTCTGAAGTGTATCCAGGGCAAAGGCATTGTTAACTCTATCTCGATGAAGAAGAGGGCGT  1388

Qy   1497  GGACGACTTCTTGGAGAAGGCCAGGAAGCTAAAAAAGTATAAAAGTGCTGCTATGGGTGGTCAT  1556
           | ||| |||| |  | ||  ||  || |   || |||  | |  |||||| |||||| |||
Db   1389  CGATGCCTTTATCCATCCATCACGCGAAATTGTTGGCTCGCTACGTCGTGCGCAGTAGTGTGGTAAT  1448

Qy   1557  GGCTTTTGATGAAGACGACAGGCAACAGAAACAGACACAAAAATCAGAGTGCACCCG       1616
           |||||| || | || |||||| || || || |  |||| || |  |  | | || |
Db   1449  GGCCTTTGACGAACAGGGACAGGCCGATACTCCGCACGCAGAAATCGAAATTGCCGTCG      1508

Qy   1617  GGCCTACCATCTGCTTGCTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCC  1676
           |||| | ||||  || ||  | || || || || || |  || || | |||| |  |||
Db   1509  GGCGTACAAAATCCTCACCGAGAGGTTGGCTTCGCATTGAAGAGCAGCAACTACCGCAGGACTTTAT  1568

Qy   1677  TAATATCCTAACCATTGGGACTGGAATGCAGAATGGAGGAACACAACTTCGTATGCCATTAATTTTAT  1736
           | | | ||| |  ||||  ||  ||  | | || | ||| || || || |  | |  |||| ||
Db   1569  AAACATCTTCGCGGTGGCGCGGGTGCGCTGTCGCAGAGCAGCATCATTGAAGAGCAGCATCACCGTTAT  1628

Qy   1737  CCATGCAACAAAGTCATTAAGAGAACATTACCTGCGCAGAATAAGTAGGCCAGAATAAGTGAGGTCTTTC  1796
           || || |||| ||| ||| ||   | ||| | ||||| | ||| ||  ||||| | ||
Db   1629  CGGCGCGTGTGAAGACATCAAACGCAACTGCGACGCTGAGGCGCCACGCGTGATTTCCGGCGCGTATC  1688

Qy   1797  CAACTTGTCCTTCCTTCCTTCGGGGGGACATGGGGTTT                              1856
           || ||| | || || | | || || || || || ||
Db   1689  TAACGTTTTCTTTCTCTCGGTTCCGTGGCAACGATCCGGATCGTGCGCGACGCGGTGAACGCCAGTGTT  1748

Qy   1857  CCTTTACCATGCAATCAAGTCTGGCATGGACATAGTGGAGAAGTGAATGCTGGAAACCTCCC       1916
           || || | |||| ||  | ||| ||||  |  || | ||| ||| | ||  | ||
Db   1749  CCTTCTACTACGTTATTCGCAATGTGGCATGGATGGATAGTGTCGTCAACGCGCGGGCCAACTGCC     1808

Qy   1917  TGTGTATGATGATATCCATAAGAACTTCTCTGCAGCTCGTGTGAAGATCTCATCTGGAATAA        1976
           || |||| | ||| | |||| | ||||  | ||| |  ||| |  ||| || | ||  ||
Db   1809  GATTTACGACGACCACCACCGCGTCGAACTGCCGCTGGAGCTGCGGCTGAAGATGTGATTCTTAATCG   1868

Qy   1977  AGACCCTGAGGCCCACTGACTCTTACGTTATGCGCCAAGGC----------AC           2027
           ||| |  |  | |||  ||| | | | | | || ||| ||  
Db   1869  TCGCGACGATGCACCGAGCGTTGCCGAGCGTTGCCGAGAAATATCGCGCAGCAGCAAAAC      1928

Qy   2028  AGGAGGGAGAAAGTCATTCAGACTGATAGGCGGGCATTGAAATATTGAAGAACGGCCT       2087
           |||  |  || || || || ||| || |  || || |||| |  | ||| || || |
Db   1929  CGACGACACCACCGCCAACTCAGACGCAGAGGGAGTCGGCTCGCGTGTCGAGAAATAAACGTCT       1988

Qy   2088  TGAGTATGCCCTTGTGAAGGGCATTGAAAGAAAAATATTGAGGACTAGGAGGACCCCTGATGAATGCC    2147
           || || |||| | ||| | ||| ||  | | ||| ||  || || | |||  || |||
Db   1989  GGAATACTGCGTGTGTCAAAGGCATTTATTCGGAGTTTATCGAGAGATACCGGAGGAGC---          2045

Qy   2148  GTTAAACCAAAAAAATATCCCCGACCTCTCAATATAATTAATTGAAGTGATTGATGAATGCG       2207
           ||      | ||  | | | |  ||  |   || ||  ||  |||||  | |||   ||||
Db   2046  ------CGGCCAGCGTACGGCGCCCGATTGGAGCTGAAAATGTTTCTACCTCAGGTTATAAA       2099

Qy   2208  AATGAAAATTGTTGGTGATCTTTTGAGCTGAAACATTGGAGAGGCGGCTG               2267
           | ||| || | ||  | | ||  || || || | |   | ||  ||||| |
Db   2100  CATGAAGTGGTCGGCGGACTGTTTGTTGGCGAAGGGGAAAAATGTTCCTGCCACAGGTGGTCAA    2159

Qy   2268  GTCAGCCCGGGTTATGGAGGAAGGCTCGTTGGCCACCTTATCCCTTCATGGAAAAGAAAG      2327
           || | || | | || ||| ||| | ||||| ||  |||  || | || | ||  |||||
Db   2160  ATCGGCGCGGTCATGAAACAGGCGGTGCCTCTCACCGGTTATTGAAGCCAGCA-            2218

Qy   2328  GTCAGCGCCGGGTATGGAGGAAACATCAGAAGAGAGAAGAGACCCTTACCACGGGCACCAT     2387
           | |   | | ||  | || || | | || | | |||||||  |  | |  ||||  ||
Db   2219  -----------------AAGAGCAGGGCGAAAACCAACCGCAAGAACATAGTTGGAGTAGT      2246

Qy   2388  CGTGCTGGCCACTGTTAAAGGCCACTGTTAAAGGCCACATAGTGAGTAGT              2447
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Left column:

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Db  2247 GGTGATCGCCACCGTGAAGGGCGACGTCCACGACATCGGTAAAAATATCGTTGGTGTGGT 2306
          ||| |||| || ||||| |||| | ||  |||||||||  ||||| ||| || || |||
Qy  2448 CCTTGGCTGCAATAATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGAT 2507

Db  2307 GCTGCAATGTAACAACTACGAAATTGTCGATCTCGGCGTTATGGTGCCTCGCGGAAAAAT 2366
          ||| |||| || || ||| || ||| ||| ||  |||| ||| ||||| ||  ||||||
Qy  2508 ACTGAAAGCTGCTCTTGACCACCAAGCAGATATAATTAATTGGCCTGTCGTCAGGACTCATCACTCC 2567

Db  2367 TCTCCGTACCGCTAAAGAAGTGAATGCTGATCTGATCTGATTGGCCTTTCGGGGCTTATCACGCC 2426
          ||| |||| || ||  ||||| ||| || |||  || ||| |||||| ||||| ||  || ||
Qy  2568 TTCCCTGGATGAAATGATTTTTGTTGCCAAGAAATGGAGAGATTAGCTATAAGGATTCC 2627

Db  2427 GTCAGGCTGGACGAGATGGTTAACGTGGCGAAAGAGATGAGCGGTCAGGGCTTCACTATTCC 2486
          ||  |||| || ||| || ||| ||||| ||||| || || ||| ||| ||| ||| ||
Qy  2628 ATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAG 2687

Db  2487 GTTACTGATTGGCGGCGACGACCTCAAAAGCGGTGAAAATCGAGCAGAA 2546
          ||| || ||||| || || || ||  ||||| ||||||||| || |||
Qy  2688 ATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGTGTCCCA 2747

Db  2547 CTACAAGCGGCCCGACGGTGTATGTGCAGAATGCCTCGCGTACCGTTGGTGTGGTGGCGGC 2606
          ||   || || ||  || || |||| || || || |||| ||| || |||| |||| |
Qy  2748 GCTGTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATCGAAGAAATGAGA 2807

Db  2607 GCTGCTTTCCGATACCCGAGCCGTGATGAGTTTTGTCGCTCGTACCGAGCAAGAGTACGAAAC 2666
          ||| ||  |||| |||| || || || ||| ||| |  ||  ||  || || || ||| ||
Qy  2808 TATTAGACAGGACCATTATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGC 2867

Db  2667 CGTACGTATTCAGCACGGGCGCCAAGAAACCGCGCACCACCGGTCACGCTGGAAGCGGC 2726
          || ||  || || ||  || || ||||| |||| ||||||| || || ||||| || |
Qy  2868 CAGAAAAAGTGGTTTCCAAATGGATTGGCTCTGAACCTCACCCAGTGAGCTGGAGCCCACGTT 2927

Db  2727 GCGCGGATAACGATTTCGCTTTGACTGGCAGGCTTACACGCGCCGGGTGGCGCACCGTCT 2786
          || |  ||||| || ||||| |||| || || || ||||| || |||| || ||  ||
Qy  2928 TATTGGGACCCAGGTCTCTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTG 2987

Db  2787 CGGCGCAGGAGTC------GAAGCCAGCATCGAAACGTCGCTGCGTAATTACATCGACTG 2840
          |||| || || |       || || |||| | ||  || || ||  ||| ||| |||||
Qy  2988 GAAGCCTTTCTTTGATGTCTCGGCCAGCTCCGGGCAAGTGCCCAGGAAGTCTACGAGGCTTCCCCAA 3047

Db  2841 GACACCGTTCTTTATGACCTGGTCGTCGGGGAAGTATCCG---------CG 2885
          || |  || || || ||| ||| || ||  |||| |||           ||
Qy  3048 GATATTTAACGACAAAACGTAGGTGGAGAGGCCAGAAGTGTCTACGATGATGCCCACA 3107

Db  2886 CATTCTGGAAGATGAAGTGGTGGGCGTTGAGGCGCGCGTTTAAAGACGCCAACGA 2945
          |||| ||||| || ||   || || ||  || ||   || ||| || || ||
Qy  3108 CATTCTCGGCTAACTACTGTCTCGCTGACTTCGTTGCGGCCCAAGCTTTCTGTGTAAAGCAGA 3167

Db  2946 CATGCTGGATAAATTAAGCGCCGAGAAACGCTGAATCCTGAATCTACCGTGAAAAGCGCGTACCCATG- 3005
          |||| |||| ||  | |||| || ||| || || |  ||  || |||| ||||   ||||| || |
Qy  3168 TTACATCGGCGCATTGCCGTGACTGGCGGCGGAGCAGCGACCGCACGGGACTGCCTGATGCCTT 3227

Db  3006 CCCGGCAAACCGTGTGGGCGATGACATTGAAATCTACCGTGACATTGAAATCTACCGTGAAAAGCGCGTACCCATG- 3064
          ||| || |  |||| ||  || || ||  |||| ||| ||||  ||||||  ||| ||||||||| ||
Qy  3228 CTACCTGGGCCGTGTTGCCGTTGCCTCGTTTGGGGTAGAGAG----CTGAGCAAGGCCTA 3287

Db  3065 -------------TGATCAACGTGCCTCCTCAGACTTCATCGGTCTTGCATTCTCCCTGCCCTCCTGGAA 3107
                       || ||||||| |||| ||| || || ||  |||| || |||| || ||||| ||
Qy  3288 CACGGAGCCATACTACTACTGCACGACTTCATCCTCCGAACTTCTGTAAAGCAGA 3347

Db  3108 AGGCTTCGCTAACTACTGTCTCTCGCTGACTTCGTTGCGGCCCAAGCTTTCTGTGTAAAGCAGA 3167
          ||| ||  ||||| || || || ||| ||| ||||| ||| ||  ||| ||  ||||||||||
Qy  3348 CTACCTGGGCCGTGTTGCCGTTGCCTCGTTTGGGGTAGAGAG---CTGAGCAAGGCCTA 3404

Db  3168 TTACATCGGCGCATTGCCGTGACTGGCGGCGGAGCAGCGACCGCACGGGACTGCCTGATGCCTT 3227
          |||| ||| | ||   ||||| || ||||| || || ||||||||||  |||  ||||| |||
Qy  3405 TGAGGATGATGGTGACGACTACAGCAGCATCATGGTCAGGCGCGTGGGGACCGGCTGGC 3464

Db  3228 TGAAGCGGCGCACGATGATTACAACAAAATCATGGTGAAAGCGTTTAGC 3287
          ||||| || || |||||  ||| | |||||||||||| | ||  |||||
Qy  3465 AGAGGCCTTTGCAGAGAGAGACTCCATGAAGAGAAAGTTCGCCCGACGAGTTCGCCGAGACTGTGTG 3524
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Right column:

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Db  3288 CGAAGCCTTTGCGGAGTATCTCCATGAGCGTGTGCGTAAAGTCTACTGGGGCTATCGCC 3347
          || ||| ||||| |||||||||| |||  ||| || ||||| ||| ||||| ||| ||
Qy  3525 CAGTGAGCAGTCGGACGTCGCGAGACCTGCGACCTGGAAGGTTGCGGTACAAGGCATCCGCCCCGGC 3584

Db  3348 GAACGAGAACCTCAGCAACGAAGAGCTGATCCGCGAAAACTACCAGGGCATCCGTCGGC 3407
          ||  ||||| || ||||| ||||| ||| || ||  ||| ||||| |||||| || ||
Qy  3585 TCCTGGCTACCCCAGCCAGCCCGACCACACGAGAAGCTCACCCATGTGGAGACTGCGCAGA 3644

Db  3408 ACCGGGCTATCCGCCTGGACGTGGAACATACGGAAAAAGCCACCATCTGGGAGCTGCTGGA 3467
          || || |||||| || ||| |||||  || || ||||||| ||||  || || ||||| |
Qy  3645 CATCGAGCAGTCTACGAGGCATTAGCTGGTTAACAGAATCATTAGCAGTTCC 3704

Db  3468 AGTGAAAACACACTGGCATGAAACTCACAGAATCTTTCGCCATGTGGCCGGTGCATC 3527
          ||||||| | || ||| |||| |  ||||| |||| ||||| ||| || ||||  ||
Qy  3705 AGTCTCAGGCCCTCTACTTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGAAGATTTC 3764

Db  3528 GGTTTCGGGGTTGGTACTTCAGCCACCCGGACCAAGCAAGTACTACGGTGTAGCACAAATTCA 3587
          ||||| || ||||| ||  |  ||||  ||| || || ||| ||||| || || |||||||
Qy  3765 CAAGGATCAGGTTGAGGATTATGCATTGAGAAGAACATATCTGTGCGTGAGGTTGAGAA 3824

Db  3588 GCGGGATCAGGTTGAAGATTATGCCCCGTAAAGGTGATGAGCGGTTACCGAAGTTGAGCG 3647
          |||||||||||||| |||||||||  || ||||| ||||||  || |||||| |||| ||
Qy  3825 ATGGCTTGGACCCCATTTTGGGGATAATGATACAGACTAA 3861

Db  3648 CTGGCTGGCACCGGAATCTCGGGGTATGACGCCGGACTGA 3684
          ||||||||||||  |||| ||||| ||||||| |||||||
Qy  3825 ATGGCTTGGACCCCATTTTGGGGATAATGATACAGACTAA 3861
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  Query Match             3.6%;     Score 141.4;  DB 6;     Length 1275;
  Best Local Similarity  99.3%;     Pred. No. 6.1e-29;
  Matches  142;  Conservative   0;  Mismatches   1;  Indels   1;  Gaps   0;

Qy  1874 AGTCTGGCATGGACATGGACATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCC 1933
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   562 AGTCTGGCATGGACATGGGCATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCC 503

Qy  1934 ATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTG 1993
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   502 ATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTG 443

Qy  1994 AGAAGCTCTTACGTTACGTATGCCCAG 2016
          ||||||||||||||||||||||||||
Db   442 AGAAGCTCTTACGTTACGTATGCCCAG 420
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RESULT 3
US-11-116-881A-1611/c
; Sequence 1611, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
;
; SEQ ID NO 1611
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-11-116-881A-1611

Query Match   3.5%;   Score 135.8; DB 9; Length 494;
Best Local Similarity   56.2%; Pred. No. 1.3e-27;
Matches   276; Conservative   0; Mismatches 212; Indels   3; Gaps   1;

Qy   260 ACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACCAAATCCATAAGGAATACT 319
                |||||| ||| | | || ||||| || ||||| | ||| || |||| ||| || |||
Db   494 ACAACGACCTGCTGGTACTCAGTAAACCGGAAGTGATCGCCGCTATCCACAACGCCTACT 435

Qy   320 TGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCAGCACTAGTATTGCCCAAG 379
                ||| || || || | |||| || || |||| |||| | || || || ||||||
Db   434 TTGAAGCGGGGCGCGGGATATCATCGAAACCCAACTCCACGACCATTGCGATGG 375

Qy   380 CTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGTGCTCTGCAGGAGTGGCCA 439
                || ||||||| || || ||| ||| || |||| |||||||| | ||| ||| |||
Db   374 CGGATTACCAGATGGAATCCCTGTCGGCGGAAATCAACTTTGGCGGCGAAACTGGCGC 315

Qy   440 GA--AAAGCTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGAGGTTTGTGGCAGGGG 496
                || | || ||| || | ||| || || ||| || || | || || || |||
Db   314 GAGCTTGTGCTGACGAGTGGACCGCGCGGCACGCCAGAGAAACCGCGCTACGTTGCCGGTG 255

Qy   497 CTCTGGGTCCGACTAATAAGACACATCTCTCTGTGTCCCATCTGTGGAAAGGCCGGATTATA 556
                || || || || || || ||| | | | |||| ||||||| || ||||| |
Db   254 TTCTCGGCCCGACCACGGCACGGCGTCTTATTCTCCGAGCGTCAAGGATCCGGCATTTC 195

Qy   557 GGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGAGGCCAAAGACTTCTGG 616
                |||| ||||| || ||| || ||| | | |||| || ||| || ||||| |||||||
Db   194 GTAATATCACTTTTGACGGCTGTGGCGCCTTATGCGGAGTCACCAAAGCGCTGGTGG 135

Qy   617 ATGGCGGGGTTGATAATCTTACTCATTGAAACTATTTTGATACTGCCAATGCCAAGGCAG 676
                ||||| || | ||||| || | || |||| | || ||| || || ||| |||| |
Db   134 AAGGTGGCGCGGATCCTGATTGAAACCGGTTTCGACACCCTTAACGCCAAAGCGG 75

Qy   677 CCTTGTTGTTGCACTCCAAAATCTTTTTGAGGAGAAAATATGCTCCCCGGCCTATCTTTATTT 736
                ||| | || ||| | || || | | || ||| | ||||| || |||| ||| || ||

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Qy   2473  ATTGATTTAGGAGTCATGACTCCATGTGATAGATACTGAAAGCTGCTCTTCGACCACAAA  2532
           ||||  |||| ||||||| ||||| |||||||||||||| |||| || ||||||| |||||
Db   2471  GTGAACTTGGGCATCAAGCAGCCACTGTCCCGCCATGTTGGAGCAGCGGAGAACACAAA  2530

Qy   2533  GCAGATAAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGATGAAATGA  2584
           ||||| ||||| ||||||| |||||   |||||||||||||| |||||||
Db   2531  GCAGACGTCATCGGCATGTCGGGACTTCTTGTGAAGTCCACCGTGGTGATGA  2582
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RESULT 5
US-11-055-822-709
; Sequence 709, Application US/11055822
; Publication No. US2005026070γA1
; GENERAL INFORMATION:
;   APPLICANT: Pompejus, Markus
;   APPLICANT: Kroger, Burkhard
;   APPLICANT: Schroder, Hartwig
;   APPLICANT: Zelder, Oskar
;   APPLICANT: Haberhauer, Gregor
;   TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
;   TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
;   FILE REFERENCE: BGI-121CPCN
;   CURRENT APPLICATION NUMBER: US/11/055,822
;   CURRENT FILING DATE: 2005-02-11
;   PRIOR APPLICATION NUMBER: 09/606,740
;   PRIOR FILING DATE: 2000-06-23
;   PRIOR APPLICATION NUMBER: 60/141,031
;   PRIOR FILING DATE: 1999-06-25
;   PRIOR APPLICATION NUMBER: 60/142,101
;   PRIOR FILING DATE: 1999-07-02
;   PRIOR APPLICATION NUMBER: 60/148,613
;   PRIOR FILING DATE: 1999-08-12
;   PRIOR APPLICATION NUMBER: 60/187,970
;   PRIOR FILING DATE: 2000-03-09
;   PRIOR APPLICATION NUMBER: DE 19930476.9
;   PRIOR FILING DATE: 1999-07-01
;   PRIOR APPLICATION NUMBER: DE 19931415.2
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931418.7
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931419.5
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931420.9
;   PRIOR FILING DATE: 1999-07-08
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 709
;   LENGTH: 2599
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(2599)
;   OTHER INFORMATION: RXN02198
US-11-055-822-709

Query Match   2.9%; Score 112.8; DB 12; Length 2599;
Best Local Similarity 45.4%; Pred. No. 1.2e-20;
Matches 650; Conservative 0; Mismatches 737; Indels 45; Gaps 5;

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Qy   1162  CCGTACACCAACTTGTTAACATTGGAGAGCCCTGTAATGTTGCAGGATCAAGGAAGTTT  1221
           ||||| || ||| |||  ||| ||||||||| ||||  ||||| ||||||||  |||||
Db   1187  CAGGAAACCGGCATTTCCATGATCGGTGAGCGCACCAACTCCAACGGTTCCAAGGCATTC  1246

Qy   1222  GCTAAACTCATCATGGCAGGAAACTATGAGAGAAGCCTTGTGTGTTGCCAAAGTGCAGGTG  1281
           |||   ||  ||| |||||||||  || ||  || ||||| || |||||  |||| ||||
Db   1247  CGTGAGGCAATGCGTCTGTCTGGCGATTGGGGAAAAGTGTGTGGGATATTGCCAAGCAAACC  1306

Qy   1282  GAAATGGGAGCCCAGTGTTGCAACATGGATGATGCCATGCTAGATGGTGTCCAAGT  1341
           || |||||||| ||||||| |||||   || ||| |||  ||| |||||||| |||
Db   1307  CGGCGATGGTGCACACATGCTCGATCTTTGTGTGGATTACGTTGGGACGACGGCACCGGCC  1366
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Db   1367  GATATGGCGACCTTGGCAGCACTTCTTGCTAC--------CAGCTCCACTTGCCAATC  1417
           |||||||| ||||||||||||||||||||||||        |||| || |||| ||
Qy   1402  TGCATCGACTCCTCCAATTTTGCTGTGTGATTGAAGCTGGTCGCAAGGGAAG  1461
           ||||||||| |||||||||| |||| || |||||||||| || ||||||||
Db   1418  ATGATTGACTCCACCGAGCCAGAGGTTATTCGCACAGGCCTTGGGTGACGA  1477

Db   1462  TGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGACGA--------CTTCTTGGAG  1512
           ||||||  |  ||| |||||||||||||||||||||||||        |||||||||
Qy   1478  AGCATCGTTAACTCCGTCAACTTTGAAGACGGCGATGGCCCCGAGTCCCGTACCAGCGC  1537

Db   1513  AAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGCGTGGTCATGCGTTTTGATGAAGAA  1572
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Qy   1538  ATCATGAAACTGGTAAAGCAGAACAGACACAAAAATCAGAGTGTGCACCCGGGCCTACCATCTGCTT  1597

Db   1573  GGACAGGCAACAGAAACAGACAGAAAAATCAGAGTGTGCACCCGGGCCTACCATCTGCTT  1632
           ||||| ||| || ||||||||| |||||||||||||||| |||| ||||
Qy   1598  GGCCAGGCACGTACCCGTGAGCACCAGGTGCCATTGCTAAACGACTGATGACGATATC  1657

Db   1633  GTGAAAAAACTGGGCTTTAATCAAATGACATTATTTTGACCCTAATATCCTAACCATT  1692
           || || |||||||| |||| ||| ||  || ||||| || ||| |||| |||||
Qy   1658  ACCGGCAGCTACGGCCTGGATATCAAAGACATCGTTCGGACGTGCCTGCCTGACCTTCCCGATC  1717

Db   1693  GGGACTGGAATGGAGGAACACAACTTGTATGCCCATTAATTTTATCCATGCAACAAAAGTC  1752
           || || | ||||| |||  | ||||   ||| |||| ||  || ||||||| || ||
Qy   1718  TCTACTGGCCAGGAAGAAACCAGGCAGATGCATTGAAACCATCGAAGCCATCCGCGAG  1777

Db   1753  ATTAAAGAAACATTACCTGGACCAGAATAAGTGGAGTCTTTCCAACTTGTCCTTCTCC  1812
           || |||||| ||| ||||||| |||| ||||||||| ||||||| | |||| || |||
Qy   1778  CTGAAGAAGCTCTACCAGAATCCACCACCACCCCTGGGTCTGTTCCAATATTTCCTTCGGC  1837

Db   1813  TTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTTCTTTTACCATGCAATC  1872
           ||||||||||||||||||||||  | || |||||| || |||||| |  | ||||| |||
Qy   1838  CTG------AACCCTGTCGCACGCCAGGTTCCTTAACTCGTGTTCCCAATGAGTGCATT  1891

Db   1873  AAGTCTGGCATGACATGGAAGTAGTGAATGCTGAAAACTCCCCTGTGTATGATGATATC  1932
           |||| ||||| |||| ||||| |||  |||  |||||||||  || |||||||||
Qy   1892  GAGGCTGGTCTGGACTCTGCGATTGCGCAGACTCCAAGATTTTTGCCGATGAACCGCATT  1951

Db   1933  CATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACT  1992
           |||| ||||||| | | |  || |||||| || ||| ||||| ||||  |||||
Qy   1952  GATGATCGGCCAGCGCGAAGTGGCGTTGGATATGATGGTCTATGATGCGCCACCGAGGATTAC  2011

Db   1993  GAGAAGCTCTTACGTTACGGTTATGCCCAGACTCAAGGCAGAGGAGGAAAGTCATTCAGACT  2052
           |||||||| ||  |||| |  |||||||||||||| || ||||| || || ||||||||
Qy   2012  GATCCGCTGCAGGAATTCATGCAGCGTGTTTGA---GGGCGGTTTCTGCTGCCGATGCCAAG  2068

Db   2053  GATGAGTGGAGAAATGGCCCCTGTCGAAGAACGCCCTTGGTGAGTATGCCCTTGTGAAGGGCATT  2112
           |||| ||  | ||||| |||| ||||| ||| | ||| |||  |||||  || || ||| |||
Qy   2069  GATGCTCGCGCTGGAACAGCTGGCCGCTATGCCTATGGCGTTTCTTGAGCGTTTGGCCACAGCGCATC  2128

Db   2113  GAAAAACATATTATTGAGGAGTACTGAGGAAGCCAGGTTAAACCAAAAAAATATCCCCGA  2172
           ||||  ||||| |||||||| ||  |  | |||||||  |||  |||||| ||
Qy   2129  ATCGACCGGATAAGAATGGGCTCATGGCGATGATCTCGAAGCAGAGGAGAAGTCT  2188

Db   2173  CCTCTCAATATAATTGAAGGACCCCCTGATGAATGGAAATGAAAATTGTGGTGATCTTTTT  2232
           ||| | | | || ||||||||  ||| |||||| | || |||
Qy   2189  CCTATTGCGATCATCAACGAGACCTTCTCAACGGCATGAGACCGTGGGTGAGCTGTTTT  2248

Db   2233  GGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCGGGTTATGAAGAGAGGCT  2292
           ||||| |||| |||| ||| | || |||| ||||| |||  |||  ||| ||||| | |
Qy   2249  GGTTCCGGACAGATGCGAGCTGCCATTCGTGCTGCAATCGGCAGAAACCATGAAAACTGCG  2308

Db   2293  GTTGGGCACCTTATCCTTTCATGGAAAAGAAAGAGAAACCAGAGTGCTTAACGGC  2352
           ||  | || || | |  |||| || ||||||  ||||| ||||||  || |
Qy   2309  GTGGCCTATTTGGAACCGTTCATGGAAGGATGAGGAAGCAGAAGCTACCGGATCT--------  2359

Db   2353  ACAGTAGAAGAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTTAAAGGCGAC  2412
           ||| |
Qy   2360  --------GCGCAGGCGAGGGCAATGGCGCAAAATCGTCGTTGGCCACCGTCAAGGGTGAC  2410

Db   2413  GTGCACGACATAGGCAAGAACACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCCGAGTT  2472
           ||||||||| | ||||||||||  |||||| |||| |||| |   |    |||| ||||||
Qy   2411  GTGCACGATATCGGCCAAGAACTTGGTGGACATCATTTTGTCCAACAACGGTTACGACGTG  2470
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Qy  1342 GCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCGCAGACATCGCGAAAGTACCTTTG 1401
              ||||||||              |||||||
Db  1367 GATATGGCGACCTTGGCAGCACTTCTTGCTAC--------CAGCTCCCACTTTGCCAATC 1417

Qy  1402 TGCATGCTGACTCCTCCAAATTTTGCTGTGTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAG 1461
              ||||||||||||
Db  1418 ATGATTGACTCCCACCGAGCCAGAGGTTATTCGCACAGCCTTGAGCACTTGGGTGACGA 1477

Qy  1462 TGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACGA--------CTTCTTGGAG 1512
              ||||                                      |||||||||
Db  1478 AGCATCGTTAACTCCGTCAACTTTGAAGCGCCTGAGTCCGGTCACCGTGGTGATGA 1537

Qy  1513 AAGGCCAGGAAGATTAAAAAGTATGGAGCGTGCTATGGTGGTCATGGGTTTTGATGAAGAA 1572
              |||||||||||
Db  1538 ATCATGAAACTGGTAAAGCAGCACGCGGTGCGGCCGGTGTGGCACCCGGCCTACCCATCTGCTT 1597

Qy  1573 GGACAGGCAACAGAACAGACACAAAATCAGAGTGTGCACCCGGGCCTACCATCTGCTT 1632
              |||||||||
Db  1598 GGCCAGGCACGTACCGCGTGAGCACAAGTGCGCATTGCTAAACGACTGATTGACGATATC 1657

Qy  1633 GTGAAAAAACTGGGCTTTAATCCAAATGCATTATTTTTGACCCTAATATCCTAACCATT 1692
              |||||||                 |||
Db  1658 ACCGGGCAGCTACGGCCTGGATATCAAAGACACATCGTTGTGGACATCGTCTGCCTGACCTCGATC 1717

Qy  1693 GGGACTGAATGCGATGGAGGAACACAACTTGTATGCCATTAATTTATCCATGCAACAAAGTC 1752
              |||||||||||
Db  1718 TCTACTGCCGCAGAAGAAACCAGGCGACGATGGCATTGAAACCATCCGGCATCCGCGAG 1777

Qy  1753 ATTAAAGAAACATTACCTGGAGCCCAGAATAAGTGAGGTCTTTCCAACTTGTCCTCTCC 1812
              |||||||||||
Db  1778 CTGAAGAAGTCTCACCCAGAAATCCACACACCGGTCTGTCGTCCGATAATTTCCTTCGGC 1837

Qy  1813 TTCCGAGGAATGGAAGCCATTCGAGAGCAATGCATGCATGGGGTTTTCCTTACCATGCAATC 1872
              |||||                   |||
Db  1838 CTG------AACCCTGCTGCACGCCAGGTTCTTAACTCGTGTTCCCAATGAGTGCATT 1891

Qy  1873 AAGTCCTGCATGACATGAGATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATC 1932
              ||||||||||
Db  1892 GAGGGCTGGCTCTGAGACTCTGCGATTGCCGACAGCTCCAAGATTTTGCCGATGAACCGCATT 1951

Qy  1933 CATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAGCGCCACT 1992
              |||||
Db  1952 GATGATCGCAGCGCGAAGTGGCGTTGGAATGTCTATGATGTCTATGATCGCCGCACCGAGGATTAC 2011

Qy  1993 GAGAAGCTCTTACGTTACGTATGCCCAGACTCAAGGCACACGAGGAGGAAGAAAGTCATTCAGACT 2052
              ||||||                  ||||
Db  2012 GATCCGCTGCAGGAATTCATGCGAGCTCGTTTGA--GGGCGTTTCTCGCTGCCGATGCCAAG 2068

Qy  2053 GATGAGTGGGAGAAATGGCCCTTGCGAAGAACGCCTTGAGTATGCCCTTGTGAAGGGCATT 2112
              |||||||||||
Db  2069 CAGGAAAACCGGCATTTCCATGTCGCTATGCCGCCTGGCTCCCTTTGTTGTTGAGCAGGCATTC 2128

Qy  2113 GAAAACATATATTATTGAGGAATACTGAGGAAACGAGTTAAACCAAAAAATATCCCGA 2172
              |||||
Db  2129 ATCGACGCGATAAGAATGGCCTTGAGGATGATCTGAGGATGCAGGCAGGAAGTGTGGATATTGCCAAGCAGCAAACC 2188

Qy  2173 CCTCTCAATATAATTGAAGATGAGAAAATTGTTGGTGATCTTTT 2232
              ||||||||||||
Db  2189 CCTATTGCGATCATCAACGGAGACCTTCTCACGAGGATGGTGGGTGAGCTGTTT 2248

Qy  2233 GGAGCTGGAAAATGTTTCTACCTGATTATAAAGTTGCAGCCCGGGTTATGAGAAGGCT 2292
              |||||||                 |||
Db  2249 GGTTCCGGACAGAGTGCAGCTGGCCATTCGTGCTGTCGTGCTCAATGGGCAGAAAAACCATGAAAACTGCG 2308

Qy  2293 GTTGGCCACCTTATCCCTTCATGGAAGAAGAGAAGAAAACCAGAGTGCTTAACGGC 2352
              |||||                   ||||
Db  2309 GTGGCCTATTTGGAACCGTTCATGGAAGGAAGAGAAGAAGCTTGGGTGGGGACGA 2359

Qy  2353 ACAGTAGAAGAGAGGAACATAGGCAAGAACACATAGTTGGAGTAGTTGGAGTGCTATGGGTGCTATGGGTCATGGTCGTATGGTGGTCAT 2412
                                  --------        |||||||
Db  2360 --------GCGCAGGCAGAGGGCAAGGGCAAATCGTCGTCGTGGCCAAAATCGTCCGTCAACGGGTGAC 2410

Qy  2413 GTGCACGACAGACATAGGCAAGAACACATAGTTGGAGTGTCCTTGGGTGACTGCTATGGGTCATGGTCGTATGGTGGTCATGAAGAA 2472
              |||||||||||
Db  2411 GTGCACGATATCGGCAAGAACACTTGGTGTGGTGGACATCATTTTTGTCCAACACGGTTACGTACGACGTG 2470

Qy  2473 ATTGATTTAGGAGTCATGACTCCATGTGTATAAGATACTGAAAGCTGCTCTTGAACAACACAA 2532
              ||||||||||
Db  2471 GTGAACTTGGGCATCAAGCAGCACTGTCCGCCGCATGTTGGGAGCAGCCGGAAGAACACAA 2530

Qy  2533 GCAGATAATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAAATGA 2584
              |||||||||||
Db  2531 GCAGACGTCATCGGCATGTCGGGGACTTCTTGTGAAGTCACCGTGGTGATGA 2582
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RESULT 6
US-10-858-730-260
; Sequence 260, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 4.0
; SEQ ID NO 260
; LENGTH: 3666
; TYPE: DNA
; ORGANISM: Coryne-bacterium glutamicum
US-10-858-730-260

Query Match   2.9%; Score 112.8; DB 8; Length 3666;
Best Local Similarity 45.3%; Pred. No. 1.5e-20;
Matches 659; Conservative 0; Mismatches 752; Indels 45; Gaps 5;

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Qy  1162 CCGTACCACCAACTTGTTAACATTGGAGAGCGCGTGTAATGTTGCAGGATCAAGAAGTT 1221
              |||||||||||
Db  1087 CAGGAAAACCGGCATTTCCATGTCGCTATGCCGCCTGGCTCCCAACGCGTTCCAAGGCATTC 1146

Qy  1222 GCTAAACTCATCATGGCAGGAAACTATGAAGAAGAGCCTTGTGTGTTGCCAAGCAGCAAACC 1281
              |||||||||||
Db  1147 CGTGAGGGCAATGCGTCTGCGATTGGCGATTGGGAAAAGTGTGGATATTGCCAAGCAGCAAACC 1206

Qy  1282 GAAATGGGAGCCCAGGTGTTGATGATGGCATGCATGGTCAACATGGGTCGAGATGGTCCAGT 1341
              ||||||||                 |||
Db  1207 CGCGATGGTGCACACATGCTGATGATCTTTGTGTGGCGATTACGTGGCCAGACATCGCAAAGGTACCTTTG 1266

Qy  1342 GCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCGCAGACATCGCGAAAGGAGGCT 1401
              |||||                   ||||
Db  1267 GATATGGCGACCTTGGCAGCACTTCTTGCTAC-------CAGCTCCCACTTTGCCAATC 1317

Qy  1402 TGCATCGACTCCTCCAAATTTGCTGTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGGAG 1461
              |||||
Db  1318 ATGATTGACTCCCACCGAGCCAGAGGTTATTCGCACAGCCTTGAGCACTTGGGTGGACGA 1377

Qy  1462 ACAGTAGAAGAGAGGAACATAGGCAAGAACACATAGTTGGAGTAGTTGGAGTGCTATGGGTGCTATGGGTCATGGTCGTATGGTGGTCAT 1512
                                  --------        |||||||
Db  1378 AGCATCGTTAACTCCGTCAACTTTGAACGCGCCTGAGTCCGGTCACCGTGGTGATGA 1437

Qy  1513 AAGGCCAGGAAGATTAAAAAGTATGGAGCGTGCTATGGGTGGTCATGGGTTTTGATGAAGAA 1572
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Db   2491 CTTGAGGAGATGAACA 2506

RESULT 7
US-11-055-822-213
; Sequence 213, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 213
; LENGTH: 2578
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(2578)
; OTHER INFORMATION: FRXA02198
US-11-055-822-213

Query Match   2.9%; Score 112.4; DB 12; Length 2578;
Best Local Similarity 45.5%; Pred. No. 1.5e-20;
Matches 640; Conservative 0; Mismatches 721; Indels 45; Gaps 5;

Qy   1162 CCGTACCAACCTTGTTAACATTGGAGAGCGCGTGTAAATGTTGCAGGATCAAGGAAGTTT 1221
          ||| ||||| ||| |||| |||| | ||||||||| |||| |||| |||| |||| ||
Db   1187 CAGGAAACCGGCATTTCCATGATGCGGTGAGCGCACCACCTTCCAAGGCATTC 1246

Qy   1222 GCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGTGTGTTGCCAAAGTGCAGTG 1281
          | |||||||||||| |||||| ||| |||| || || ||| || ||||||||| |||
Db   1247 CCTGAGGCAATGCGTGTCTCGGCCATTGGCGAAAAGTGTGGGATAATTGCCAAGCAGCAAACC 1306

Qy   1282 GAAATGGGAGCCCAGGTGTTGCCAGGTGTGGATGTCAACATGGATGATGGGCATGCTAGAGTGTCCAAGT 1341
          | || ||||| |||||||| |||| ||| |||| |||||||||| ||||||||| ||| |||| |||||
Db   1307 CGCGATGGTGCACACATGCCTGGATCTTTGTGTGGATTACGTTGGGACGAGACGGCACCGCC 1366

Qy   1342 GCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCAGACATCGCAAAGGTACCTTTG 1401
          || |||| |||| |||||| |||| | ||||| || ||| ||| ||
Db   1367 GATATGCGACCTTGGCAGCACCTTCTTGCTAC-------CAGCTCCACTTTGCCAATC 1417

Qy   1402 TGCATCGACTCCTCCAATTTTGCTGTGATTGAAGGTGGTTAAAGTGCTGCCAAGGGAAG 1461
          | |||||| || || ||||||| ||||| ||| ||||| | || |||| |||||
Db   1418 ATGATTGACTCACCAGCCAGAGGTTATTCCGCACAGGGCCTTGAGCACTTGGGTGGACGA 1477

Qy   1438 ATCATGAAACTGGTAGCAGCAGCACGGTGCGCGGCCGGTTGCGTGTTGCACCGGCCTACCCATTGATGAGGAA 1497
          |||| | ||||| | ||| | || |||||||| |||| ||| |||| |||| |||| || | |||||| |||
Db   1573 GGACAGCAACAGAACAGACACAAAAAATCAGAGTGCGCACCCGGGCCTACCATCC 1632

Qy   1498 GGCCAGCGCACGTACCGCTGAGCACACAAGCTGCGCCATTGCTAAACGACTGATTGACGATATC 1557
          | | ||| | || || ||||| |||| | | || |||| ||| |||||||| |||| | ||
Db   1633 GTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATATCCTAACCATT 1692

Qy   1558 ACCGGCAGCTACGGGCCTGGATATCAAAGACATACGTGTGGACTGCCTGCCTTCCCGATC 1617
          |||||| || || || ||||| || | ||||| | | ||| ||| | ||||||||||
Db   1693 GGGACTGGAATGGGAGGAACACAACTTGTATGCCATTAATTTTATCCATGCAACAAAAGTC 1752

Qy   1618 TCTACTGGCCAGGAGGAAGAAACCAGGCGAGATGCATTGAAACCATCGAAGCCATCCGGCGAG 1677
          || | | ||| ||| ||||| | | |||| ||| |||| || || ||| | |||||| | ||
Db   1753 ATTAAAGAAACATTACCTGAGCCAGAAATCCACACCGGGTCTTCCAACTTGTCCTTCTCC 1812

Qy   1678 CTGAAGAAGCTCTACCCAGAAAATCCACACCCCTGGGTCTGTCCAATATTTCCTTCGGC 1737
          ||| |||||| || ||||| ||| || ||| || |||||| || || || ||||| |
Db   1813 TTCCGGGAATGGAAGCCAATTCGAGAGCAATGCATCGAGAGCAATGCATGGGGTTTTCCTTTACCATGCAATC 1872

Qy   1738 CTG------AACCCTGCTGCACGCGCAGGTTCTTAACTCTGTTCCTCCAATGAGTGCATT 1791
          ||| || ||||||||| | |||| ||||| ||| |||||| | |||||||
Db   1873 AAGTCTTGGCATGGACATGGAGATAGTGAATGCTGGAAACCTCCCCGTGTGTATGATGATATC 1932

Qy   1792 GAGGCTGGTCTGGACTCTGGCGATTGCGCAGCTCCAAGATTTTGCCGATGAACCGCATT 1851
          ||||| ||| ||| | || || ||| ||| || ||| ||||| || ||| ||||||
Db   1852 GATGATCGCCAGCGCGAAGTGGCGTTGGATATGGTCTATGATGCGCCGCAGCCGAGGATTAC 1911

Qy   1852 CATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACT 1992
          || | ||||| | || || | ||| | ||||| ||| ||| | | ||| || |||
Db   1912 GATCGCCGCTGAGCAGAAGATTCATCGCTGTGTTGA---GGGCGTTTCTGCTGCCGATGCCAAG 1968

Qy   1993 GAGAAGCTCTTCTTACGTGTTATGCCCAGACTCAAGGCACAGGAGGAGGAAGAAAGTCATTCAGACT 2052
          |||||||| | || || || ||| || ||||| || |||||| || |||| |||| |||| | |
Db   1969 GATGCTCGCGCTGCAACAGCTCGGCCGCCGTATGCGGCTATGCCTTTGTTGTTGGAGCACCAGCGCATC 2028

Qy   2053 GATGAGTGGAGAAATGCCCTGTCGAAGAACGCCTTGAGTAGTGCCCTTGTGAAGGGCATT 2112
          |||||||| || || ||| || ||||| |||| ||| | || |||| |||| |||
Db   2113 GAAAAACATATATTATTGAGGAGTACTGAGGAAGAAAGAGAAAAAGAAGAAGAAACCAGAGTGCTTAACGGC 2172

Qy   2113 GAAAAACATATATTATTGAGGATACTGAGGAAGAAAGAGAAAAAGAAGAAGAAGAAACCAGAGTGCTTAACGGC 2172
          ||| | | |||| |||| || || |||||||| || |||||||||| ||||| |||||| ||||||
Db   2029 ATCGACGGCGATAAGAATGGGCCTTGGAGGATGATCTCGAAGACGGCAGCGGCATGAAGCAGGAAGTCT 2088

Qy   2173 CCTCTCAATATAATTGAAGGACCCCCTGATGAAATGAAAATTGTTGGTGATCTTTT 2232
          || | | || ||||| |||| |||| ||||| ||| ||| |||| || || ||||
Db   2089 CCTATTGCGATCATCAACGAGGACCTTCTCAACGGCATGAAAATCCTCGTGTGAAGTCCACCGTGGAGCTGTGTT 2148

Qy   2233 GGAGCTGGAAAAATGTTCTACCTCAGGTTATAAAGTCAGCCGGGTTATGAAGAAGGCT 2292
          |||||| || | ||| | || | ||| | || | || || ||| |||| |||| ||
Db   2149 GGTTCCGGACAGCTGCAGCTGCAGGATGCAGATGCGTGCTGCAATCGGCAATCGGCAATCGGCAGAAAAACCATGCG 2208

Qy   2293 GTTGGGCCACCTTATCCCTTTCATGGAAAAAGAAGAAGACCAGAGTGCTTAACGGC 2352
          ||||||||| || || ||| ||||| |||||| || | ||| ||| ||||||
Db   2209 GTGGGCCTATTTGGAACCGGTTCAGGATGGAAGCAGAAGCTACC----------- 2253

Qy   2353 ACAGTAGAAGAAGAGAGACCCTTACCAGGGCACCATCGTGCTTGGCCACTGTTAAAGGCGAC 2412
          || || ||||| |||| ||| || ||| || || |||| | || | ||| ||| ||||
Db   2254 ---GGATCGCGCCCAGCAGAGGGCAAGGGCAAAATCCGTCGTGGCCACCGTCAAGGGTGAC 2310

Qy   2413 GTGCACGACATAGGCAAGAACATAGTTGGAGTGAGTGCTCCTTGGCTGCAATAATTTCCGAGTT 2472
          |||| ||||| || ||| | | | |||| || || |||| || ||| || ||| |||||
Db   2311 GTGCAGCAGATATCGGCAAGAACTTGGTTGGACATCATTTGTCCAACAACGGTTACGACGTG 2370

Qy   2473 ATTGATTTAGGAGTCATGAGTCCATGTGATAAGATACTGAAAGCTGTCTTGACCACAAA 2532
          ||||| || || || | | ||| || | | | | || ||| || |||| |||||
Db   2371 GTGAACTTGGGGCATCAAGCAGCCACTGTTGGAAGCAGCGGAAGAACAAA 2430

Qy   2533 GCAGATATAATTGGCTTGTCAGGACTCATCACTCCTTCCCTGGATGAAATGATTTTTGTT 2592
          ||||| ||| ||||| | || ||||| ||| | ||| | ||||||| | || |||||
Db   2431 GCAGACGTCATCGCGCATGTCGGGACTTCTTGTGAAGTCCACGTGGTGATGAAGGAAAAC 2490

Qy   2593 GCCAAGGAAATGGAGA 2608
          || || ||||| | |

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Qy   2533  GCAGATATAATTGGCCTGTCAGGACT  2558
           ||||||||||| ||||||||||||||
Db   2531  GCAGACGTCATCGGCATGTCGGGACT  2556
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RESULT 8
US-11-055-822-711
; Sequence 711, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
;   APPLICANT: Pompejus, Markus
;   APPLICANT: Kroger, Burkhard
;   APPLICANT: Schroder, Hartwig
;   APPLICANT: Zelder, Oskar
;   APPLICANT: Haberhauer, Gregor
;   TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
;   TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
;   FILE REFERENCE: BGI-121CPCN
;   CURRENT APPLICATION NUMBER: US/11/055,822
;   CURRENT FILING DATE: 2005-02-11
;   PRIOR APPLICATION NUMBER: 09/606,740
;   PRIOR FILING DATE: 2000-06-23
;   PRIOR APPLICATION NUMBER: 60/141,031
;   PRIOR FILING DATE: 1999-06-25
;   PRIOR APPLICATION NUMBER: 60/142,101
;   PRIOR FILING DATE: 1999-07-02
;   PRIOR APPLICATION NUMBER: 60/148,613
;   PRIOR FILING DATE: 1999-08-12
;   PRIOR APPLICATION NUMBER: 60/187,970
;   PRIOR FILING DATE: 2000-03-09
;   PRIOR APPLICATION NUMBER: DE 19930476.9
;   PRIOR FILING DATE: 1999-07-01
;   PRIOR APPLICATION NUMBER: DE 19931415.2
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931418.7
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931419.5
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931420.9
;   PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 711
;   LENGTH: 2578
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(2578)
;   OTHER INFORMATION: FRXA02198
US-11-055-822-711

Query Match   2.9%; Score 112.4; DB 12; Length 2578;
Best Local Similarity   45.5%; Pred. No. 1.5e-20;
Matches 640; Conservative   0; Mismatches 721; Indels 45; Gaps 5;

Qy   1162 CCGTACCACCAACTTGTTAACATTGGAGAGCGCCTGTAATGTTGCAGGATCAAGGAAGTTT 1221
           ||||| ||||||||||||||| ||||||| |||||||||||||| ||| ||| ||||
Db   1187 CAGGAAACCGGCATTTCCATGATCGGTGAGCGCACCACCAACTCCAACGGTTCCAAGGCATTC 1246

Qy   1222 GCTAAACTCATCATGGCAGGAAACTATGGAAACCTTGTGTGTTGCCAAAGTGCAGGTG 1281
           ||||| || ||| || |||| |||| | ||| | |||| ||| ||||
Db   1247 CGTGAGGCAATGCTGTCTCGGCGATTGGATGGAAAAAGTGTGGATATTGCCAAGCAGCAGCAAACC 1306

Qy   1282 GAAATGGAGCCCAGGTGTTGAGATGTCAACATGGATGATGGCATGCTAGATGGTCCAAGT 1341
           |||| | ||| ||| || || ||| || |||| |||| |
Db   1307 CGCGATGGTGCACACATGCTGGATCTTTGTGTGGATTACGTGGACGAGACGGCACCGCC 1366

Qy   1342 GCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGACATCGCAAAGGTACCTTTG 1401
           ||||||| | |||| || | | || | ||||||
Db   1367 GATATGGCGACCTTGGCAGCACTTCTTGCTAC--------CAGCTCCACTTTGCCAATC 1417

Qy   1402 TGCATGACTCCTCCAATTTTCGTGTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAG 1461
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Qy   1462  TGCATTGTCAATAGCATTAGTCTGAACGAAGAGAGGACGA--------CTTCTTGGAG  1512
Db   1478  AGCATCGTTAACTCCGTCAACTTTGAAGACGGCGATGGCCCTGAGTCCGTACCACGCGC  1537

Qy   1513  AAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGCTGTCATGGCTTTTGATGAAGAA  1572
Db   1538  ATCATGAAACTGGTAAAGCAGCAGCACGTGCGGCCGTGTTGCGGCCATTGATGAGGAA  1597

Qy   1573  GGACAGGCAACAGAAGACAGACACAAAAATCAGAGTGTGCACCCGGGCTACCATCTGCTT  1632
Db   1598  GGCCAGGCACGTACCGCTGAGCAATGCGCATTGCTAAACGACTGATTGACGATATC  1657

Qy   1633  GTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATATCCTAACCATT  1692
Db   1658  ACCGGGCAGCTACGGCCCTGGATATCAAAGACATCGTTGTGGACTGCTGCCTGCCCCCATC  1717

Qy   1693  GGGACTGCGAATGGAATACCTGGACCCAGATAAGTAGTGAATGCGAATTTTATCCATGCAACAACAAAAGTC  1752
Db   1718  TCTACTGGCCAGGAAGAAAACCAGGCGAGATGGCATTGAAACCATCGAAGGCCATCCGCGAG  1777

Qy   1753  ATTAAAGAAACATTACCTGGACCCAGAGATAAGTGGAGCTCTTTCCAACTGTCCTTCTCC  1812
Db   1778  CTGAAGAAGCTCTACACCGAGAATCCACCACCCCTGGGTCTGTTGCCAATATTTCCTTCGGC  1837

Qy   1813  TTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCCATGGGGTTTTCCTTTACCATGCAATC  1872
Db   1838  CTG------AACCCTGCTGCACGCCAGTTCTTAACTCGTGTTCCTCCAATGAGTGCATT  1891

Qy   1873  AAGTCTCGGCATGCATGGACACTGGAGATAGTAGTGAATGCTGGAAAACCTCCCTGTGTGATGATATC  1932
Db   1892  GAGGCTGGTCGTTGGACTTCTGCCGATTGCGCACAGCTCCAAGATTTGCCGATGAACCGCATT  1951

Qy   1933  CATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACT  1992
Db   1952  GATGATCGCCAGCCGCGAAGTGGCGTTGGATGTGGTCTATGATCCGCCGCCGAGG---AT  2008

Qy   1993  GAGAAGTCTTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAGTCATTCAGACT  2052
Db   2009  TACGATCCGCTGCAGGAATTCATGCAGCTGTTTGAGGCGTTTCTGCCGATGCCAAG  2068

Qy   2053  GATGAGTGGGAGAAATGGCCCTGTCGAAGAACCGCCTTGTGCCCTTGTGAAGGGCATT  2112
Db   2069  GATGCTCGGCGTGAACAGCTGGCCGCGCTATGCCTTTGTTGAGCGTTTGGCACAGCGCCATC  2128

Qy   2113  GAAAAAACATATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAATATCCCCGA  2172
Db   2129  ATCGGCGATATAAGAATCGGATGAATGGCAGGAGGCATGAGAGGAGAGTCT  2188

Qy   2173  CCTCTCAATATAATTGAAGGACCCCCTGATGAATGGAAATTGTTGGTGATCTTTTTT  2232
Db   2189  CCTATTGCGATCATCATCAACGAGCATCGAGAACCTCTCAACGGCATGAGAACCGTGGGTGAGCTGTGTT  2248

Qy   2233  GGAGCTGAGAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCGGGTTATGAAGAGAGGCT  2292
Db   2249  GGTTCCGGACAGATGCAGCTGCCATTCGTGCTGCAATCGGCAGAAACCATGAAAAACTGCG  2308

Qy   2293  GTTGGGCCACCTTATCCCTTCATGAGAAAAGAGAAGAAAGACCAGAGTGCTTAACGGC  2352
Db   2309  GTGGGCCTATTTGGAACCGTTCATGGAGAACGGATGGAGAGGAGCAGAGAAGTCTACC------  2353

Qy   2353  ACAGTGAAGAAGAGAGACCCTTACCAGGGGCACCATCCGTGCTGGCCACTGTTAAGGCGAC  2412
Db   2354  ---GGATCTGCGCGGAGGAGAGGGCAAAATCGTCGTGGCCACCGTCAAGGGGTGAC  2410

Qy   2413  GTGCACGACATAGGCGAAGAACATAGTTGGACTAGTCCTTGGCCTGCAATAATTTCCGAGTT  2472
Db   2411  GTGCACGACGATATCGCAAGAACTTGGTCGACATCATTTTGTCCAACAACGGTTACGACGTG  2470

Qy   2473  ATTGATTTAGGAGTCATGAGTCCATGTGATAAGATACTGAAAGCTGCTCTTGACCACCAAA  2532
Db   2471  GTGAACTTGGGCATCATCAAGCAGCAGCAGCCACTGTGCCCGCCACTGTTGGAAGCAGCAGCAGGCAGCAGGGAAG  2530
```

```
Db   2471 GTGAACTTGGGCATCAAGCAGCCACTGTCCGCCATGTTGGAAGCAGCGGAAGAACACAAA 2530

Qy   2533 GCAGATAATTGGCCTGTCAGGACT 2558
               |||| ||  ||| |||| ||||||
Db   2531 GCAGACGTCATCGGCATGTCGGGACT 2556
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RESULT 9
US-09-925-065A-697175/c
; Sequence 697175, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 697175
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-697175

Query Match   2.6%; Score 101.4; DB 6; Length 616;
Best Local Similarity 97.1%; Pred. No. 7.7e-18;
Matches 102; Conservative   1; Mismatches 2; Indels 0; Gaps 0;

Qy   2739 GTGTTCCCAGCTGTTAGATGAAGAAATCTAAAGGATGAAATACTTTGAGGAAATCATGGAAGA 2798
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 GTGTTCCCAGCTGTTAGATGAAGAAATCTAAAGGATGAAATACTTTGAGGAAATCATGGAAGA 75

Qy   2799 ATATGAAGATATTAGACAGGACCATTATGAGTCTCTCAAGGAGAG 2843
          ||||||||||||||||||||||||||||||||||||||||||
Db   74 ATATGAAGATATTAGACAGGRCCATTATGAGTCTCTCAAGGTAAG 30
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RESULT 10
US-10-858-730-141
; Sequence 141, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10

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Db   1418 ATGATTGACTCCACCGAGCCAGAGGTTATTCGCACAGGCCTTGAGCACTTGGGTGACGA 1477
               || |||||| || || ||||      ||                      ||
Qy   1462 TGCATTGTCAATAGACATTAGTCTGAAGGAAGGAGGAGGACGA-------CTTCTTGGAG 1512
               ||| |                                           ||
Db   1478 AGCATCGTTAACTCCGTCAACTTGAAGACCGCGATGGCCCTGAGTCCGCTACCAGCGC 1537

Qy   1513 AAGGCCAGGAAGAGATTAAAAAGTATGAGAGCTGCTATGGTGGTCATGGCTTTTGATGAAGAA 1572
               |||||      || |||||||||
Db   1538 ATCATGAAACTGGTAAAGCAGCACGACAGACAAAAATCAGAGTGTGCACCCGGGCTACCATCTGCTT 1597

Qy   1573 GGACAGGCAACAGAAACAGAACACAAAAATCAGAGTGTGCACCCGGGCTACCATCTGCTT 1632
               ||||
Db   1598 GGCCAGGCACGTACCCGCTGAGCGACAAGGTGCGCCATTGCTAAACGACTGATTGACGATATC 1657

Qy   1633 GTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTTAATATCCTAACCATT 1692
               || |
Db   1658 ACCGGCTACGCCGGGATATCAAAGACACATCGTTGTGGACTGCCTGACCTTCCCGATC 1717

Qy   1693 GGGACTGGAATGGAAGAACACAACTTGTATGCCATTAATTTTATCATGCAACAAAAGTC 1752
               ||| || |
Db   1718 TCTACTGGCCAGGAGAAAACCAGGCGAGATGCATTGAAACCATCGAAGCCATCCGCGAG 1777

Qy   1753 ATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTGTCCTTCTCC 1812
               || | |||| ||     |  ||
Db   1778 CTGAAGAAGCTCTACCCAGAAATCCAACCACCACCCTGGGTTTCCAATATTTCCTTCGGC 1837

Qy   1813 TTCCGGGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTCCTTTACCATGCAATC 1872
               ||
Db   1838 CTG------AACCCTGTGCACGCCAGGTTCTAACTCGTGTTCCTCAATGAGTGCATT 1891

Qy   1873 AAGTCTCGGCATGGACATGGAGATAGTGAATGCTGGAAAACCTCCCTGTGTATGATGATATC 1932
               |||
Db   1892 GAGGCTGGTCTGGACTCTGGACTTCTGCAGCTCTGAAGATCTCATCTGGAATAAAGACCCACT 1951

Qy   1933 CATAAGGAAACTTCTGCAGCTCTGTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACT 1992
               ||  |||
Db   1952 GATGATCGCCAGCCGCGAAGTCGCGTTGGATATGGTCTATGATGCGCCGCGACGGAG---AT 2008

Qy   1993 GAGAAGCTCTTACGTTATGCCCAGACTCAAGGCCACAGAGGCGGAAGAAAGTCATTCAGACT 2052
               ||
Db   2009 TACGATCGCGTCGCAGGAATTCATGCAGCTGTTTGAGGCGGTTTCTGCTGCCGATGCCAAG 2068

Qy   2053 GATGAGTGGAGAAATGGCCCCTGTCGAAGAACGCCCTGTGTAGTGCCCTTGTGTGAAGGGCATT 2112
               ||| |
Db   2069 GATGCTCGCGCTGGAACAGCTGGCCGCTATGCCGTATGCCTTTGTTGGCGTTTGGCCACAGCGCATC 2128

Qy   2113 GAAAAACATATTATTGAGGAATACTGAGGAAGCCAGGTTAAACCAAAAAAATAATCCCCGA 2172
               |||
Db   2129 ATCGACCGGCGATAAGAATGGCCGATGATTCTGAGGAGCAGGCATGAGGAGGAGTCT 2188

Qy   2173 CCTCTCAATATAATTGAAGGACCCCCTGATGAATGAAATTGTTGGTGATCTTTTT 2232
               ||    |||
Db   2189 CCTATTGCGATCATCAACGAGACCTTCTCAACGGCCAAAATCCTCGTGGCCAAGGGTGTTT 2248

Qy   2233 GGAGCTGGAAAAATGTTGTTCTACCTCAGGTTATAAAGTCAGCCCGGGGTTATGGAAGAGGCT 2292
               ||||||
Db   2249 GGTTCCGGACAGATGCAGCTGCAGCTGCCATTCGTGCTGCAATCGGCAGAAACCATGAAAACTGCG 2308

Qy   2293 GTTGGGCCACCTTATCCCTTTCATGGAAAAAGAAGAAGAACCAGAGTGCTTAACGGC 2352
               ||||||
Db   2309 GTGGCCTATTGTGGAACCGTTCATGGAAGAGGAAGCAGGAAGCTACC------------ 2353

Qy   2353 ACAGTGAAGAAGAAGAGACCCCTTACCAGGGCACCATCCGTGCTGGCCACTGTTAAAGGCGAC 2412
               ||  ||||||                   ||     |||
Db   2354 ---GGATCTGCGCAGGCGCAGAGGGCAAGGGCAAAAATCCTCGTGGCCACCGTCAAGGGTGAC 2410

Qy   2413 GTGCACGACATAGGCAAGAACATAGTTGGAGTAGTGCTTCCTGCAATAATTTCCGAGTT 2472
               |||||| |||||  ||||||||   || | |         | ||
Db   2411 GTGCACCAGATATCGGCCAAGAACTTGGTCGACATCATTTTGTCCAACAACGGTTACGACGTG 2470

Qy   2473 ATTGATTTAGGAGTCATGACTCCGATGTGATAAGAATACTGAAAGCTGCTCTTGACCACAAA 2532
               || || |                ||      ||      |||
```

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; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 3477
; TYPE: DNA
; ORGANISM: Thermobifida fusca
US-10-858-730-141

Query Match        2.4%;  Score 93.4; DB 8; Length 3477;
Best Local Similarity 43.6%;  Pred. No. 4.3e-15;
Matches  628;  Conservative  0; Mismatches 766; Indels 45; Gaps  3;

Qy 1145 AGCCCTTCAGGATTGGACCGTACCACCAACTTTGTTAACATTGGAGACGCGCTGTAATGTTG 1204
Db  980 AGAGGGTCCCGTTCCGGCCAGGACACCAGCTACCTGGCGATCGGGGAACGCACCAACGCCCA 1039

Qy 1205 CAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGAAAACATGAAGAAGCCTTGTGTG 1264
Db 1040 ACGGCTTCAAGGCGTTCCGCGAAGCCATGCTCGCGGAACGGTCACGACGACTGTGTGGAGA 1099

Qy 1265 TTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTGTTGGATGTCAACATGGATGATGGCA 1324
Db 1100 TCGCCCGCCAGCAGATCCGGCCGGCGGCGATCGGGGACGTCGACCTGCGTCGACTATGTGG 1159

Qy 1325 TGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTAATTGCTTCCGAGCCAGACA 1384
Db 1160 GACGCGACGGCGGGTGCGGGAGCTGGCTTCCCGGCTGGCCACCGCCTCCACGC 1219

Qy 1385 TCGCAAAGTGTACCTTTTGTGCATCGACTTCCTCCAATTTTGCTGTGATTGAAGCTGGGTTAA 1444
Db 1220 TGCCGGCTCGTACTGGACTCCACCGAGTAGCCGTACTGGGACTGGAGATGCTGG 1279

Qy 1445 AGTGCTGCCAAGGGAAGTGCATTGTCAATAGACATTAGTCTGAAGGAAGGAGGAGGACT 1504
Db 1280 GCGGGCGCGCCCGTGCTCAACTCGGTCAACTACGAGAGACGGCCCTGACTCCCGGT 1339

Qy 1505 TCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGTCATGGCTTTTG 1564
Db 1340 TCGCCAAGTGCCGCGGCTGGCCGTGGCTGGAGCACGGGGGCCCTCATGGCGCTGACCATCG 1399

Qy 1565 ATGAAGAAGGAGCAGGCAACAGAGCAACACAGAAAAATCAGAGTGTGCACCCGGGCTACC 1624
Db 1400 ACAGACAGGGGGCAGGGCGCGGCAGCCGGGACGGAAAGTGGAGGTCGCCGAAAGTGCGGCTCATCC 1459

Qy 1625 ATCTGCTTGTGTGAAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATATCC 1684
Db 1460 GGCAGCTCACCACCGAGTACGGCCATCCGCAAGCACGACATCATCGTGACTGCTGCCTGACCT 1519

Qy 1685 TAACCATTGGGACTGGAATGGAAGGAGGAACAACTTGTATGTCCATTAAATTTATCCATGCAA 1744
Db 1520 TCACGATCGCAACCGGACAGGAGGAGTCGCGCGCGGACGACGACGAGCTCTCGGAAACCATCGAGGCGA 1579

Qy 1745 CAAAAGTCATTAAGAAAAGCATTAGCCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTGT 1804
Db 1580 TCCGTGAACTGAAGCGGCGCCACCCGGACGTGCGAGACGCTGGGCCGTGTCAA----- 1634

Qy 1805 CCTTCTCCTTCGGCGAGAGGAATGAAGGCCATTGAGAAGCAATGCATGGGGTTTCCTTTACC 1864
Db 1635 -CGTCTCCTTCGGGCTCAACCCGGCTGCCCGGATTGTGCTCAACTCGGTGTTCCTCCACG 1693

Qy 1865 ATGCAATCAAGTCTGGCATGGACATGGAGACATAGTGAAATGCTGAAAACCTCCCTGTGTATG 1924
Db 1694 AGTGCGTCCAGGCCGGCCGGTTGGACTCCGGATCGTGCACGACGTCTCCAAGATCCTGCCGATCA 1753

Qy 1925 ATGATATCCATAAGGAACTTCTGCAGCTTCTGTGAAGATCTCATCTGAATAAAGACCCTG 1984
Db 1754 ACCGGCATCCCCGAGGAGCAGCGGCAGGTGGCGTTGGACATGAATCTTACGACCGCCGCACCG 1813

Qy 1985 AGGCCACTGAGAAGTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAGGAGAAAGTCA 2044
Db 1814 ATGACTACGACCCGCTGCAAGCGTTCCTGCAGCTTTTCGAAGAGGAGTGACGCGCAGGCGA 1873

Qy 2045 TTCAGACTGATGAGTGAGGAAATGGCCCTGTCGAAGAACGCCCTTGAGTATGCCCTTGTGA 2104
```

(Right column)

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Db 1874 T---GCGCGCCTGCGCGGAGGAGAAGAGAGTGGCCGCGCTGCCGCTGTGTGGGAGGCGGCTGGAGC 1930

Qy 2105 AGGGCATTGAAAAACATATTATTGAGGATACTGAGAGAGCCAGTTAAACCAAAAAAAT 2164
Db 1931 GCCGTATCGTCGACGGGGAAGCCGCCGGCATGGAAGCCGGACCTGGACGAAGCGGCTCACCC 1990

Qy 2165 ATCCCCGACCTCAATATAATTGAAGACCCCTGATGAATGAAAATTGTTGGTG 2224
Db 1991 AGCGGTCCGGCGCTGGACATCATCAACAACCACGCTGCTGCGGGGATGGAAGACCGTCGGCG 2050

Qy 2225 ATCTTTTTGGAGCTGAAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGTTATGA 2284
Db 2051 ACCTGTTCGGCTTCGGGCAGGATGCAGCTCCCGTTCGTCGTGCTGAAGTCGGCGAGGTGATGA 2110

Qy 2285 AGAAGGCGTGTTGGCCACCTTATCCCTTTCATGGAAAAGAGAGAAAGAAACCAGAGTGC 2344
Db 2111 AGGCCGGCGCCGTGCCTATCTGGAGCCGCCACATGGAGGTG--------- 2151

Qy 2345 TTAACGGCACAGTAGAAGAAGGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTTA 2404
Db 2152 --------GACGGCGACCTCGGCAAGGCGGGATCGTGCTGGGCCACGGTCA 2194

Qy 2405 AAGGCGACGTGCGACGACTAGGCAAGAACATAGTTGGAGTAGTGCTTGGCTGGTCGCAATAATT 2464
Db 2195 AGGGCGACGTCCACGACATCGGCAAGAACCTTGTGGACATCATCCTGTCCAACAACGGCT 2254

Qy 2465 TCCGAGTTATTGATTTAGGAGTCATGAGTCATGTGATAGAATACTGAAAGCTGCTCTTG 2524
Db 2255 ACGAGGTCATCAACCTGGGGATCAAGCAGCCCATCTCCGGATTCTGAGAGGCGCCGAGC 2314

Qy 2525 ACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGATGAAATG 2583
Db 2315 GGCACCGCGCCGACGTGATCGGCATGTCCGGCCATGTCGGCGCTGCGTGGAAGTCCACGGTGTGATG 2373
```

```
RESULT 11
US-10-858-730-142
; Sequence 142, Application US/10858730
; Publication No. US20050255568A1
GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Vorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 3513
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-858-730-142

Query Match        2.3%;  Score 91.4; DB 8; Length 3513;
Best Local Similarity 44.3%;  Pred. No. 1.6e-14;
Matches  642;  Conservative  0; Mismatches 741; Indels 66; Gaps  4;

Qy 1145 AGCCCTTCAGGATTGGACCGTACCACCAACTTTGTTAACATTGGAGAGCGCGCTGTAATGTTG 1204
```

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Db  1019 ||||||  |  |||  |||  ||| ||  |||||||  ||||||  ||
         AGACCGTGCCCTTCCGCGACACCTCCTACCTGGCCATCGGCGACGCCACCAACGCCA 1078

Qy  1205 CAGGATCAAGAAGAAGTTTGCTAAACTCATCATGGCCAGGAAACTATGAAGAGAGCCTTGTGTG 1264
Db  1079 ACGGGTTCCAAGAGAGTTCCGCGAGGGCCATGCTGGACGGCGACTGCGTCGAGA 1138

Qy  1265 TTGCCAAAGTGCAGGTGGAAATGGGAAGGGCGCACAGGTGTTGGATGTGATGATGGCA 1324
Db  1139 TGGCCCGCGACCAGATCCGCGAAGGGCGCACATGCTGCGTCTTGCGTCGACTACGTCG 1198

Qy  1325 TGCTAGATGGTCCAAGTGCAATGACCAGATTTGCACTTAATTGCTTCCGAGCCAGACA 1384
Db  1199 GCCGGGGACGGCGTCGGCGACATGCGAGGAACTGGCCGCGGTTGGCCACCGCCTCCACGC 1258

Qy  1385 TCGCAAAGGTACCTTTGTCGATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTTAA 1444
Db  1259 TGGCCGATCGTCCTCGACTCCACCGGAGTCGACGTCATCGGCCGCGGTCATCGGGAGAAGCTCG 1318

Qy  1445 AGTGCTGGCCAAGGGAAGGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGACGACT 1504
Db  1319 GCGGGCCGCGCGGCCGGTGATCAACTCGGTCAACTACGAGGACGGGCGGCCCGGCCGGAGTCCCGGT 1378

Qy  1505 TCTTTGGAGAAGGCCAGGAAGAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTTTTG 1564
Db  1379 TCGCCCCGCGTCACGAGCTCGCCCGGGAGCACGCGGCCGCGATCGATCGCCGTGATCACCATCG 1438

Qy  1565 ATGAAGAAGGACAGGCAACAGAACAGAGACACAAAAATCAGAGTGTGCACCCGGGCCTACC 1624
Db  1439 ACGAGGTGGGACAGGCCCGACACCGCCCGAGAGAAGAGGTCGAGATCGCGCAAGCGGCTCATCG 1498

Qy  1625 ATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTTGACCCTAATATCC 1684
Db  1499 ACGACCTCACCCGGCATCGGGCATCCAGATTCCACAGTCCGACTCCGTCGACTGCCTGACCT 1558

Qy  1685 TAACCATTGGGACTGGAATGGAGGAACACACTTGTATGCCATTAATTTTATTCATCATGCAA 1744
Db  1559 TCACCCATCTGCACCGGCACGGCACGGAGTCCCCAAGGACGGCCTGGCCACCATCGCGAGGGCA 1618

Qy  1745 CAAAGTCATTAAAGAGAAACATTTACCTGGAGCCAGGAATAAGTGCAGGTCTTTCCAACTTGT 1804
Db  1619 TCCGGGAACTCAAGCGACCACGCGCCCACCCGACGTGCAGACCACGCTCGGCCTGTCGAACCATCT 1678

Qy  1805 CCTTCTTCCTTCCGAGGAATGGAAGCTCATTCGAGGTTATGCCCAGACTCAAGGCATGGGGTTTCCTTTACC 1864
Db  1679 CCTTCGGCCTC------AACCCGCGCCGCCGAGGGACTGGCGCCGCCTCTTCCTCCGAGACG 1732

Qy  1865 ATGCAATCAAGTCTGGCATGACATGGACATGTGGCATAGTGAATGCTGGAAACCTCCCTGTGTATG 1924
Db  1733 AATGCGTCAAGGCCGCGGCCGGACTCGGCGACTGCACGCGCAGCAAGATCCTGCCCGATCG 1792

Qy  1925 ATGATATCCATAAGGAAACTTCTGCAGCTCTGCGTCGAAGATCTCATCTGGAATAAAGACCCCTG 1984
Db  1793 CCCGCTTCGACGAGGAGCAGGTCCACCAGGGCTCACCACGCGGCCGGGCGCGCG 1852

Qy  1985 AGG-------CCACTGAGAAGCTCTTACGGTTATGCCCAGACTCAAGGCACAGAGGAGGGA 2035
Db  1853 AGGGCTACGACCCCCTGCAAAAGCTCATGCAGCTCTTCGAGGGGCGGCCCCAAGCTCGC 1912

Qy  2036 AGAAAGTCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGCCCTTGAGTATG 2095
Db  1913 TGAAGGCCTCCAAGGGCGAGGAGCTGCCCGCGCCCTCCCGCTGGAGCGGCCTTCAAGCGCC 1972

Qy  2096 CCCTTGTGAAGGGCCATTGAAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACC 2155
Db  1973 GCATCATCGACGGCGAGAAGACGGCCTCGAACAGGACCTCGACGAGGCC------ 2022

Qy  2156 AAAAAAAATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAATGAAAA 2215
Db  2023 --CTCCGGGAGCGCCCCGCCGAGGTATGAAGG 2080

Qy  2216 TTGTTGGTTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCGCCC 2275
```

```
Db  2081 TCGTCCGGCGGAGCTGTTCGGCCGGCAGATGCAGTCAGCTGCCGTCGGTCGTGCTCCAGTCCGGCG 2140
Qy  2276 GGGTTATGAAGAGGCGTTGTTGGGCCACCTTATCATCCTTTCATGGAAAAAGAGAAGGAAGAA 2335

Db  2141 AGTCATGAAGAAGACCCGCGGTGGCCACCTGGAGCCGACCATGACGAGGCCGACGACG 2200
Qy  2336 CCAGAGTGCTTAACGCACAGTAGAGAAGAGAGACCCTTACCAGGGCACCATCGTGCTGG 2395

Db  2201 GCA----------------------AGGGCACGATCGTGCTGG 2221
Qy  2396 CCACTGTTAAAGGCGACGTGACGACGTGCGACGACATAGGCGACGAAGACACATAGTTGGAGTAGTCCTTGGCT 2455

Db  2222 CCACCGTTCCGCGGCGACGTCCACGACATGCGGCAAGAACCTCGTCGACATCATCCGTGTCCA 2281
Qy  2456 GCAATAATTTCCCAGTTATTGATTTAGGAGTCATGACTCCATCGATAAGATACTGAAAG 2515

Db  2282 ACAACGGCTACAACGTCGTCAACCTCGTCCGCGGCCATGTCCGGATCCTGAAG 2341
Qy  2516 CTGCTCTTGACCACAAAGCAGATATAATTGGGCTGTCAGGACTCATCACTCCTTCCCTGG 2575

Db  2342 CGGCCGACGAGCACCGGGCCGCACGTCATCGGCGATGTCCGGATCCTCCTCAAGTCCACGG 2401
Qy  2576 ATGAAATGA 2584

Db  2402 TGATCATGA 2410
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RESULT 12
US-10-858-730-144
; Sequence 144, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Mycobacterium leprae
US-10-858-730-144

Query Match   2.3%; Score 89.6; DB 8; Length 3621;
Best Local Similarity 44.1%; Pred. No. 5.2e-14;
Matches 1039; Conservative 0; Mismatches 1199; Indels 120; Gaps 11;

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Qy  234 AGATCATGCCAGGCCGCTGAAAGGCAACAATGACATTTTAGTATAACTCAGCCTGATGT 293
Db  123 AGATGATTTCCGCGGCCTGGACGGGCTGCAACGATTCTCAACGAAACGCGTCCTCAAGCGT 182

Qy  294 CATTACCAAATCCATAAGGAATACTTGCTCGGCGGCAGATATCCATTGAAACAAATAC 353
Db  183 GCTGGAAACCATCCACCGACACCACCACCTCGAGGCAGCAGGTGCGGACGACCACCAC 242

Qy  354 TTTTAGCACTAGTATTGCCCAAGCTGACTAGGCCTATGGCCTTGAACACTTGGCCTACCGGAT 413
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Qy  1476 CATTAGTCTGAAGGAAGGAGGAGGACGACTTCTTGGAGAAGGCCAGGAGAGATTAA------ 1529
              |||||||||||||||| |||| | ||  |||||  ||| | || |
Db  1341 CGTCAACTACGAGGACGGTGACGGTCCGAGTCAGGTTGTCGAAGACCATGGAGTCGT 1400

Qy  1530 ---AAAGTATGGAGCTGCTATGTGGTCATGGCTTTTGATGAAGAAGAACAGGCAACAGA 1586
            |||| | | ||  ||||||||||||||||||||||||||||||
Db  1401 CGCCGAGCACCGAGCGGCGGTCGTTGCGCACCATCGACCGTCAGGTCCCGCAC 1460

Qy  1587 AACAGACACAAAAATCAGATGTCACCCGGGCTACCATCGCTCGTGTGAAAAAACTGGG 1646
             |||||||||||||||||||||||||||||||||||||||||||
Db  1461 CGTTGAGAAGAAGGTCGAAGTCGGACGCTTATCGAGCTTGATGACATTACGACTAACTGGGG 1520

Qy  1647 CTTTAATCCAAATGACATTATTTTGACCCTAATATCCTAACCATTGGGACTGGAATGA 1706
             ||||| | |||||||||||||||||||||||||||||||||||||
Db  1521 CGTTGATAAATCGGCGATTCTCATCGATTGCTTTACTGTTTTACTATTGCCACTGGCCAGA 1580

Qy  1707 GGAACCAACTTGTATGCCATTAATTTTATCCATGCAACAAAAGTCATTAAAGAAAACATT 1766
             ||||||||||||||||||||||||||||||||||||||||||||
Db  1581 GGAGTCACGCAAAGACAACCGCATTCGAGTCGTGAGCGTGAAGAAGCCGGCA 1640

Qy  1767 ACCTGGAGCCAGAATAAGTGGAGGTCTTCCAACTTGTCCTTCCTTCCGAGGAATGGA 1826
             |||||||||||| || |||||||||||||||||||
Db  1641 CCCAGGCGTGCAGACTACGCGTGGGGTTGTGTCCAA------CATCTCCTTCGGTCTCAATCC 1694

Qy  1827 AGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTACCATGCAATCAAGTCTGGCATGA 1886
             |||||||||||||||||||||||||||||||||||||||
Db  1695 TTCTGCACGCCAAGTTCTTAACTCTGTTTTTCACATGAATGTCAGGAGCAGGACTGA 1754

Qy  1887 CATGGAGATAGTGAATGCTGAAATCTCCCTGTGTGTGATGGAATAATTGAAAAATG 1946
             || ||||||||||||||||||||||||||||||||||||||
Db  1755 TTTCGGCGATTGTGCACCGTCAAAGATATTGGCCATCAACCCGATACCCGAAGAACAGCG 1814

Qy  1947 GCAGCTCTGTGAAGATCTCATCTGGAAT-------- 1997
             |||||||||||||
Db  1815 CCAGGCTGCGCTGGATCTTAGTGTTATGACGAGCCGTCCGCGGAAGGCCGAAGGTCTGCAGAA 1874

Qy  1998 GCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAGTCATTCAGACTGATGA 2057
             |||||||||| |||||||||||||||||||||||
Db  1875 GCTGATGTGGTTATTCAAAGGTGTGTCGCGCCATCGTGAAGGGAAACACGGAGGCAGA 1934

Qy  2058 GTGGAGAAATGGCCCTGTGAGTGAACGCCTTGTGAGTATGCCCTTGTGAGGGGCATTGAAAA 2117
             |||||||||||||||||||||||||||||||||||||
Db  1935 ACTCGCTAAGTGCCGTTGTTGCACCGGATCGTCGACGCGGATCGTCCGGGGAAGT 1994

Qy  2118 ACATATTATTGAGGATCTGAGAGTGAAGCCAGGTAAACCAAAAAAAATATCCCGACCTCT 2177
             ||||||||||||||||||||||||||
Db  1995 CGGGTTAGATGTTGATCTGACGAGGCAATGACCCCAGAAA--------CCGCCGTT 2042

Qy  2178 CAATATAATTGAAAGGACCCCTGATGAATGGAATGAAAATTGTTGTGATCTTTTGGAGC 2237
             |||||||||||||||||||||||||||||||
Db  2043 GGCGCATCATCAACGAGAAGCCTGCTGGACGCGGATTGTGTCTGGCTCGGTCGGGCTC 2102

Qy  2238 TGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTATGAGAAGAAGGTGTTGG 2297
             |||||||||||||||||||||||||||||||
Db  2103 TGGGCAGATGCAGCTGCGTGTTTCGTTTGCAGTGCAGTCGGGTTATGAAAGCAGCGGTGGC 2162

Qy  2298 CCACCTTATCCCTTCATGGAAAAAGAAGAAATGGGAGGCCCA 2357
             ||||||||||||||||||
Db  2163 TTATCTACGAAAACCGCCGCACACCGAGAAT--------TCCGACTGTGA 2198

Qy  2358 AGAAGAGGAGACACCCTTACCAGGGCACACTGCTGGCCACTGTGTTAAGGCGACGTGCA 2417
             |||||||||||||||||||||||||||||
Db  2199 CTTCGGTAAGGGGTTAGCGCGGGTCGGACGGATTGTGCTCGGCTACCGTCAAAGGAGAGTGTGCA 2258

Qy  2418 CGACATAGGCAAGAACACATAGTTCGAGTAGTCCTTGGCTCGCAATAATTTCCGAGTTATTGA 2477
             |||||||||||||||||||||
Db  2259 CGATATTGGCAAAAAACCTCGTCGATATCATTCTGAGCAACAACGGCTACGAAGTGGTAAA 2318

Qy  2478 TTTAGGAGTCATGACTCATGTGCCAAGGGAAGTGCATTGTTCAATAG 2537
             |||||||||||||||
Db  2319 CCTCGGCCATCAAGCAGCCGCAGATTACCAACATTCTCGAGTGGTCGCGAGCAGGACAAAAAGCGCCGA 2378



Db   243 TTTCGGCTGCAACCTGTCCAACCTTGGTGACTACGACATCGCCGACAAGATCAGGGACTT 302
             ||||||||||||| |||||||| |||||||||||||||
Qy   414 GAACATGTGCTCTGCAGGAGTGCCAGCAGAAAAAGCTGCCGAGGAGGTAACTTCCAGACAGG 473

Db   303 GTCGCAGCGGGGCACCGTGATTGCGCGACGCGGTCGCCGAGCGTGACCACCC---CCGA 359
             ||||||||||||||||||||||||||||||
Qy   474 AATTAAGAGAGGTTTGTGGCAGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCC 533

Db   360 CCACAAGCGATACGTGCTGGGGTCGATGGGAACATCACAGGTTGCCCAACCCTGGGCCA 419
             ||||||||||||||||||||||
Qy   534 ATCTGTGTGGAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCA 593

Db   420 CACCGAGTACCG------GTCGTTCGAGACGCCTACAC 452
             ||||||||||
Qy   594 AGAGCAGGCCAAAGGACTTCTCGATGGCGGGGGTTGTGATATCTTTACTCATTGAAACTATTTT 653

Db   453 CGAGTCGGCGTAGGCATGCTGGACGCTGCACTCGTTGCGCTACTCGTTGAAACCTGTCA 512
             ||||||||||||||||||||||
Qy   654 TGATACTGCCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTTGACGGAGAAATA 713

Db   513 GGACTTGCTGCTGCCAGTCAAGGCTCTCAAGGCTCGGCGTGCGCGGCGCCGGATGACAGAGCCGG 572
             ||||||||||||||||||||||
Qy   714 TGCTCCCCGGCCTATCTTATTTCAGGGACGGATCGTTGATAAAAGTGGGCGGCCGACTCTTTC 773

Db   573 TCGGACATTCCGGTCTTCGTCCACGTGACGTGCTGAGAGCGACCGGAACGATGCTGCCTGGGG 632
             ||||||||||||||||||||||
Qy   774 CGGACAGCAGGAGAGGAGGATTTGTCATCAGCTGTCTCATGGAGAACCACCACTCGCATTGG 833

Db   633 AAGTGAGATCGGCGCGCTGCCACTCGGCTGCGAGCCGCGTCGGTGTC---GACATGATCGG 689
             ||||||||||||||||||||||
Qy   834 ATTAAATTGTGCTTTGGGTGCAGCTGAGCATGAGACCTTTATTGAAATAATTGAAAAATG 893

Db   690 TTTGAACTGCGCAACGGCGGCAATGAATGAGTGAGTGGCACTGTGCGGCATCTGTCCAAGCA 749
             ||||||||||||||||||
Qy   894 TACAACAGCCATGTCCTATGTGTTGTAAGCTAGAGTTCACACCTTTGGTGACTA 953

Db   750 TGCCGCATCCCGGTGTCGGTGATGCCCAACGCGGTCGGGCGTGCGGTGCCAAGGG 809
             ||||||||||||||||||
Qy   954 TGATGAAACGCGCCCTTCATGATGATGGCTAGAGGATTTTGCTATGGATGGCTTGGT 1013

Db   810 AGCTGAATACCCGCTGCGGCGAATTGGCTTCGGCTTTGGCTGGTTCATCGCTGA 869
             ||||||||||||||||
Qy  1014 CAAT------ATAGTTGGAGGATGTCGTGGTCAACACCAGATCATATCAGGGAAAT 1064

Db   870 ATTTGGTCTTTCGTTGGTTCGGTGTGGCTGCTGTTGGTTGTACCACCCGACCACATCCCGGGAAGT 929
             ||||||||||||||||||||
Qy  1065 TGCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTTCCACCTGCCACTGCTTTTGAAGACA 1124

Db   930 GGCCGGCAGCGGTAGCCAGATGCAACGACACGGGACAGTGCCACGCGGTCATGTGTGAC 989
             ||||||||||||||||
Qy  1125 TATGTTACTGTCTGGTCTAGAGCCCTTCAGGATGGACCGTACACCAACT----T 1175

Db   990 CTATGAGCCGTCGATCTGTCGCTGTATACAGCCATTCGCCCAAAAACCCTCGGT 1049
             ||||||||||||||||||
Qy  1176 TGTTAACATTGGAGAGCGCCTGTAATGTTGCAGATCAAGGAAGTTTGCTAAACTCATCAT 1235

Db  1050 ATTTGGTCTTTCGTTGTTTTTCGTGAGGCAATGAT------TGGACTCTAC 1109
             ||||||||||||
Qy  1236 GGCAGGAAACTATGAAGAACCCTTGTGTTGCCAAGTGCAGGTGAAATGGGAGGCCCA 1295

Db  1110 CGCCGAGGACTATCAAAAGTGTCTAGATATCGGCAACGACCAAACCCTGGCGGCGCACA 1169
             ||||||||||||||||
Qy  1296 GGTGTTGGATGGTCAACATGGCATGTGATGATGGCATCGGCATGCTAGATGTCGTCAAGATT 1355

Db  1170 CCTGCTGGATCTGTGTGTCGCGAATTACGTCGGCCGCAACATGGCCGACATGAGGGCGTT 1229
             ||||||||||||||||||
Qy  1356 TTGCAACTTAATTGCTTCGGAGCCAGCATCGCATTTGTGTCATCGGACTCCTC 1415

Db  1230 GGCCGGGGCTTGAGCGTGTGCAGACATTGCCGATCATGC------TGGACTCTAC 1280
             ||||||||||||
Qy  1416 CAATTTTGCTGTGATTGAAGCTGGGCAGGTTTGGAGCTGCGTGCATTGTCAATAG 1475

Db  1281 CGAAATACCGGGTTGCTGCAGCCTGGCGGCCGGCGCGGGGAAGTGGCCGAGGGTGATCAATTC 1340
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RESULT 13
US-10-858-730-143
; Sequence 143, Application US/10858730
; Publication No. US2005025556A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-858-730-143

Query Match   2.3%;   Score 88.2; DB 8; Length 3579;
Best Local Similarity 43.2%;   Pred. No. 1.3e-13;
Matches 706;   Conservative   0; Mismatches 878; Indels 51; Gaps 4;

Qy   974 TGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAGTTGGAGGATGCT 1033
           ||||||| || ||| | | |||||| |||||| || || | || |||| | |||
Db   833 TGGCCGAGGGCGTGGGCGCGGCTTCATCCGCCGAGTTCCGCTTGGTCGGTGGCGGCTGCT 892

Qy   1034 GTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCGTGTGAAAAATTGTAAGCCTA 1093
           | |||| || | | | | || | | |||| || ||| ||| | |
Db   893 GCGGCACCACCCCGGCCCATATCCGGAAGTGGCTGCCGGTTGCAACATCAAGGGTC 952

Qy   1094 GAGTTCCACCTGGCCACCTGCCACTGTCTTTTGAAGGACATATGTTTACTGTCTGTCTTCA 1153
           ||||||||| || |||||| |||| | | ||| | ||| ||| || |||||| ||
Db   953 CCGAGGCACAGGTCA------GCTACGAGCCGTCGGTGTCGTGGTCGCTGTCACCGGCAATCC 1006

Qy   1154 GGATTGACCGTACACCAACTTGTTAACATTGGAGAGCGCGTGTAATGTTCAGGATCAA 1213
           |||| | ||| | ||| ||||| | || || ||| ||| | ||||| | || |||
Db   1007 CGTTCGCGCCAGGACGCCTCGGTTCTGGTCGGTTGATCGGGGAGCGGAGCGACGGCCACG 1066

Qy   1214 GGAAGTTGCTAAACTCATCATGGCAGGAAACTATGAAGAGAGCCTTGTGTTGCCAAAG 1273
           || | |||| ||| | | | ||| | | | | |||| | |||| ||| |||| |||
Db   1067 AGGGTTTTCGTGAGGGAATGGATGATCCCGAGTCCGGAGACTACCAGAGTGCCTGGTTG 1126

Qy   1274 TGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGCATGCTAGATG 1333
           || ||| |||| | | | ||||| | | || | || | || | | | | |
Db   1127 ACCAGAGCCCGCGACGCGCCCACCTGTGTGTGGACTACGTGGGCCGCGACG 1186

Qy   1334 GTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGACATCGCAAAGG 1393
           |||||| || | || || | ||| | ||| | || | || ||||||| ||| ||
Db   1187 GTGTGGCCGACATGAAGGCGCTCGGACTGCTGGCACGCGTTCCTCGACGCGTCGCCGATCA 1246

Qy   1394 TACCTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTTAAAGTGCTGCC 1453
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Db   1247 TGCTGGACTCCACGAAACCGGGTGCTGCGAGGCGGTTTGGAGCATTCGGGTGGCCGTT 1306

Qy   2538 TATAATTGGCTGTCAGG 2555
           | ||| ||| |||
Db   2379 CCTAGTCGGGGATGTCGGG 2396

Qy   1454 AAGGGAAGTGTCAATAGCATTAGTCTGAAGAAGGAGGAGGACGACTTCTTGGAGA 1513
           || | || | || ||| | | || ||| ||| || || || | ||||
Db   1307 GCGGGATCAACTCGGTCGAGGACGGCGGCCGGAATCGCGCTTTGACCGATCGAGAAGAAGA 1366

Qy   1514 AGGCCAGGAAGATTAAAAGTATGAGACGTGCTCATGGTGGTCATGGCTTTGATGAAGAAG 1573
           || | |||| | | | || | | | || || |||| ||||| ||| |||| | |
Db   1367 CCATGGCGGCTGTGCCGAGCGCAGGAGCAGCAAAAATCGAGTGTCGCCGTGAACGGCATCG 1426

Qy   1574 GACAGGCAACAGAAACAGCCGGCAGCAGAAGAAATCAGAGTGTCGACATCGCCGGGCGTCG 1633
           | || | || | | || ||| | | |||||||| | || | | |||| |||
Db   1427 GCCAGGCCGCCACCGCCGCCGCAGAGAAGGTCGAGATCGCCGAGTCGTGATCAACGACATCA 1486

Qy   1634 TGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATATCCTAACCATTG 1693
           | | || | || | | | | ||||| | | | | | | | | || |
Db   1487 CCGGCAACTGGGCGTCGACGAATCATCCATCCTCATCGACACTTGACGTTCACCATCG 1546

Qy   1694 GGACTGGAATGAGGAACACAACTTGTATGCCATTAATTTTATCATGCAACAAAAGTCA 1753
           | | |||||| | | || || ||| | | | | | |||| | | || | |||
Db   1547 CCACCGGTCAGGAGGAGTCCCGCGACGGCATCGAGACCACCTGGTCTGTCTCCAACA 1606

Qy   1754 TTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGTCTTTCCAACTTGTCCTTCCT 1813
           | | | | | || ||| || | ||| || ||| |||| || | | |||
Db   1607 TGAAAAAGCGCCACCCGGATGTGCAGACAGCAGCCACACTGTGTCGTCCAACA------TCTCGT 1660

Qy   1814 TCCGAGAATGAAGCCATTCGAGAGCAATGCATCATGGGTTTTCCTTTACCATGCAATCA 1873
           | |||| | | | || | ||| | | | | | || || || ||| | |||
Db   1661 TTGGTCTCAATCCGCAGCGCCCAGGTGCTCAACTCGGTGTTCCTGCACGAATGCCAAG 1720

Qy   1874 AGTCTGGCATGACATGGATGAGTAGTGAAATGCTGGAAACCTCCCTGTGTATGATGATATCC 1933
           || | ||| || | | | | | | | | || || | | ||| ||| | |||| ||
Db   1721 AAGCGGGGGCTGATTCGGCGGATTCGGCGGTCGCACGCGTCGAGATCCTGCGACGCCGGATTC 1780

Qy   1934 ATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGAGAATAAAGACCCTGAGGCCACTG 1993
           | | ||| | | | | || | | | | | | | ||| | | | |||| || |||
Db   1781 CCGAGGAGCAACGCAACGTCGCCCTGGATCTGGTCTACGACCGGCGGGAGGACTACG 1840

Qy   1994 AGAAGCTCTTACGTTATGCCCAGACTCAAGCACAGGAGGGAAGAAAGTCATTCAGACTG 2053
           || | | | | | | || | | | ||| | || ||| | ||| || ||| |
Db   1841 ATCCGC---TGCAGGAGCTGATGCGGCTGTGCGGCGTGTCGGCGCCTCCTCGGAAAG 1897

Qy   2054 ATGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTAGTGCCCTTGTGAAGGGCATTG 2113
           ||||| |||| |||| | | ||||||| | | | ||| | || || |||||| |||
Db   1898 AGGACCGACTGGCTGAACTAGCTGGCGGTCTGGAAGCAGGTTAAACCAAAAAAATATCCCCGAC 1957

Qy   2114 AAAAACATATTATTGAGGACGCAAGCGTGTGAAGCTGGCGATGGAATGAAAATTGTGGTGAC 2173
           | | | | ||| || || || | | || || | ||| | | | ||| || | ||
Db   1958 TCGACGGCGAGCGCAAGTGGCTGGACGACGATGACCGTTGCGAACAATCAAGGGTC 2017

Qy   2174 CTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAAATTGTTGGTGATCTTTTTG 2233
           | | || | | | | | | | |||| | ||| || | | | | | ||
Db   2018 CGCTTTCAGATCATCAACGAACATCTGCTCGGCCGGCGCGATCTCGCGGCTCGGCTCTTCG 2077

Qy   2234 GAGCTGGAAAAATGTTTCTACCTCAGGTTAAAGTCAGCCCGGGTTATGAAGAAGGCTG 2293
           |||| |||| | ||| |||| | | ||||| || | || | || || || | |||
Db   2078 GCTCCGGCCAGATGCAGCGTCCGTCGTGTGCTGGAGTAATGAAAGCCCCGG 2137

Qy   2294 TTGGCCACCTTATCCCTTTCATTGGAAAAAGAAGAAGATCATGGAAGAAACAGAGTGCTTAACGGCA 2353
           | | | | ||| | ||| | | | | |||| | || | | | | | || | | |||
Db   2138 TCGCGTATCTGGAACCGCACATGGAGCGGCTCG------------------------- 2169

Qy   2354 CAGTAGAAGAAGAGGACCCTTACCAGGCACCATCGTGCTGCGCCACTGTTAAAGGCGACG 2413
           || | |||| | || || | | | || || || | ||| || | || ||| || |||
Db   2170 -------GACGACGATTCGGGCAAGGGACGCCATCGTTCTGCGGCCGTCAAGGGGCGACG 2221

Qy   2414 TGCACGACATAGGCAAGAACATCAGTAGTCCTGGCTGCTCCGAGCACATCGCAAAGG 2473
           || || | | | || | | | | | ||| ||| | || | | || ||
Db   2222 TGCACGACATCGGCGACATCGGTCGACATCATCTTGAGCAACAACGGCTACGAAGTGG 2281

Qy   2474 TTGATTTAGGAGTCATGACTCATGTGATAAGATACTGAAAGTGCTCTTGACCACAAAG 2533
           | | | || || | | | || || | | | ||| | | |||| || || |||
Db   2282 TCAACATCGGCATCAAGCAGCCAATCGCCACCATCCTCGAAGTCGCCGAGGACAAGAGCG 2341

Qy   2534 CAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGCGATGAAATGATTTTTGTTG 2593
           | || | ||| || ||| | | || | || | | ||| ||| | | | | ||
Db   2342 TGCTCGGACTCCACCGAAACCGGGTGCTGCGAGGCGGTTTGGAGCATCTCGGGTGGCCGTT

Db   2342 CCGACGTGGTCGGCATGTCGGCGGCCTGCTGGTGGTGAAGTCGACCGTGGTGATGAAGGAAAACC 2401
                     ||| | |||||||| || || | || | ||||
Qy   2594 CCAAGGAAATGGAGA   2608
                     | ||||| ||| ||
Db   2402 TCGAGGAGATGAACA 2416

Db   302 TTCACACATTTTTTTCCAAGTAATATTTGGAAATACTTTATCTCAACACCAGTATTAG 243
Qy   3781 GATTATGCATTGAGGAGGAAGAACATATCTCGTGGCTGAGGTTGAGAAATGCTTGGACCCATT 3840
                   ||||||| |||||| || | ||||| ||| | |||||| | ||| ||
Db   242 GATTTTGTTGGAATTAAATTATATCTATAGATAAATTTAGGGGTCTTGGTAAACT 183
Qy   3841 TTGGGATATGATACAGACTAACTTTTTTTTTTTTTGC 3880
                   ||||||||||||||
Db   182 ATTGATTCTCATACAGACTATGCTAGTTCTATGTTCTTAC 143

RESULT 14
US-11-175-859-4373
; Sequence 4373, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
;   APPLICANT: Affymetrix, Inc.
;   APPLICANT: Liu, Guoying et al.
;   TITLE OF INVENTION: Method of Analysis of Human Polymorphism
;   FILE REFERENCE: 3690.1
;   CURRENT APPLICATION NUMBER: US/11/175,859
;   CURRENT FILING DATE: 2005-07-05
;   PRIOR APPLICATION NUMBER: US 60/585,352
;   PRIOR FILING DATE: 2004-07-02
;   NUMBER OF SEQ ID NOS: 116251
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4373
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: homo sapien
US-11-175-859-4373

  Query Match   1.2%; Score 46.4; DB 12; Length 50;
  Best Local Similarity   94.0%; Pred. No. 0.0052;
  Matches   47; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   2794 GAAGAATGAAGAATATTAGACAGGACCCATTATGAGTCTCTCAAGGAGAG 2843
            |||||||||||||||||||||||| ||||||||||||||||||||| ||
Db   1 GAAGAATGAAGAATATTAGACAGGRCCATTATGAGTCTCTCAAGGTAAG 50

RESULT 15
US-09-925-065A-483679/c
; Sequence 483679, Application US/0925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 483679
;   LENGTH: 616
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-483679

  Query Match   1.1%; Score 43.2; DB 6; Length 616;
  Best Local Similarity   54.4%; Pred. No. 0.21;
  Matches   87; Conservative   0; Mismatches   73; Indels   0; Gaps   0;

Qy   3721 TTCTCCAATTTGAAGTCCAAATATTTGCTGGTGGGGAAGAATTCCAAGGATCAGGTTGAG 3780
            ||| | |||| ||| |||||| |||| |||||||| || | |||| | | | ||| | |||

Search completed: March 6, 2006, 19:47:06
Job time : 713 secs

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               GenCore version 5.1.7
               Copyright (c) 1993 - 2006  Bioccceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    March 7, 2006, 01:52:43 ; Search time 13579 Seconds
                                     (without alignments)
                                     13503.099 Million cell updates/sec

Title:   US-10-607-712-1
Perfect score: 3919
Sequence:  1 ggtcacctgtggagagcacg.........ctccaaggaaatacaaacctag 3919

Scoring table: OLIGO_NUC
               Gapop 60.0 , Gapext 60.0
Searched: 41078325 seqs, 2339354122B residues
Word size : 18
Total number of hits satisfying chosen parameters:    312259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 1000 summaries

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         2:  gb_est2:*
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         7:  gb_est6:*
         8:  gb_est7:*
         9:  gb_gss1:*
        10:  gb_gss2:*
        11:  gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		2460	62.8	3711	11	DQ037675	DQ037675 Homo sapi
2		839	21.4	4888	4	CR859882	CR859882 Pongo pyg
3		681	17.4	863	3	BM450887	BM450887 AGENCOURT
4		660	16.8	721	1	AL598311	AL598311 DKFZp313F
5		651	16.6	871	5	BX390174	BX390174 BX390174
6		637	16.3	943	5	BU189680	BU189680 AGENCOURT
7		623	15.9	698	7	CN414972	CN414972 170004180
8		545	13.9	583	3	BP313585	BP313585 BP313585
9		529	13.5	582	3	BP336553	BP336553 BP336553
10		501	12.8	583	3	BP337383	BP337383 BP337383
11		497	12.7	560	3	BP220649	BP220649 BP220649
12		490	12.5	490	1	AL041796	AL041796 DKFZp434B
13		490	12.5	3677	11	DQ037676	DQ037676 Pan trogl
14		480	12.2	582	3	BP336015	BP336015 BP336015
15		448	11.4	1043	3	BQ062840	BQ062840 AGENCOURT
16		440	11.2	626	5	BX485695	BX485695 DKFZp686C
17		404	10.3	404	7	CV334327	CV334327 IL3-NT028
18		363	9.3	937	5	BQ960377	BQ960377 AGENCOURT
19		350	8.9	874	2	BE879762	BE879762 601491666
20		332	8.5	579	3	BP268350	BP268350 BP268350
21		323	8.2	527	3	BX470290	BX470290 DKFZp779J
22	c	321	8.2	523	1	AW277117	AW277117 xp63a10.x
23		315	8.0	506	3	BQ364647	BQ364647 MR2-SN000
24		315	8.0	997	3	BG258321	BG258321 602379766
25		314	8.0	961	5	BX332266	BX332266 BX332266
26	c	298	7.6	574	7	CV344680	CV344680 MR1-HN006
27		287	7.3	587	5	BP336596	BP336596 BP336596
28		267	6.8	623	7	BX498595	BX498595 DKFZp779G
29		267	6.8	587	5	CR629973	CR629973 DKFZp469I
30		251	6.4	583	5	BP332632	BP332632 BP332632
31		236	6.0	466	3	BX484356	BX484356 DKFZp686H
32		232	5.9	581	3	BP348983	BP348983 BP348983
33		231	5.9	592	5	BP249465	BP249465 BP249465
34		216	5.5	496	7	BU429497	BU429497 UI-HF-BN0
35		212	5.4	618	5	CV356711	CV356711 MR4-RT002
36		205	5.2	292	5	AA356439	AA356439 EST64989
37	c	201	5.1	356	3	BX955050	BX955050 DKFZp781F
38		180	5.1	581	3	BP248483	BP248483 AGENCOURT
39	c	158	4.6	996	5	BU184298	BU184298 AGENCOURT
40		154	4.0	668	7	AI872333	AI872333 wm57h11.x
41	c	142	3.9	477	7	CV363529	CV363529 PM1-CN009
42		136	3.6	552	2	CR767594	CR767594 DKFZp469O
43	c	134	3.5	226	7	BF749082	BF749082 MR2-BN038
44		129	3.4	486	7	CR773515	CR773515 DKFZp459D
45		128	3.3	444	5	CR751928	CR751928 DKFZp469P
46		127	3.3	1168	5	BQ960236	BQ960236 AGENCOURT
47		124	3.3	269	9	CR853354	CR853354 DKFZp469J
48		117	3.2	857	9	AQ744889	AQ744889 HS_5507_A
49		114	3.2	735	10	AG092782	AG092782 Pan trogl
50		98	3.0	153	6	CF135946	CF135946 UI-HF-BN0
51		98	2.9	436	1	AU077264	AU077264 AU077264
52	c	98	2.5	517	3	BQ311389	BQ311389 PM3-BN017
53		96	2.5	554	3	BP380788	BP380788 BP380788
54		96	2.5	599	8	CD675851	CD675851 fs29a02.y
55		96	2.4	623	7	DN996221	DN996221 TC120000
56		88	2.4	639	7	CN414973	CN414973 170005999
57		86	2.2	550	3	BP380920	BP380920 BP380920
58		81	2.2	252	7	BI027486	BI027486 CM3-MT029
59	c	68	2.1	607	7	CR770704	CR770704 DKFZp469I
60	c	68	1.7	581	8	DN279755	DN279755 1160811 M
61		60	1.7	715	8	DN280822	DN280822 1161963 M
62	c	57	1.5	551	9	AQ411010	AQ411010 HS_2257_B
63	c	54	1.5	248	9	BE929041	BE929041 PM2-GN001
64		54	1.4	217	10	CL211992	CL211992 M064F08 G
65		54	1.4	458	7	CK389585	CK389585 L045E03-
66	c	54	1.4	539	6	CF165176	CF165176 B0753B09-
67		52	1.4	658	6	CB455191	CB455191 712318 MA
68	c	51	1.3	727	6	CB600441	CB600441 AGENCOURT
69		50	1.3	1326	10	AG448662	AG448662 Mus muscu
70	c	50	1.3	2150	4	CV363529	CV363529 PM1-CN009
71	c	47	1.3	162	6	AK037599	AK037599 Mus muscu
72	c	47	1.2	538	7	BF852392	BF852392 MR3-EN008
73		46	1.2	365	2	CB454749	CB454749 711558 MA
74		43	1.1	365	7	CK465144	CK465144 936226 MA
75	c	41	1.0	445	1	CK467246	CK467246 938530 MA
76		41	1.0	544	7	BF515662	BF515662 UI-H-BW1-
77		41	1.0	648	3	CR751294	CR751294 DKFZp469H
78		40	1.0	717	3	AJ448453	AJ448453 AJ448453
79		39	1.0	452	3	AJ724456	AJ724456 AJ724456
80	c	38	1.0	520	2	AJ724468	AJ724468 AJ724468
81		38	1.0	571	2	CN690949	CN690949 E0302G11-
82		38	1.0	548	8	BI345164	BI345164 373893 MA
83		38	1.0	617	2	BI345087	BI345087 373795 MA
84		38	1.0	633	6	BE684351	BE684351 184729 MA
85		38	1.0	678	4	CK620511	CK620511 m113b08.y
86		38	1.0	758	1	BB662292	BB662292 BB662292
87		37	1.0	909	9	BB039567	BB039567 BB039567
88		37	0.9	915		CK228713	CK228713 MBM08606
89				954		BG918727	BG918727 602819207
90				1788		BQ954233	BQ954233 AGENCOURT
91				156		CA786770	CA786770 AGENCOURT
92				501		AK085987	AK085987 Mus muscu
93			0.9	809		AA285223	AA285223 PMY0833 K
94			0.9			BM088286	BM088286 501720 MA
95	c		0.9		9	BZ873476	BZ873476 CH240_250

No.	c	Score	E	Length	N	Accession	Accession	Description
96		35	0.9	397	2	BB813231	BB813231	BB813231
97		35	0.9	822	7	CK846954	CK846954	969526 MA
98		34	0.9	292	2	BB241066	BB241066	BB241066
99	c	34	0.8	389	9	AZ485259	AZ485259	1M0312N03
100	c	32	0.8	688	10	CE401545	CE401545	tigr-gss-
101		32	0.8	798	10	CG843722	CG843722	Ynhw4336
102		31	0.8	591	5	BX510153	BX510153	DKFZp686H
103	c	30	0.8	402	3	BQ365637	BQ365637	MR2-GN003
104		30	0.8	566	10	CE321611	CE321611	tigr-gss-
105		30	0.8	698	5	BW782486	BW782486	BW782486
106		29	0.7	363	5	AI604746	AI604746	vc20d02.y
107		29	0.7	398	6	CA531346	CA531346	C0318D05-
108		29	0.7	436	9	AA387056	AA387056	vc20d02.r
109	c	29	0.7	486	9	AZ765154	AZ765154	1M0561M20
110		29	0.7	551	2	CL352328	CL352328	RPCI44 40
111		29	0.7	589	10	BI065590	BI065590	pgf1n.pK0
112		29	0.7	613	1	AL872457	AL872457	AL872457
113		29	0.7	627	1	AL875075	AL875075	AL875075
114		29	0.7	657	9	CC249505	CC249505	RRF186 Ba
115		29	0.7	665	7	BB156044	BB156044	BB156044
116		29	0.7	812	7	CR575710	CR575710	CR575710
117		29	0.7	885	6	CF548421	CF548421	AGENCOURT
118	c	29	0.7	161	7	BI376557	BI376557	BFLG3_000
119	c	28	0.7	225	6	BE005215	BE005215	CM1-BN011
120	c	28	0.7	230	9	AZ844485	AZ844485	2M0143F24
121		28	0.7	518	7	CO596140	CO596140	DG8-12I15
122		28	0.7	622	7	CN537801	CN537801	UI-M-H50-
123		28	0.7	669	1	AJ724454	AJ724454	AJ724454
124		28	0.7	693	6	BU290174	BU290174	604161924
125		28	0.7	717	6	CF739229	CF739229	UI-M-HD0-
126		28	0.7	728	7	BU372990	BU372990	603811666
127	c	28	0.7	738	1	AJ724471	AJ724471	AJ724471
128	c	28	0.7	758	10	AG546553	AG546553	Mus muscu
129		28	0.7	914	8	BU343179	BU343179	603524953
130		27	0.7	101	8	CV994689	CV994689	IpCGFr3_8
131		27	0.7	263	2	BF733369	BF733369	MRI-AN003
132		27	0.7	421	6	AJ825014	AJ825014	AJ825014
133		27	0.7	453	6	CB077007	CB077007	h47e10.g
134		27	0.7	510	10	CL336386	CL336386	RPCI44_26
135		27	0.7	579	10	CL321842	CL321842	CH242_15G
136		27	0.7	691	10	CW861380	CW861380	shS2k48-
137		26	0.7	193	10	CE781142	CE781142	tigr-gss-
138		26	0.7	202	6	BI298055	BI298055	UI-R-CV2-
139		26	0.7	210	6	CB857501	CB857501	NISC_na07
140		26	0.7	210	1	CB857502	CB857502	NISC_na07
141		26	0.7	220	1	AJ703441	AJ703441	AJ703441
142		26	0.7	321	3	BM031265	BM031265	496621 MA
143		26	0.7	331	2	BE852434	BE852434	uw20d04.x
144		26	0.7	370	5	BM958744	BM958744	PLATE_16
145		26	0.7	377	5	BU727434	BU727434	UI-E-CQ1-
146		26	0.7	410	6	BI291331	BI291331	UI-R-CV2-
147		26	0.7	424	10	CE447107	CE447107	tigr-gss-
148	c	26	0.7	424	11	CR894413	CR894413	Sus scrof
149	c	26	0.7	457	10	CE506288	CE506288	tigr-gss-
150	c	26	0.7	463	7	CO609245	CO609245	DG8-80e18
151		26	0.7	476	6	CV554309	CV554309	UI-D-GC1-
152		26	0.7	512	7	CV529297	CV529297	BX529297
153		26	0.7	515	11	CR922091	CR922091	Sus scrof
154		26	0.7	540	9	AZ869000	AZ869000	2M0180M20
155		26	0.7	543	5	CO089397	CO089397	UI-CF-DU1
156		26	0.7	566	7	CU080299	BU680299	GR_Ea08N
157	c	26	0.7	574	9	AZ554775	AZ554775	RPCI_23-2
158		26	0.7	596	11	CR894944	CR894944	Sus scrof
159		26	0.7	597	7	AW637729	AW637729	b16ih07.w
160		26	0.7	599	7	CJ016456	CJ016456	CJ016456
161		26	0.7	600	7	CV585887	CV585887	L_AH-aaa3
162		26	0.7	613	6	CV585764	CV585764	L_AH-aaa3
163	c	26	0.7	613	6	CB975827	CB975827	CAB40001
164		26	0.7	618	5	CU680966	BU680966	UI-CF-ECl
165		26	0.7	631	7	BU623815	BU623815	UI-H-FG1-
166		26	0.7	640	7	CN412664	CN412664	17005325
167		26	0.7	646	3	BM980620	BM980620	UI-CF-EN1
168		26	0.7	653	6	CA424914	CA424914	UI-H-FE1-
169		26	0.7	656	6	CB528401	CB528401	UI-H-FT2-
170		26	0.7	658	2	BB657977	BB657977	BB657977
171		26	0.7	708	5	CA763245	CA763245	BR060012B
172		26	0.7	725	5	BQ780303	BQ780303	UI-R-FF0-
173		26	0.7	727	7	CR433139	CR433139	CR433139
174		26	0.7	746	3	BQ003913	BQ003913	UI-H-EI1-
175		26	0.7	752	7	CV598811	CV598811	L_AH-aaa3
176	c	26	0.7	757	7	AJ724469	AJ724469	AJ724469
177		26	0.7	778	6	CA307248	CA307248	UI-H-FT1-
178		26	0.7	806	1	AJ724455	AJ724455	AJ724455
179		26	0.7	812	5	BX752969	BX752969	BX752969
180		26	0.7	826	7	CK197521	CK197521	FGAS00599
181	c	26	0.7	1094	11	AL322116	CNS055JF	AL322116 Tetraodon
182	c	26	0.7	1105	9	CC184546	CC184546	CH261-52N
183		25	0.6	78	10	CN545963	CN545963	EST 17911
184	c	25	0.6	95	6	BX120837	BX120837	BX120837 Danio rer
185	c	25	0.6	102	6	CB376734	CB376734	Hb06D03 L
186		25	0.6	103	6	CF510960	CF510960	CAbud0001
187		25	0.6	105	6	CF215276	CF215276	CAST0001
188	c	25	0.6	109	10	AI340607	AI340607	tb31h02.x
189	c	25	0.6	110	6	CF269835	CF269835	Fcy1cold1
190	c	25	0.6	110	7	CN385319	CN385319	LE2TR03E1
191		25	0.6	115	7	CN545789	CN545789	EST 17733
192		25	0.6	117	7	CN545605	CN545605	EST 17549
193		25	0.6	117	7	CN546348	CN546348	EST 18300
194		25	0.6	118	6	CF518976	CF518976	CAP0006_I
195		25	0.6	124	6	CF512448	CF512448	CAbud0003
196		25	0.6	127	7	CN546260	CN546260	EST 18212
197		25	0.6	129	6	CF212016	CF212016	CGF100066
198		25	0.6	129	6	CF212499	CF212499	CGF100065
199		25	0.6	132	6	CB978871	CB978871	CAB4000_6
200	c	25	0.6	132	8	DN837912	DN837912	SmoC-1_01
201	c	25	0.6	136	6	AI275354	AI275354	qw66e02.x
202	c	25	0.6	136	6	CF518719	CF518719	CAP0007_
203		25	0.6	143	5	BU531347	BU531347	AGENCOURT
204		25	0.6	143	6	BU531590	BU531590	AGENCOURT
205		25	0.6	143	6	CB610600	CB610600	ALBEDO000
206		25	0.6	144	6	CF205875	CF205875	RR890915I
207		25	0.6	144	6	BU563912	BU563912	AGENCOURT
208		25	0.6	145	6	CD769674	CD769674	AGENCOURT
209		25	0.6	146	5	BU534815	BU534815	AGENCOURT
210		25	0.6	146	6	BU842656	BU842656	AGENCOURT
211		25	0.6	146	6	CF511584	CF511584	CAbud0002
212	c	25	0.6	147	5	BU530443	BU530443	AGENCOURT
213		25	0.6	147	5	CD768528	CD768528	AGENCOURT
214		25	0.6	148	5	BU844094	BU844094	AGENCOURT
215		25	0.6	148	6	CB237919	CB237919	AGENCOURT
216		25	0.6	149	5	BU563335	BU563335	AGENCOURT
217		25	0.6	149	6	CD769174	CD769174	AGENCOURT
218		25	0.6	150	5	BU530986	BU530986	AGENCOURT
219		25	0.6	150	6	BU531230	BU531230	AGENCOURT
220	c	25	0.6	150	5	BU531608	BU531608	AGENCOURT
221		25	0.6	151	6	CB976825	CB976825	AGENCOURT
222		25	0.6	151	6	CD769343	CD769343	AGENCOURT
223		25	0.6	152	6	BU531635	BU531635	AGENCOURT
224		25	0.6	152	5	CD768990	CD768990	AGENCOURT
225		25	0.6	153	5	BU529255	BU529255	AGENCOURT
226		25	0.6	153	5	BU554957	BU554957	AGENCOURT
227		25	0.6	154	6	BU563541	BU563541	AGENCOURT
228		25	0.6	154	6	CD768221	CD768221	AGENCOURT
229	c	25	0.6	154	6	CD769714	CD769714	AGENCOURT
230	c	25	0.6	155	6	CF512543	CF512543	CAbud0003
231		25	0.6	156	1	AI343315	AI343315	tb81e08.x
232		25	0.6	159	5	BU556412	BU556412	AGENCOURT
233		25	0.6	159	6	CD769459	CD769459	AGENCOURT
234		25	0.6	162	6	BU556005	BU556005	AGENCOURT
235		25	0.6	163	3	BM121849	BM121849	L0502D03-
236		25	0.6	163	6	CN385655	CN385655	LE2TR04D0
237		25	0.6	164	6	CB971610	CB971610	UI-H-FG1-
238		25	0.6	164	6	CAB10005	CAB10005	CAB10005
239	c	25	0.6	165	6	CN385177	CN385177	LE2TR02Ol
240		25	0.6	167	5	BU842470	BU842470	AGENCOURT
241		25	0.6	168	5	BU958197	BU958197	AGENCOURT

Left portion:

	#					Accession	Accession	Description
c	242	25	0.6	5	174	BU564407	BU564407	AGENCOURT
c	243	25	0.6	5	176	BU963383	BU963383	AGENCOURT
	244	25	0.6	2	179	BI184493	BI184493	UNL-P-FN-
	245	25	0.6	5	185	BU536826	BU536826	AGENCOURT
	246	25	0.6	3	190	BI345093	BI345093	373801 MA
c	247	25	0.6	5	195	BU944994	BU944994	AGENCOURT
c	248	25	0.6	6	196	CA728416	CA728416	wdilc.pk0
	249	25	0.6	6	206	CB304413	CB304413	FLAVEDO00
	250	25	0.6	6	207	CF212679	CF212679	CGF100065
	251	25	0.6	6	211	CF202630	CF202630	RR890915N
c	252	25	0.6	1	212	AW302865	AW302865	xr57h11.x
c	253	25	0.6	2	213	AW492883	AW492883	UI-M-BH3-
	254	25	0.6	5	213	BU566667	BU566667	AGENCOURT
c	255	25	0.6	2	216	BE043416	BE043416	hk37h12.y
	256	25	0.6	2	217	BF414917	BF414917	UI-R-BJ2-
c	257	25	0.6	2	220	BE857902	BE857902	7d66b11.x
c	258	25	0.6	5	220	BU929970	BU929970	AGENCOURT
	259	25	0.6	7	220	CV022671	CV022671	Rasgscb02
c	260	25	0.6	5	221	BU587985	BU587985	AGENCOURT
	261	25	0.6	7	222	CK937767	CK937767	CGF100448
c	262	25	0.6	5	223	BU844150	BU844150	AGENCOURT
c	263	25	0.6	6	226	CB975354	CB975354	CAB30006_
	264	25	0.6	5	229	BU958260	BU958260	AGENCOURT
c	265	25	0.6	6	229	CD420030	CD420030	rj18b06.y
	266	25	0.6	6	234	BE139701	BE139701	xr71e09.x
c	267	25	0.6	7	236	CV022693	CV022693	Rasgscb02
	268	25	0.6	6	239	CF795904	CF795904	892108 MA
c	269	25	0.6	6	241	CB973344	CB973344	CAB30002_
	270	25	0.6	1	243	AI845155	AI845155	UI-M-BG0-
	271	25	0.6	5	244	BU735868	BU735868	UI-E-DX0-
c	272	25	0.6	5	245	BU529994	BU529994	AGENCOURT
	273	25	0.6	6	245	CF212690	CF212690	CGF100065
	274	25	0.6	1	248	AW159099	AW159099	za52c06.x
	275	25	0.6	2	254	BB326073	BB326073	BB326073
c	276	25	0.6	6	254	CB962783	CB962783	AGENCOURT
c	277	25	0.6	1	256	AJ828936	AJ828936	AJ828936
	278	25	0.6	6	258	CF515849	CF515849	CAP0002.I
c	279	25	0.6	5	259	BU566754	BU566754	AGENCOURT
c	280	25	0.6	8	260	DN498033	DN498033	R052D11.5
	281	25	0.6	2	262	BG653057	BG653057	sad81d02.
c	282	25	0.6	1	264	AI251202	AI251202	qv38g09.x
	283	25	0.6	8	270	DR471079	DR471079	WS00952.B
c	284	25	0.6	5	272	BU957835	BU957835	AGENCOURT
c	285	25	0.6	6	274	CD446931	CD446931	E04912701
c	286	25	0.6	5	279	BU851733	BU851733	AGENCOURT
c	287	25	0.6	9	282	AQ881304	AQ881304	HS_5150_A
	288	25	0.6	8	286	CF977411	CF977411	FAR19C3_R
c	289	25	0.6	7	286	CK936787	CK936787	CGF100451
c	290	25	0.6	7	288	CN048657	CN048657	v2_p1_J13
	291	25	0.6	5	294	BU554806	BU554806	AGENCOURT
c	292	25	0.6	1	296	AI254420	AI254420	qv34c04.x
c	293	25	0.6	5	306	BU564923	BU564923	AGENCOURT
	294	25	0.6	5	308	BQ392478	BQ392478	NISC_mq24
	295	25	0.6	2	325	CD393499	CD393499	Gm_cK1303
	296	25	0.6	7	325	CN385905	CN385905	LE2TR04N2
c	297	25	0.6	7	329	CK770250	CK770250	958397 MA
	298	25	0.6	6	335	CF511129	CF511129	CAbud0001
c	299	25	0.6	6	337	CK937561	CK937561	CGF100477
c	300	25	0.6	1	343	AW268962	AW268962	xr97f12.x
c	301	25	0.6	8	349	DR647491	DR647491	EST103760
c	302	25	0.6	6	363	BP154072	BP154072	BP154072
	303	25	0.6	6	363	DR889257	DR889257	JGI_XZG38
c	304	25	0.6	2	369	BE705875	BE705875	IL3-HT005
	305	25	0.6	6	371	CB974204	CB974204	CAB30004_
c	306	25	0.6	7	374	CB358546	CB358546	rm92a01.y
	307	25	0.6	6	376	CF045510	CF045510	QCK14c09.
c	308	25	0.6	1	377	AJ825122	AJ825122	AJ825122
c	309	25	0.6	6	379	BP855124	BP855124	BP855124
c	310	25	0.6	6	388	CF801248	CF801248	rj59f11.y
c	311	25	0.6	6	389	AL587188	AL587188	AL587188
	312	25	0.6	7	389	CN729392	CN729392	11FGYSDB
	313	25	0.6	7	394	CO124510	CO124510	GR_Eb07H
	314	25	0.6	1	401	AA648376	AA648376	ns21d04.s

Right portion:

	#						Accession	Accession	Description
c	315	25	0.6	6	402	CF801155	CF801155	rj58d11.y
	316	25	0.6	1	406	AW051727	AW051727	wx27h11.x
	317	25	0.6	7	408	CO507197	CO507197	GGEZEB200
c	318	25	0.6	6	410	CF214658	CF214658	CGF100081
c	319	25	0.6	1	413	AJ791651	AJ791651	AJ791651
c	320	25	0.6	2	413	BF200242	BF200242	WHE2254_F
	321	25	0.6	6	413	CF041961	CF041961	QCI32c01.
	322	25	0.6	6	414	BQ388623	BQ388623	NISC_mq02
	323	25	0.6	6	415	CB979092	CB979092	CAB40007
	324	25	0.6	6	418	AU300742	AU300742	AU300742
	325	25	0.6	8	419	DR872137	DR872137	JGI_CABG1
	326	25	0.6	6	423	CF529746	CF529746	UI-1-BC1p
	327	25	0.6	2	427	BI792918	BI792918	ie49b03.x
	328	25	0.6	5	435	AI983889	AI983889	wz55b05.x
c	329	25	0.6	7	435	CO375246	CO375246	tah25f02.
	330	25	0.6	7	437	B31144	B31144	HS-1007-A1-
	331	25	0.6	10	437	CNS010VU	ALO99492	Drosophil
c	332	25	0.6	11	438	BG897135	BG897135	HOA60-1-E
	333	25	0.6	11	445	CR918808	CR918808	Sus scrof
	334	25	0.6	6	446	CF212858	CF212858	CGF100065
c	335	25	0.6	2	450	BF414918	BF414918	UI-R-BJ2-
	336	25	0.6	2	450	CN725698	CN725698	17ACDHMS
c	337	25	0.6	8	450	DR889166	DR889166	JGI_XZG36
	338	25	0.6	7	453	CO205478	CO205478	WS0064.B2
	339	25	0.6	3	459	BQ029178	BQ029178	UI-H-DT0-
	340	25	0.6	7	464	CN543304	CN543304	UI-R-DO1-
	341	25	0.6	7	466	CR565013	CR565013	CR565013
	342	25	0.6	8	471	CX510124	CX510124	JGI_XZG35
	343	25	0.6	7	475	CN547892	CN547892	EST_15530
	344	25	0.6	7	477	CK927534	CK927534	hags017xm
	345	25	0.6	8	481	CX889240	CX889240	JGI_CAAM2
	346	25	0.6	2	484	BE118107	BE118107	UI-R-BS1-
	347	25	0.6	9	484	CE064329	CE064329	tigr-gss-
	348	25	0.6	7	487	CK933466	CK933466	CGF100428
	349	25	0.6	5	490	BQ392721	BQ392721	NISC_mq26
	350	25	0.6	2	490	BX751340	BX751340	BX751340
c	351	25	0.6	10	491	CL412078	CL412078	RPCI44_43
	352	25	0.6	8	492	DN388645	DN388645	LIB3893-0
	353	25	0.6	2	496	BI293645	BI293645	UI-R-DK0-
	354	25	0.6	9	498	BH005747	BH005747	BMBAC10B0
	355	25	0.6	8	502	CB756874	CB756874	AGENCOURT
c	356	25	0.6	1	504	AW543914	AW543914	C0175F06-
	357	25	0.6	2	509	BF392858	BF392858	UI-R-CA0-
	358	25	0.6	2	514	BX783275	BX783275	BX783275
c	359	25	0.6	8	514	BE705878	BE705878	IL3-HT005
c	360	25	0.6	8	515	DR716817	DR716817	AGENCOURT
c	361	25	0.6	5	516	DR809825	DR809825	ZM_Bfb003
c	362	25	0.6	6	517	CF803584	CF803584	rg73a08.y
	363	25	0.6	5	517	CN385739	CN385739	LE2TR04G1
c	364	25	0.6	6	519	CA814909	CA814909	CA12EI201
	365	25	0.6	10	519	BX996407	BX996407	Forward_s
c	366	25	0.6	11	521	CN725738	CN725738	17ACDHMS
	367	25	0.6	2	521	CR885386	CR885386	Sus scrof
	368	25	0.6	6	522	BE103267	BE103267	UI-R-BX0-
c	369	25	0.6	9	539	BE737662	BE737662	60157224 6
	370	25	0.6	3	540	CO123800	CO123800	GR_Eb06D
	371	25	0.6	6	543	CA814867	CA814867	CA12EI201
	372	25	0.6	6	543	A2737128	A2737128	RPCI-24-1
	373	25	0.6	8	544	BX119703	BX119703	BX119703
	374	25	0.6	3	544	BM348712	BM348712	MEST299-E
c	375	25	0.6	6	547	CB979272	CB979272	CAB40007
	376	25	0.6	8	554	BB968696	BB968696	601650142
c	377	25	0.6	8	554	DN507004	DN507004	HL01019B2
	378	25	0.6	5	557	BM332118	BM332118	MEST152-F
	379	25	0.6	8	554	BI398720	BI398720	MI-P-AY1-
	380	25	0.6	8	554	DN904018	DN904018	or04d06.y
	381	25	0.6	11	555	CR875564	CR875564	Sus scrof
	382	25	0.6	7	556	CF920895	CF920895	gmthRww3-
	383	25	0.6	9	557	A2974199	A2974199	2M0248M08
c	384	25	0.6	11	557	CR877998	CR877998	Sus scrof
	385	25	0.6	8	559	CX602488	CX602488	CT02032B2
c	386	25	0.6	6	560	BM334253	BM334253	MEST134-F
c	387	25	0.6	1	565	AJ825542	AJ825542	AJ825542

c	No.	Len	Thr	Value	Score	Accession	Description
	388	25	0.6	565	8	DR148466	DR148466 49100001
	389	25	0.6	566	8	BX687988	BX687988 BX687988
	390	25	0.6	568	5	BF401678	BF401678 UI-R-CA0-
c	391	25	0.6	570	6	CF212602	CF212602 CGF100065
	392	25	0.6	570	6	DR405936	DR405936 CSAJ-PNP1
	393	25	0.6	574	2	BF729281	BF729281 1000075B0
	394	25	0.6	579	6	CD776467	CD776467 UI-M-AQ0-
	395	25	0.6	580	5	CN726470	CN726470 3ETMS UP
c	396	25	0.6	589	11	CR886685	CR886685 Sus scrof
	397	25	0.6	594	5	BU677874	BU677874 UI-CF-BC0
	398	25	0.6	595	1	AV717635	AV717635 AV717635
c	399	25	0.6	597	6	CF206271	CF206271 RR890915I
	400	25	0.6	603	10	CB827724	CB827724 tigr-gas-
c	401	25	0.6	607	5	BW961259	BW961259 BW961259
	402	25	0.6	609	5	AJ813188	AJ813188 AJ813188
	403	25	0.6	614	6	CD488859	CD488859 T15_D07 T
	404	25	0.6	614	6	CV916072	CV916072 PP058B3 s
c	405	25	0.6	615	6	CF215370	CF215370 CAST0001
c	406	25	0.6	615	7	CN384794	CN384794 LE2TR01O0
	407	25	0.6	617	11	CR149657	CR149657 Reverse s
	408	25	0.6	620	2	BB631852	BB631852 BB631852
c	409	25	0.6	627	5	AL884520	AL884520 AL884520
c	410	25	0.6	633	3	BQ206970	BQ206970 UI-R-D2I-
	411	25	0.6	635	2	CK320026	CK320026 L2P01g08
c	412	25	0.6	637	2	BF132027	BF132027 601821023
	413	25	0.6	640	7	BF213454	BF213454 601845222
c	414	25	0.6	644	7	CN443884	CN443884 Mdfw20011
	415	25	0.6	644	7	CN385045	CN385045 LE2TR02I2
	416	25	0.6	645	8	CN385216	CN385216 LE2TR02I2
c	417	25	0.6	649	6	CN385234	CN385234 CSAB-PNP1
	418	25	0.6	658	2	BB630813	BB630813 BB630813
	419	25	0.6	660	2	BB630813	BB630813 BB630813
	420	25	0.6	660	8	CB339464	CB339464 CA23EI03I
c	421	25	0.6	661	8	DR472524	DR472524 WS00739.B
	422	25	0.6	662	4	AY440238	AY440238 Armigeres
	423	25	0.6	663	9	AQ488364	AQ488364 RPCI-11-2
c	424	25	0.6	665	8	CF794201	CF794201 889689 MA
	425	25	0.6	665	8	DN128468	DN128468 1142541 M
c	426	25	0.6	671	6	CX448696	CX448696 JGI_XZG26
	427	25	0.6	674	1	CF792835	CF792835 885817 MA
	428	25	0.6	680	6	AL901343	AL901343 AL901343
	429	25	0.6	680	6	CB983173	CB983173 CAB70007
	430	25	0.6	680	11	CR924367	CR924367 Sus scrof
	431	25	0.6	685	1	AV733869	AV733869 AV733869
c	432	25	0.6	687	6	DR575043	DR575043 WS00739.B
	433	25	0.6	688	11	CB241449	CB241449 UI-CF-FN0
	434	25	0.6	688	11	CR903632	CR903632 Sus scrof
	435	25	0.6	692	3	BM993076	BM993076 UI-H-DTO-
c	436	25	0.6	692	7	CK814475	CK814475 Rasgsc502
	437	25	0.6	692	10	CL367328	CL367328 RPCI44_36
c	438	25	0.6	693	8	CX895119	CX895119 JGI_CAAM6
c	439	25	0.6	703	7	CD237523	CD237523 FNPAMC03
	440	25	0.6	703	7	CN106864	CN106864 EC2CAA2RA
c	441	25	0.6	707	1	AV716035	AV716035 AV716035
	442	25	0.6	707	7	AV716035	AV716035 AV716035
	443	25	0.6	708	7	BX691192	BX691192 BX691192
c	444	25	0.6	712	11	CR267126	CR267126 Reverse s
	445	25	0.6	714	6	CK738577	CK738577 BR060013B
	446	25	0.6	714	11	CR922773	CR922773 Sus scrof
	447	25	0.6	721	6	CD238347	CD238347 FNPAZA12
c	448	25	0.6	724	7	CD238943	CD238943 FNPBIB08
c	449	25	0.6	725	11	BU850746	BU850746 AGENCOURT
	450	25	0.6	728	5	CR800132	CR800132 GR0AAAI9C
c	451	25	0.6	729	7	CD239530	CD239530 FNPBVE12
	452	25	0.6	730	7	CN047319	CN047319 V2_p12_F8
	453	25	0.6	732	8	CB982531	CB982531 CAB70006
c	454	25	0.6	732	7	DR811302	DR811302 ZM_BFb003
	455	25	0.6	736	7	CK814424	CK814424 Rasgsc493
c	456	25	0.6	740	6	CD238545	CD238545 FNPBBG04
c	457	25	0.6	740	10	CE553122	CE553122 tigr-gas-
	458	25	0.6	743	9	CC310782	CC310782 TAM32-20N
	459	25	0.6	744	7	CV276358	CV276358 WS0179.B2
	460	25	0.6	749	11	CR194187	CR194187 Reverse s
	461	25	0.6	754	7	CK784592	CK784592 UI-D-GC1-
	462	25	0.6	755	5	BX761543	BX761543
	463	25	0.6	755	9	BH107066	BH107066 RPCI-24-3
	464	25	0.6	766	10	AG484585	AG484585 Mus muscu
	465	25	0.6	780	5	BX761207	BX761207
	466	25	0.6	787	5	BX684116	BX684116
c	467	25	0.6	796	7	CO108108	CO108108 GR_Eb003
	468	25	0.6	796	1	AU117063	AU117063
c	469	25	0.6	798	5	SSC561049	BU589598 AGENCOURT
	470	25	0.6	812	8	CX825761	CX825761 JGI_CAAK4
	471	25	0.6	814	11	BU842689	AJ561049 Sus scrof
	472	25	0.6	817	6	CB235818	BU842689 AGENCOURT
c	473	25	0.6	842	6	AG827284	CB235818 AGENCOURT
	474	25	0.6	854	10	BX756706	AG827284 Sus scrof
	475	25	0.6	856	5	CB998656	BX756706 BX756706
c	476	25	0.6	859	6	BX763164	CB998656 AGENCOURT
	477	25	0.6	866	10	AG827256	BX763164 BX763164
	478	25	0.6	868	7	CR430666	AG827256 Sus scrof
	479	25	0.6	872	10	DU039766	CR430666 CR430666
	480	25	0.6	879	7	BG243773	DU039766 24696 Tom
	481	25	0.6	884	6	CO385194	BG243773 602357086
	482	25	0.6	886	10	AG827168	CO385194 AGENCOURT
	483	25	0.6	893	6	CD756153	AG827168 Sus scrof
	484	25	0.6	898	10	CK194558	CD756153 AGENCOURT
	485	25	0.6	904	7	BU588050	CK194558 FGAS00298
	486	25	0.6	907	5	CK814312	BU588050 AGENCOURT
	487	25	0.6	924	7	CN384923	CK814312 Rasgsc472
	488	25	0.6	927	7	CK157081	CN384923 LE2TR02D2
	489	25	0.6	944	8	DN583815	CK157081 FGAS03815
	490	25	0.6	1070	2	BB878913	DN583815 CH261-107
c	491	25	0.6	1096	6	CN384845	BB878913 90928688
	492	25	0.6	1101	7	CA789790	CN384845 LE2TR02A1
c	493	25	0.6	1121	2	AJ885370	CA789790 AGENCOURT
	494	25	0.6	1148	6	C2505378	AJ885370 Equus cab
	495	25	0.6	1199	10	DU050209	C2505378 GMW2-10J1
	496	25	0.6	1244	10	CO387678	DU050209 144777 To
	497	25	0.6	1248	7	BU300629	CO387678 AGENCOURT
	498	25	0.6	1503	5	CC287888	BU300629 603611639
c	499	25	0.6	1805	10	CNS00FKS	CC287888 CH261-107
c	500	25	0.6	2222	10	AL070916	AL070916 Drosophil
	501	25	0.6	4021	9	CC201777	CC201777 CH261-5C4
	502	24	0.6	52	9	AL567420	AL567420 AL567420
	503	24	0.6	69	8	DR145973	DR145973 49098853
	504	24	0.6	70	8	DN809815	DN809815 77080735
	505	24	0.6	109	8	BM452402	BM452402 AGENCOURT
	506	24	0.6	116	3	BG500956	BG500956 602546539
	507	24	0.6	121	10	CL078548	CL078548 CH216-151
	508	24	0.6	127	10	BC018960	BC018960 603611639
	509	24	0.6	134	4	CNS0A4LN	CNS0A4LN
c	510	24	0.6	138	4	BF632484	BF632484 NF039G06D
	511	24	0.6	158	2	CV623286	CV623286 L_AJ-aaa1
	512	24	0.6	166	7	CV623393	CV623393 L_AJ-aaa2
	513	24	0.6	167	7	CV615513	CV615513 L_AI-aaa2
c	514	24	0.6	168	1	CB344090	CB344090 CA48EN000
c	515	24	0.6	178	1	AI305645	AI305645 qw72g09.x
	516	24	0.6	179	2	BI135249	BI135249 UI-M-BH3-
c	517	24	0.6	180	3	CB344144	CB344144 CA48EN000
c	518	24	0.6	191	1	AI224731	AI224731 qx25c09.x
c	519	24	0.6	199	3	BP145280	BP145280 BP145280
c	520	24	0.6	199	2	BY082908	BY082908 BY082908
c	521	24	0.6	199	5	BU590216	BU590216 Sus scrof
c	522	24	0.6	204	2	BE110172	BE110172 UI-R-BJ1-
c	523	24	0.6	212	11	BF215451	BF215451 60188I004
c	524	24	0.6	215	2	CR910000	CR910000 Sus scrof
	525	24	0.6		1	BF508454	BF508454 UI-H-BI4-
	526	24	0.6		1	BF733479	BF733479 MR0-AN003
	527	24	0.6		1	AA910608	AA910608 ok61a06.s
	528	24	0.6		1	AI251235	AI251235 qv55g01.x
	529	24	0.6		2	AI733997	AI733997 qv55g01.x
c	530	24	0.6		10	BF402224	BF402224 UI-R-CA1-
	531	24	0.6		10	CL346304	CL346304 RPCI44_27
	532	24	0.6		7	CL361144	CL361144 RPCI44_34
	533	24	0.6			CO220941	CO220941 WS01011.B

Left block:

	idx			num		accession	accession	n	description
	534	24	0.6	221		AW522595	AW522595	1	AW522595 UI-R-BOO-
c	535	24	0.6	225		AI046577	AI046577	1	AI046577 uh27e06.r
	536	24	0.6	228		AI792898	AI792898	1	AI792898 qv55g01.y
	537	24	0.6	231		BE111168	BE111168	2	BE111168 UI-R-BJ1-
c	538	24	0.6	232		DR904169	DR904169	8	DR904169 JGI_XZT65
	539	24	0.6	245		DN104664	DN104664	8	DN104664 1100462 M
	540	24	0.6	247		CL330693	CL330693	10	CL330693 CH242_4P1
	541	24	0.6	249		AL962690	AL962690	1	AL962690 AL962650
	542	24	0.6	249		AW526512	AW526512	1	AW526512 UI-R-BO1-
c	543	24	0.6	251		AA823304	AA823304	1	AA823304 vp37c07.r
	544	24	0.6	256		CN267265	CN267265	7	CN267265 170004708
	545	24	0.6	257		AI568036	AI568036	1	AI568036 tr88e10.x
	546	24	0.6	259		DN110163	DN110163	8	DN110163 1107825 M
c	547	24	0.6	259		DN110511	DN110511	8	DN110511 1108209 M
	548	24	0.6	263		BB562944	BB562944	2	BB562944 BB562944
	549	24	0.6	265		BU735805	BU735805	3	BU735805 UI-E-DXO-
c	550	24	0.6	269		BM812123	BM812123	2	BM812123 fx14f06.y
	551	24	0.6	272		BI044595	BI044595	2	BI044595 PMO-OTO21
	552	24	0.6	274		AL875163	AL875163	1	AL875163 AL875163
	553	24	0.6	282		AA516315	AA516315	1	AA516315 ng68h11.s
	554	24	0.6	290		AW292572	AW292572	1	AW292572 UI-H-BI2-
	555	24	0.6	291		CN083700	CN083700	7	CN083700 EC2BBA23A
	556	24	0.6	294		AA355995	AA355995	1	AA355995 EST64648
c	557	24	0.6	296		CF722804	CF722804	6	CF722804 E04_LKF00
	558	24	0.6	299		BX289619	BX289619	10	BX289619 Arabidops
c	559	24	0.6	302		DN104986	DN104986	8	DN104986 1100846 M
	560	24	0.6	305		BI296776	BI296776	3	BI296776 UI-R-DKO-
	561	24	0.6	306		AI355451	AI355451	1	AI355451 qt95e07.x
	562	24	0.6	310		AI955112	AI955112	1	AI955112 wr48h04.x
	563	24	0.6	315		CL411220	CL411220	10	CL411220 RPCI44_42
	564	24	0.6	318		CL370729	CL370729	10	CL370729 RPCI44_29
c	565	24	0.6	321		AG203964	AG203964	10	AG203964 Pan trogl
	566	24	0.6	323		AI593222	AI593222	1	AI593222 vt86b02.x
	567	24	0.6	324		AW321058	AW321058	1	AW321058 uo17e11.x
c	568	24	0.6	327		CE797793	CE797793	10	CE797793 tigr-gss-
	569	24	0.6	336		AW449516	AW449516	1	AW449516 UI-H-BI3-
c	570	24	0.6	337		BF661503	BF661503	2	BF661503 maa78b05.
	571	24	0.6	339		CB084012	CB084012	6	CB084012 hq07h06.b
	572	24	0.6	342		CX125445	CX125445	8	CX125445 1326056 N
	573	24	0.6	348		AW016332	AW016332	1	AW016332 UI-H-BI0-
	574	24	0.6	348		CL362961	CL362961	10	CL362961 RPCI44_38
	575	24	0.6	362		AW048768	AW048768	1	AW048768 UI-M-BH1-
	576	24	0.6	363		CE411596	CE411596	10	CE411596 tigr-gss-
	577	24	0.6	364		BE234499	BE234499	2	BE234499 141628 MA
	578	24	0.6	365		BQ160489	BQ160489	3	BQ160489 WHE1821-1
	579	24	0.6	367		DN139422	DN139422	8	DN139422 SGP264260
	580	24	0.6	373		BP804554	BP804554	5	BP804554 BP804554
c	581	24	0.6	374		CA296841	CA296841	6	CA296841 SCUTSD208
	582	24	0.6	381		AI044248	AI044248	1	AI044248 UI-R-C1-k
	583	24	0.6	381		AI706215	AI706215	1	AI706215 UI-R-AB1-
	584	24	0.6	382		AI161157	AI161157	1	AI161157 qc89h04.x
	585	24	0.6	386		BY097208	BY097208	5	BY097208 BY097208
	586	24	0.6	388		CL352603	CL352603	10	CL352603 RPCI44_40
	587	24	0.6	390		CR899706	CR899706	11	CR899706 Sus scrof
	588	24	0.6	396		BQ601516	BQ601516	3	BQ601516 MI-P-H4-a
	589	24	0.6	399		BU822195	BU822195	3	BU822195 UB33BF09
	590	24	0.6	401		BI403623	BI403623	3	BI403623 MI-P-CP1-
	591	24	0.6	402		AI619980	AI619980	1	AI619980 ty46g01.x
	592	24	0.6	404		AI521110	AI521110	1	AI521110 to43b08.x
	593	24	0.6	404		BI388085	BI388085	3	BI388085 BFL26_002
	594	24	0.6	405		CR872320	CR872320	11	CR872320 Sus scrof
c	595	24	0.6	406		AI032161	AI032161	1	AI032161 os76f08.s
	596	24	0.6	406		BX484831	BX484831	5	BX484831 DKFZp686K
	597	24	0.6	407		BM151093	BM151093	2	BM151093 TCBAP1D13
c	598	24	0.6	411		BP650014	BP650014	5	BP650014 BP650014
	599	24	0.6	413		AV744909	AV744909	4	AV744909 AV744909
	600	24	0.6	416		AW055257	AW055257	1	AW055257 wz16a09.x
	601	24	0.6	416		BE114328	BE114328	2	BE114328 UI-R-BJ1-
	602	24	0.6	418		AI043943	AI043943	1	AI043943 UI-R-CO-j
	603	24	0.6	420		CB241920	CB241920	6	CB241920 UI-CF-FNO-
	604	24	0.6	424		BF199042	BF199042	2	BF199042 249086 MA
	605	24	0.6	425		CK785785	CK785785	7	CK785785 UI-D-GC1-
	606	24	0.6	432		AW534664	AW534664	1	AW534664 UI-R-BS0-

Right block:

	idx		24	0.6	accession	accession	n	description
	607		24	0.6	BQ032062	BQ032062	3	BQ032062 UI-1-CF0-
	608		24	0.6	AW457182	AW457182	1	AW457182 UI-M-BH3-
c	609		24	0.6	AV740541	AV740541	4	AV740541 AV740541
	610		24	0.6	AW632847	AW632847	1	AW632847 b101a07.x
c	611		24	0.6	CN644374	CN644374	7	CN644374 ILLUMIGEN
c	612		24	0.6	BG348216	BG348216	2	BG348216 dg39f08.y
c	613		24	0.6	CR902053	CR902053	11	CR902053 Sus scrof
	614		24	0.6	BE490944	BE490944	2	BE490944 db40b10.x
	615		24	0.6	BQ031536	BQ031536	3	BQ031536 UI-1-CF0-
	616		24	0.6	AW298014	AW298014	1	AW298014 UI-H-BW0-
c	617		24	0.6	DR805882	DR805882	8	DR805882 ZM_BFb003
	618		24	0.6	AW074271	AW074271	1	AW074271 xb10c10.x
	619		24	0.6	AJ700742	AJ700742	1	AJ700742 AJ700742
c	620		24	0.6	DN139438	DN139438	8	DN139438 SGP264276
	621		24	0.6	AI885486	AI885486	1	AI885486 wm24f05.x
	622		24	0.6	AJ280852	AJ280852	1	AJ280852 4A3A-AAY-
	623		24	0.6	AW136703	AW136703	1	AW136703 UI-H-BI1-
	624		24	0.6	BQ391277	BQ391277	3	BQ391277 NISC_mq17
	625		24	0.6	AQ310697	AQ310697	5	AQ310697 CITBI-E1-
	626		24	0.6	BH552392	BH552392	5	BH552392 BOGNF66TR
	627		24	0.6	BY566085	BY566085	5	BY566085 BY566085
	628		24	0.6	BX107687	BX107687	5	BX107687 BX107687
	629		24	0.6	BX568221	BX568221	5	BX568221 BX568221
	630		24	0.6	CW066231	CW066231	10	CW066231_104_313_1
	631		24	0.6	CK784232	CK784232	7	CK784232 UI-D-GC1-
c	632		24	0.6	CL370447	CL370447	5	CL370447 RPCI44_29
	633		24	0.6	BX762998	BX762998	5	BX762998 BX762998
	634		24	0.6	BM714864	BM714864	3	BM714864 UI-E-EJ0-
	635		24	0.6	BM935083	BM935083	3	BM935083 UI-M-BH3-
	636		24	0.6	BM675378	BM675378	3	BM675378 UI-E-EJ0-
	637		24	0.6	BH090249	BH090249	9	BH090249 RPCI-24-3
c	638		24	0.6	CB151011	CB151011	9	CB151011 tigr-gss-
	639		24	0.6	AW632884	AW632884	1	AW632884 b101d08.x
	640		24	0.6	AL134552	AL134552	1	AL134552 DKFZp547A
	641		24	0.6	DR103310	DR103310	8	DR103310 JH030A10
	642		24	0.6	BX113834	BX113834	5	BX113834 BX113834
c	643		24	0.6	CW490786	CW490786	10	CW490786_f6bb001f2
c	644		24	0.6	AQ207299	AQ207299	5	AQ207299 HS_3242_A
	645		24	0.6	BI379779	BI379779	3	BI379779 BFLGl_001
c	646		24	0.6	BU824240	BU824240	5	BU824240 UB62BPA07
	647		24	0.6	DR130839	DR130839	8	DR130839 49078376
	648		24	0.6	AA997646	AA997646	1	AA997646 UI-R-CO-h
	649		24	0.6	BU824195	BU824195	5	BU824195 UB61BPF06
	650		24	0.6	BG379298	BG379298	2	BG379298 UI-R-CS0-
c	651		24	0.6	CX693530	CX693530	8	CX693530 ydc82h04.
	652		24	0.6	AM004437	AM004437	11	AM004437 AM004437
	653		24	0.6	AL742979	AL742979	1	AL742979 Danio rer
	654		24	0.6	DN435011	DN435011	11	DN435011 LIB4217-1
c	655		24	0.6	AG829138	AG829138	10	AG829138 Sus scrof
	656		24	0.6	BF389909	BF389909	2	BF389909 UI-R-BS2-
	657		24	0.6	CO000974	CO000974	7	CO000974 OB073 pre
	658		24	0.6	DR033904	DR033904	8	DR033904 OD2_pre-o
	659		24	0.6	BQ398314	BQ398314	3	BQ398314 NISC_mo06
	660		24	0.6	CB197627	CB197627	9	CB197627 tigr-gss-
c	661		24	0.6	CZ563848	CZ563848	10	CZ563848_1_p_bw039
	662		24	0.6	CR872468	CR872468	11	CR872468 Sus scrof
c	663		24	0.6	AL036011	AL036011	1	AL036011 DKFZp564L
	664		24	0.6	BF704508	BF704508	2	BF704508 MI-P-H4-a
	665		24	0.6	AQ930618	AQ930618	5	AQ930618 RPCI-23-2
	666		24	0.6	CE251519	CE251519	9	CE251519 tigr-gss-
	667		24	0.6	CL345058	CL345058	10	CL345058 RPCI44_27
c	668		24	0.6	AZ912824	AZ912824	5	AZ912824 RPCI-24-1
c	669		24	0.6	CB135408	CB135408	9	CB135408 tigr-gss-
	670		24	0.6	DR134364	DR134364	8	DR134364 49299044
	671		24	0.6	DR142805	DR142805	8	DR142805 49101185
	672		24	0.6	DR151379	DR151379	8	DR151379 49336343
	673		24	0.6	BF711910	BF711910	2	BF711910 MI-P-O3-a
	674		24	0.6	CK433846	CK433846	7	CK433846 UI-D-GC1-
c	675		24	0.6	DR137230	DR137230	8	DR137230 49296983
	676		24	0.6	CR873261	CR873261	11	CR873261 Sus scrof
	677		24	0.6	BM987543	BM987543	3	BM987543 UI-H-COO-
c	678		24	0.6	DR138826	DR138826	8	DR138826 49159096
	679		24	0.6	CR865597	CR865597	11	CR865597 Sus scrof

C	#	E	L	Pos	N	Acc	Match / Description
	680	0.6	24	566	5	BX478587	BX478587 DKFZp686D
c	681	0.6	24	567	5	CC953015	CC953015 BOIEL23TR
	682	0.6	24	571	10	CL343128	CL343128 RPCI44_27
	683	0.6	24	573	1	AJ724453	AJ724453 AJ724453
	684	0.6	24	579	5	BX705021	BX705021 BX705021
c	685	0.6	24	582	3	BP198299	BP198299 BP198299
	686	0.6	24	582	10	CL344708	CL344708 RPCI44_27
	687	0.6	24	583	1	CV049046	CV049046 EST 14363
c	688	0.6	24	585	1	AJ724472	AJ724472 AJ724472
c	689	0.6	24	586	11	AJ920515	AJ920515 AJ920515
	690	0.6	24	586	9	DR39H21T	DR39H21T Danio rer
c	691	0.6	24	589	10	AQ634003	AQ634003 RPCI-11-4
	692	0.6	24	589	1	CL376981	CL376981 RPCI44_44
c	693	0.6	24	590	1	DR125140	DR125140 49101072
	694	0.6	24	591	8	AM009396	AM009396 AM009396
c	695	0.6	24	594	8	DR123413	DR123413 49134881
	696	0.6	24	595	8	AL046591	AL046591 DKFZp434K
c	697	0.6	24	595	10	DR128418	DR128418 49080176
	698	0.6	24	598	8	DR135701	DR135701 49291332
	699	0.6	24	598	10	BJ087381	BJ087381 BJ087381
c	700	0.6	24	598	8	CL389486	CL389486 RPCI44_28
	701	0.6	24	600	2	DR852935	DR852935 JGI_CABG9
c	702	0.6	24	603	8	BG380472	BG380472 UI-R-CT0-
	703	0.6	24	603	9	DN415940	DN415940 LIB4215-0
	704	0.6	24	608	11	CB249483	CB249483 tigr-gss-
	705	0.6	24	612	2	CR876693	CR876693 Sus scrof
c	706	0.6	24	615	3	BG529088	BG529088 602579191
	707	0.6	24	615	7	BP733570	BP733570 BP733570
	708	0.6	24	619	11	BQ597628	BQ597628 MI-P-A2-a
c	709	0.6	24	621	6	CN648794	CN648794 ILLUMIGEN
	710	0.6	24	621	3	CR882173	CR882173 Sus scrof
	711	0.6	24	624	6	CB326615	CB326615 UI-R-DZ0-
c	712	0.6	24	626	8	CL386761	CL386761 RPCI44_33
	713	0.6	24	628	9	BQ027780	BQ027780 UI-H-CO0-
c	714	0.6	24	628	8	CR898570	CR898570 Sus scrof
c	715	0.6	24	629	11	AZ099417	AZ099417 RPCI-23-4
	716	0.6	24	637	11	DN867518	DN867518 nac28d03.
	717	0.6	24	638	3	BP715100	BP715100 BP715100
	718	0.6	24	640	8	DE067677	DE067677 Oryzias 1
c	719	0.6	24	641	6	BP169174	BP169174 BP169174
c	720	0.6	24	642	2	CX486892	CX486892 JGI_XZG29
	721	0.6	24	643	3	CB348324	CB348324 CAB2SG000
	722	0.6	24	644	2	BM337023	BM337023 MEST202-C
c	723	0.6	24	646	7	BG673625	BG673625 DRNABC06
	724	0.6	24	646	8	DN901104	DN901104 naq15c01.
	725	0.6	24	648	10	CO233996	CO233996 WS0058.B2
c	726	0.6	24	648	7	CX151557	CX151557 1291991 N
	727	0.6	24	650	5	BX749766	BX749766 BX749766
	728	0.6	24	650	9	CR872579	CR872579 Sus scrof
c	729	0.6	24	652	10	CW891055	CW891055 RPCI42_11
c	730	0.6	24	655	10	CN087905	CN087905 EC2BBA29B
	731	0.6	24	655	2	AZ575185	AZ575185 336pvC1o
	732	0.6	24	656	7	AG062289	AG062289 Pan trogl
c	733	0.6	24	659	6	BM764855	BM764855 K-EST0046
c	734	0.6	24	660	10	CE000310	CE000310 tigr-gss-
	735	0.6	24	661	9	CNS04096	CNS04096 Tetraodon
c	736	0.6	24	663	11	DR884976	DR884976 JGI_CACK7
	737	0.6	24	663	7	DR884977	DR884977 JGI_CACK7
	738	0.6	24	664	11	CA344293	CA344293 674665 NC
c	739	0.6	24	664	5	CL379026	CL379026 RPCI44_42
	740	0.6	24	664	9	CR923518	CR923518 Sus scrof
	741	0.6	24	670	11	AG084650	AG084650 Pan trogl
c	742	0.6	24	671	7	BB456373	BB456373 BB456373
	743	0.6	24	671	11	DR39I22T	DR39I22T Danio rer
	744	0.6	24	673	5	CN156797	CN156797 944227 MA
	745	0.6	24	673	9	DR540888	DR540888 WS01034.B
	746	0.6	24	673	11	CR259267	CR259267 Reverse s
	747	0.6	24	675	7	BU376504	BU376504 603809946
	748	0.6	24	676	5	CW901735	CW901735 RPCI42_13
c	749	0.6	24	682	11	AZ964290	AZ964290 2M0233K22
c	750	0.6	24	683	9	CR892766	CR892766 Sus scrof
c	751	0.6	24	683	11	AJ425578	AJ425578 AJ425578
c	752	0.6	24	685	7	CO220425	CO220425 WS0109.B2
	753	0.6	24	687	8	CV796393	CV796393 UI-R-DQ1-
	754	0.6	24	692	8	CX138227	CX138227 1277433 N
	755	0.6	24	693	11	CR866681	CR866681 Sus scrof
c	756	0.6	24	694	11	CR914697	CR914697 Sus scrof
	757	0.6	24	697	2	BB865302	BB865302 BB865302
c	758	0.6	24	701	2	BE238970	BE238970 MD0626 Me
	759	0.6	24	701	7	CR420555	CR420555 CR420555
	760	0.6	24	702	6	CA811313	CA811313 CA22LI01I
	761	0.6	24	703	6	CX716569	CX716569 1332996 N
	762	0.6	24	705	2	BB865486	BB865486 BB865486
c	763	0.6	24	706	9	BP159037	BP159037 BP159037
	764	0.6	24	706	11	BZ026169	BZ026169 oei5a06.
c	765	0.6	24	706	8	CR207871	CR207871 Forward s
	766	0.6	24	710	11	CX146993	CX146993 1286945 N
c	767	0.6	24	715	3	BI382917	BI382917 BFLG2_001
	768	0.6	24	715	8	CX719257	CX719257 1335928 N
c	769	0.6	24	718	9	CC538188	CC538188 CH240_417
c	770	0.6	24	718	9	CX375037	CX375037 JGI_XZT58
	771	0.6	24	718	10	AG184527	AG184527 Pan trogl
	772	0.6	24	719	10	AG301460	AG301460 Mus muscu
	773	0.6	24	722	11	CX497433	CX497433 JGI_XZG43
	774	0.6	24	722	6	CR050194	CR050194 Reverse s
	775	0.6	24	724	6	CA363975	CA363975 638790 NC
c	776	0.6	24	725	7	CV798838	CV798838 BU01002X1
	777	0.6	24	727	7	CV260154	CV260154 WS02013.B
	778	0.6	24	727	7	CV262795	CV262795 WS0202.B2
	779	0.6	24	729	7	CV269520	CV269520 WS0208.B2
	780	0.6	24	734	11	CR415639	CR415639 CR415639
	781	0.6	24	734	7	CR925212	CR925212 Sus scrof
	782	0.6	24	735	3	CV266375	CV266375 WS02029.B
	783	0.6	24	737	9	CR423544	CR423544 CR423544
	784	0.6	24	738	3	BP455435	BP455435 BP455435
	785	0.6	24	741	8	CN972580	CN972580 2007_124
	786	0.6	24	744	9	BH086892	BH086892 RPCI-54-3
c	787	0.6	24	746	8	DN057376	DN057376 JGI_CABA1
	788	0.6	24	747	11	DN057377	DN057377 JGI_CABA1
	789	0.6	24	749	5	DE099057	DE099057 Oryzias 1
	790	0.6	24	750	5	BQ001278	BQ001278 UI-H-DH1-
c	791	0.6	24	751	8	BW976827	BW976827 BW976827
	792	0.6	24	751	8	CX718814	CX718814 1335428 N
	793	0.6	24	751	6	CC590599	CC590599 CH240_390
	794	0.6	24	752	6	CA510403	CA510403 UI-R-FS0-
	795	0.6	24	753	5	BX762190	BX762190 BX762190
	796	0.6	24	758	5	BM678941	BM678941 UI-E-E00-
	797	0.6	24	760	11	CR906699	CR906699 Sus scrof
	798	0.6	24	762	7	CR437457	CR437457 CR437457
	799	0.6	24	764	6	BW969191	BW969191 BW969191
	800	0.6	24	766	6	CD000612	CD000612 AGENCOURT
	801	0.6	24	771	7	CR425016	CR425016 CR425016
	802	0.6	24	773	4	CN509556	BX042742 Single re
	803	0.6	24	773	5	CX422367	CX422367 JGI_XZG62
	804	0.6	24	776	5	BX781246	BX781246 BX781246
	805	0.6	24	778	8	CX876111	CX876111 JGI_CAAL1
	806	0.6	24	779	5	BX734302	BX734302 BX734302
	807	0.6	24	781	8	CX567966	CX567966 UI-M-HK0-
	808	0.6	24	783	1	BZ160889	BZ160889 CH230-290
	809	0.6	24	785	8	AJ724457	AJ724457 AJ724457
	810	0.6	24	786	10	DN872774	DN872774 nad22d02.
	811	0.6	24	787	7	AG828972	AG828972 Sus scrof
	812	0.6	24	790	5	CR585029	CR585029 CR585029
	813	0.6	24	798	6	BQ771803	BQ771803 UI-H-EZ1-
	814	0.6	24	804	8	CNS03V2D	AL261886 Tetraodon
	815	0.6	24	807	11	CD513863	CD513863 AGENCOURT
	816	0.6	24	820	6	BU559835	BU559835 AGENCOURT
	817	0.6	24	820	5	DN113028	DN113028 1112267 M
	818	0.6	24	824	1	AW874684	AW874684 kdef2 Soa
	819	0.6	24	828	8	CX625298	CX625298 H29_F3 Sp
	820	0.6	24	851	5	BX742745	BX742745 BX742745
	821	0.6	24	854	7	CO913873	CO913873 AGENCOURT
	822	0.6	24	857	9	AZ688419	AZ688419 ENTL16TR
	823	0.6	24	862	8	CX370217	CX370217 JGI_XZT55
	824	0.6	24	875	9	CC553951-	CC553951 CH240_460
c	825	0.6	24	876	11	CR184556	CR184556 Forward s

	idx	E	len	pos	n	accession	accession	description
c	826	0.6	24	877	11	CR882784	CR882784	Sus scrof
c	827	0.6	24	885	7	CK019779	CK019779	AGENCOURT
c	828	0.6	24	887	2	BI101506	BI101506	
	829	0.6	24	889	5	BU854717	BU854717	AGENCOURT
	830	0.6	24	900	5	BU164249	BU164249	AGENCOURT
	831	0.6	24	920	11	SSC514471	AJ514471	Sus scrof
	832	0.6	24	938	5	BQ880486	BQ880486	AGENCOURT
	833	0.6	24	952	1	AF179479	AF179479	
	834	0.6	24	962	8	DN562478	DN562478	
	835	0.6	24	983	7	BE957745	BE957745	
	836	0.6	24	1027	5	BQ939830	BQ939830	AGENCOURT
	837	0.6	24	1052	5	DR134327	DR134327	
c	838	0.6	24	1099	8	CX817722	CX817722	D12_AGBS
c	839	0.6	24	1107	8	DR740855	DR740855	FGAS00078
	840	0.6	24	1153	8	DR123662	DR123662	
c	841	0.6	24	1166	7	CV672916	CV672916	RET7SJ_09
c	842	0.6	24	1172	8	DN262630	DN262630	Meso03860
	843	0.6	24	1201	10	CNS027L1	AL184798	Tetraodon
	844	0.6	24	1249	8	CX100315	CX100315	RECm1168
	845	0.6	24	1307	10	AG346257	AG346257	Mus muscu
c	846	0.6	24	1473	10	AJ860081	AJ860081	Brassica
	847	0.6	24	1739	10	CL136004	CL136004	ISB1-107F
	848	0.6	24	1961	4	AK051402	AK051402	Mus muscu
c	849	0.6	24	2838	4	CR858400	CR858400	Pongo pyg
	850	0.6	24	2956	4	HSM806920	BX640812	Homo sapi
	851	0.6	23	59	6	CB217739	CB217739	NISC_nb04
c	852	0.6	23	79	5	AJ737158	AJ737158	
	853	0.6	23	97	8	BQ526869	BQ526869	NISC_no19
	854	0.6	23	103	7	CN545910	CN545910	EST_17854
c	855	0.6	23	105	1	AM006188	AM006188	
c	856	0.6	23	111	6	CA811895	CA811895	CA41LN03I
	857	0.6	23	120	8	CF333073	CF333073	JMT--01-N
	858	0.6	23	121	7	CX769791	CX769791	ACAD-aab1
	859	0.6	23	124	5	AI540464	AI540464	tq24c10.x
	860	0.6	23	125	6	CA812378	CA812378	CA41LN03I
	861	0.6	23	127	11	CR897891	CR897891	Sus scrof
c	862	0.6	23	129	9	AZ077736	AZ077736	RPCI-23-4
	863	0.6	23	136	5	AI540534	AI540534	tq25f05.x
	864	0.6	23	145	3	AI843728	AI843728	UI-M-AK1-
	865	0.6	23	149	5	CV600751	CV600751	L_AH-aaal
c	866	0.6	23	150	7	CV600885	CV600885	L_AH-aaal
c	867	0.6	23	150	8	DN586294	DN586294	EST62BS_Z
	868	0.6	23	153	2	AA040237	AA040237	zk44a10.s
	869	0.6	23	157	5	BW957428	BW957428	
	870	0.6	23	158	4	AI058697	AI058697	UI-R-Cl-k
	871	0.6	23	158	9	AZ723254	AZ723254	RPCI-24-6
c	872	0.6	23	159	2	BG957829	BG957829	PM2-CT080
c	873	0.6	23	166	7	CK362261	CK362261	AGENCOURT
	874	0.6	23	168	9	AZ819262	AZ819262	2M009J14
c	875	0.6	23	171	8	BP460907	BP460907	
	876	0.6	23	172	5	AI560685	AI560685	tq55b01.x
c	877	0.6	23	178	5	BP154966	BP154966	
	878	0.6	23	180	5	AL597503	AL597503	DKFZp313E
	879	0.6	23	181	6	BU860664	BU860664	AGENCOURT
	880	0.6	23	182	8	CX907949	CX907949	JGI_CAAN6
	881	0.6	23	183	5	BU540127	BU540127	AGENCOURT
	882	0.6	23	185	3	BQ276832	BQ276832	AGENCOURT
	883	0.6	23	185	5	BQ596755	BQ596755	PfESToab2
	884	0.6	23	185	5	BU565876	BU565876	AGENCOURT
	885	0.6	23	185	5	BU587367	BU587367	AGENCOURT
	886	0.6	23	185	9	BU928581	BU928581	AGENCOURT
c	887	0.6	23	185	7	BU942925	BU942925	AGENCOURT
c	888	0.6	23	186	5	BU852006	BU852006	AGENCOURT
c	889	0.6	23	186	5	BU928649	BU928649	AGENCOURT
	890	0.6	23	186	11	CR887441	CR887441	Sus scrof
	891	0.6	23	189	1	AA746619	AA746619	nx27a05.s
	892	0.6	23	192	5	BU536052	BU536052	AGENCOURT
	893	0.6	23	193	5	BU960980	BU960980	
	894	0.6	23	195	2	BE804639	BE804639	sr84e07.y
	895	0.6	23	195	5	BU564300	BU564300	AGENCOURT
	896	0.6	23	196	5	BU928948	BU928948	AGENCOURT
c	897	0.6	23	197	5	BU554869	BU554869	AGENCOURT
c	898	0.6	23	198	3	BI298639	BI298639	UI-R-CV2-
c	899	0.6	23	198	7	CF888246	CF888246	amastc-2B
	900	0.6	23	201	2	AI933727	AI933727	wn43a11.x
c	901	0.6	23	204	2	BF577654	BF577654	602092532
c	902	0.6	23	213	5	BG296420	BG296420	602394306
	903	0.6	23	218	2	BX734913	BX734913	BX734913
	904	0.6	23	220	1	AI501906	AI501906	UI-R-C2p-
	905	0.6	23	221	1	AW531369	AW531369	UI-R-BS0-
	906	0.6	23	222	1	BF709767	BF709767	MI-P-AY0-
	907	0.6	23	222	1	AW413699	AW413699	uo91e08.x
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	914	0.6	23	241	1	AI418803	AI418803	tg33f01.x
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	916	0.6	23	245	2	AI844285	AI844285	UI-M-AL1-
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	918	0.6	23	250	2	AI071623	AI071623	UI-R-C2-m
	919	0.6	23	252	2	BB119256	BB119256	UI-R-CA0-
	920	0.6	23	253	2	BF392547	BF392547	UI-R-CA0-
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	927	0.6	23	259	1	AJ759046	AJ759046	AJ759046
	928	0.6	23	260	1	AA736595	AA736595	oa22c03.s
	929	0.6	23	261	8	CX764081	CX764081	PL_5-C6-5
	930	0.6	23	263	10	CL345026	CL345026	RPCI44_27
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	932	0.6	23	265	10	CL323384	CL323384	RPCI44_45
	933	0.6	23	266	7	AW125065	AW125065	UI-M-BH2.
	934	0.6	23	266	10	CK784345	CK784345	UI-D-GC1-
	935	0.6	23	266	7	CL412219	CL412219	RPCI44_43
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	939	0.6	23	277	10	CE311418	CE311418	tigr-gss-
	940	0.6	23	278	5	AW014864	AW014864	UI-H-BI0-
	941	0.6	23	278	7	BU754788	BU754788	UI-1-BA0-
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	944	0.6	23	286	10	BI302910	BI302910	UI-R-D00-
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	946	0.6	23	288	7	CK349134	CK349134	hggfha9B1
	947	0.6	23	290	5	BW955926	BW955926	BW955926
	948	0.6	23	292	10	CE745191	CE745191	tigr-gss-
	949	0.6	23	292	10	AW277138	AW277138	xp63e04.x
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	952	0.6	23	296	2	BB477231	BB477231	BB477231
	953	0.6	23	297	1	AI202045	AI202045	q143d07.x
	954	0.6	23	297	7	BI859231	BI859231	603385426
	955	0.6	23	297	7	CF959179	CF959179	898rsiceb
	956	0.6	23	298	1	AW078853	AW078853	xb18h04.x
	957	0.6	23	298	7	BU755026	BU755026	UI-1-BA0-
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	959	0.6	23	299	3	BP436094	BP436094	BP436094
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	962	0.6	23	303	1	AI043915	AI043915	UI-C0-j
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	964	0.6	23	306	2	AI223445	AI223445	qg54c08.x
	965	0.6	23	307	3	BP156398	BP156398	BP156398
	966	0.6	23	307	8	CV942003	CV942003	PMrpct_46
	967	0.6	23	309	10	CE534015	CE534015	tigr-gss-
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	969	0.6	23	312	3	BP157861	BP157861	BP157861
	970	0.6	23	313	3	BM987127	BM987127	UI-H-C00-
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   974  23  0.6  316   1  AW125709  AW125709 UI-M-BH2.
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   979  23  0.6  323  11  CR920588  CR920588 Sus scrof
   980  23  0.6  324   6  CF577691  CF577691 AGENCOURT
   981  23  0.6  326   1  AW450759  AW450759 UI-H-BI3-
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   983  23  0.6  327   1  AI843467  AI843467 UI-M-AQ1-
   984  23  0.6  328   1  AI835711  AI835711 UI-M-AIO-
c  985  23  0.6  328   1  BP438397  BP438397 BP438397
   986  23  0.6  329   1  AI843131  AI843131 UI-M-AK1-
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   990  23  0.6  331  10  CL359112  CL359112 RPCI44.33
   991  23  0.6  332   1  AI548502  AI548502 UI-R-C3-t
   992  23  0.6  333   1  AW633037  AW633037 b103b02.x
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   996  23  0.6  338   2  BE654713  BE654713 UI-M-BG1-
c  997  23  0.6  339  10  CL332143  CL332143 CH242.10C
   998  23  0.6  340   6  CA440983  CA440983 UI-H-EDO-
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ALIGNMENTS

ORIGIN   /locus_tag="HC7587"

Query Match   62.8%; Score 2460; DB 11; Length 3711;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2710; Mismatches 0; Conservative 0; Indels 5; Gaps 0;

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Qy 1060 GAAATTGCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCAACCTGCCACTGCTTTTGAA 1119
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Db  997 GAAATTGCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAA 1056

Qy 1120 GGACATATGTTACTGTCTGGTCTCAGAGCCCTTCAGGATTGGACCGTACCACCAACTTGTT 1179
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Db 1057 GGACATATGTTACTGTCTGGTCTCAGAGCCCTTCAGGATTGGACCGTACCACCAACTTGTT 1116

Qy 1180 AACATTGGAGAGCGCTGTAATGTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCA 1239
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Qy 1240 GGAAACTATGAAGAAGCCTTGTGTGTTGCCAAAGTGCAGGTGAAATGGGAGCCCAGGTG 1299
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Qy 1300 TTGGATGTCAACATGGATGATGGCATGGTCTAGATGGTCCAAGTGCAATGACCAGATTTGC 1359
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Qy 1360 AACTTAATTGCTTCCGAGCCAGACATCGCAAAGTACCTTGTGCATCGACTCCTCCAAT 1419
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Qy 1420 TTTGCTGTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATT 1479
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Qy 1480 AGTCTGAAGGAAGGAGGAGGAGGACGACTTCTTGGAGAAGGCCAGGAAGTATGA 1539
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Db 1417 AGTCTGAAGGAAGGAGGAGGAGGACGACTTCTTGGAGAAGGCCAGGAAGTATGA 1476

Qy 1540 GCTGCTATGGTGGTCATGGCTTTTGATGAAGAAGGACAGGCAACAGAAACAGACACAAAA 1599
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Db 1477 GCTGCTATGGTGGTCATGGCTTTTGATGAAGAAGGACAGGCAACAGAAACAGACACAAAA 1536

Qy 1600 ATCAGAGTGCACCCGGGCCTACCATCTGCTTGTGAAAAACTGGGCTTTAATCCAAT 1659
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Qy 1780 ATAAGTGGAAGTCTTTCCAACTGTCCTCCTTCCGAGGAATGGAAGCCATTCGAGAA 1839
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Db 1717 ATAAGTGGAAGTCTTTCCAACTGTCCTCCTTCCGAGGAATGGAAGCCATTCGAGAA 1776

Qy 1840 GCAATGCATGGGGTTTCCTTTACCATGCAATCAAGTCTGGCATGGATGAGATAGTG 1899
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Db 1777 GCAATGCATGGGGTTTCCTTTACCATGCAATCAAGTCTGGCATGGATGAGATAGTG 1836

Qy 1900 AATGCTGAAACCTCCCTGTGTATGATGATCCATAAGGAACTTCTGCAGCTCGTGTGAA 1959
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1837 AATGCTGAAACCTCCCTGTGTATGATGATCCATAAGGAACTTCTGCAGCTCGTGTGAA 1896

Qy 1960 GATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGACTCTTACGTTATGCCCAGACT 2019
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Db 1897 GATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGACTCTTACGTTATGCCCAGACT 1956

Qy 2020 CAAGGCACAGGAGGAGGAAGTCATTCAGACTGATGAGTGAAATGCGCCCTGTCGAA 2079
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RESULT 1
DQ037675
LOCUS   DQ037675   3711 bp   DNA   linear   GSS 02-JUN-2005
DEFINITION Homo sapiens MTR gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ037675
VERSION   DQ037675.1 GI:66888884
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 3711)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE   A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2 (bases 1 to 3711)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment. Translation starts at the beginning of
            alignment.
FEATURES   Location/Qualifiers
     source   1..3711
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
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                     /chromosome="1"
     gene   <1..>3711
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Db    1957  CAAGGCACAGGAGGGAAGAAAGTCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAA  2016

Qy    2080  GAACGCCTTGAGTAGTATGCCCTGTGAAGGGCATTGAAAAACATATTATTGAGGATACTGAG  2139
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2017  GAACGCCTTGAGTAGTATGCCCTGTGAAGGGCATTGAAAAACATATTATTGAGGATACTGAG  2076

Qy    2140  GAAGCCAGGTTAAACCAAAAAAATATCCCGACCTTCTCAATATATAATTGAAGGACCCCTG  2199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2077  GAAGCCAGGTTAAACCAAAAAAATATCCCGACCTTCTCAATATATAATTGAAGGACCCCTG  2136

Qy    2200  ATGAATGGAATGAAAAATTGTTGGTGATCTTTTGGAGCTGAAAAAATGTTTCTACACCTCAG  2259
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Db    2137  ATGAATGGAATGAAAAATTGTTGGTGATCTTTTGGAGCTGAAAAAATGTTTCTACACCTCAG  2196

Qy    2260  GTTATAAAGTCAGCCCGGTTATGAGAAGAGGCTGTTGGCCACCTTATCCCTTTCATGGAA  2319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2197  GTTATAAAGTCAGCCCGGTTATGAGAAGAGGCTGTTGGCCACCTTATCCCTTTCATGGAA  2256

Qy    2320  AAAGAAAGAGAAGAAAACCAGAGTGCTTAACGGCACAGTAGAAGAGGACCCCTTACCAG  2379
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Db    2257  AAAGAAAGAGAAGAAAACCAGAGTGCTTAACGGCACAGTAGAAGAGGACCCCTTACCAG  2316

Qy    2380  GGCACCATCGTGCTCGGCCACTGTTAAAGGCGACGTGCACGACATAGGCAAGAACAATAGTT  2439
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Db    2317  GGCACCATCGTGCTCGGCCACTGTTAAAGGCGACGTGCACGACATAGGCAAGAACAATAGTT  2376

Qy    2440  GGAGTAGTCCTTGGCTGCAATAATTCCGAGTTATTGATTTAGGAGTCATGACTCCATGT  2499
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2377  GGAGTAGTCCTTGGCTGCAATAATTCCGAGTTATTGATTTAGGAGTCATGACTCCATGT  2436

Qy    2500  GATAAGATACTGAAAGCTGCTCTTGACCACAAAGAGATATAATTGGCCTGTGTCAGGACTC  2559
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Db    2437  GATAAGATACTGAAAGCTGCTCTTGACCACAAAGAGATATAATTGGCCTGTGTCAGGACTC  2496

Qy    2560  ATCACTCCTTCCCTGATGAAATGATTTTGTTGCCAAGGAAATGGAGAGATTAGTAGTATA  2619
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Db    2497  ATCACTCCTTCCCTGATGAAATGATTTTGTTGCCAAGGAAATGGAGAGATTAGTAGTATA  2556

Qy    2620  AGGATTCCATTGTTGATTGTTGGAGGAGCAACCACTTCAAAAACCCACACAGTTAAAATA  2679
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Db    2557  AGGATTCCATTGTTGATTGTTGGAGGAGCAACCACTTCAAAAACCCACACAGTTAAAATA  2616

Qy    2680  GCTCCGAGATACAGTGCACCTGTAATCCATCGTCCTGGACGCGTCCAAGAGTGTGGTGGTG  2739
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Qy    2740  TGTTCCCAGCTGTTAGTAGAAGATGAAAATCTAAAGGATGAAATCATGAGAAGAA  2799
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Db    2677  TGTTCCCAGCTGTTAGTAGAAGATGAAAATCTAAAGGATGAAATCATGAGAAGAA  2736

Qy    2800  TATGAAGATATTAGACAGGACCATTATGAGTCTCTCAAGGAGAGGAGATACTTACCCTTA  2859
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Db    2737  TATGAAGATATTAGACAGGACCATTATGAGTCTCTCAAGGAGAGGAGATACTTACCCTTA  2796

Qy    2860  AGTCAAGCCAGAAAAAAGTGGTTTCCAAATGATTGGCTGTCTGCAAATGAACCTCACCCAGTGAAG  2919
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Qy    2920  CCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGTGTGGACTAC  2979
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Db    2857  CCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGTGTGGACTAC  2916

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Db    2917  ATTGACTGGAACCTTTCTTTGATGTCTGGCAGTCCCGGGGCAAGTACCCGGAATCGAGGC  2976

Qy    3040  TTCCCAAGATATTTAACGACAAAACAGTAGGTGGAGGAGGCCAGGAAGGTCTACGATGAT  3099
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Db    2977  TTTCCCAAGATATTTAACGACAAAACAGTAGGTGGAGGAGGCCAGGAAGGTCTACGATGAT  3036

Qy    3100  GCCCACAATATGCTGAACACACTGATTAGTCAACAGTAGTCAAAGAAACTTCGGGCCCGGGTGTTGGTT  3159
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Qy    3160  GGGTTCTGGCCAGCACAGAGTATCCAAGACGACATTCACCTGCAGAGGCTGCTGTG  3219
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Db    3097  GGGTTCTGGCCAGCACAGAGTATCCAAGACGACATTCACCTGCAGAGGCTGCTGTG  3156

Qy    3220  CCCCAGGCTGCAGAGCCCATAGCCACTTCATGGGTTAAGGCAACAGGCTGAGAAGGAC  3279
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Db    3157  CCCCAGGCTGCAGAGCCCATAGCCACTTCATGGGTTAAGGCAACAGGCTGAGAAGGAC  3216

Qy    3280  TCTGCCAGCACGGAGCCATACTACTGCCTTCAGACTTCATCGCTCCCTTGCATTCTGGC  3339
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Db    3217  TCTGCCAGCACGGAGCCATACTACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTCGC  3276

Qy    3340  ATCCGTGACTACCTGGGCCTGTTGCGTTGCGTTGGGTAGAAGAGCTGAGCAAG  3399
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Db    3277  ATCCGTGACTACCTGGGCCTGTTGCGTTGCGTTGGGTAGAAGAGCTGAGCAAG  3336

Qy    3400  GCCTATGAGGATGATGTGACGACTACAGCAGCAGCATCATGGTCAAGGGCCTGGGGGACCGG  3459
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Db    3337  GCCTATGAGGATGATGTGACGACTACAGCAGCAGCATCATGGTCAAGGGCGCTGGGGGACCGG  3396

Qy    3460  CTGGCAGAGGCCTTTGCAGAAGAGCTCCATGAAAGAGTTCGGCCGCGAGAACTGTGGGCCTAC  3519
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Qy    3520  TGTGGCAGTGAGCAGCTGGACGTCGGAGACTCGCCGAAGGTTGCGGTTGCGGTTACAAGGGCATCCGC  3579
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Qy    3580  CCGGCTCCTGGCTACCCCAGCCAGCCCGACCACCACCGGAGAAGTCACCGTGTGGAGACTC  3639
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Db    3517  CCGGCTCCTGGCTACCCCAGCCAGCCCGACCACCACCGGAGAAGTCACCGTGTGGAGACTC  3576

Qy    3640  GCAGACATCGAGCAGTCTACACAGGCATTAACAGAATCATTAGCAACATGCAATGGCACCTGCT  3699
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Qy    3700  TCAGCAGTCTCAGGCCTCAGGCCTCTCACTTCTCCAATTGAAGTCCAAATATTTGCGTGGGGAAG  3759
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Db    3637  TCAGCAGTCTCAGGCCTCCTCACTTCTCCAATTGAAGTCCAAATATTTTGCTGTGGGGAAG  3696

Qy    3760  ATTTCCAAGGATCAG  3774
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Db    3697  ATTTCCAAGGATCAG  3711
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RESULT 2
CR859882
LOCUS       CR859882          4888 bp    mRNA     linear   HTC 12-NOV-2004
DEFINITION  Pongo pygmaeus mRNA; cDNA DKFZp469P1116 (from clone DKFZp469P1116).
ACCESSION   CR859882
VERSION     CR859882.1  GI:55730633
KEYWORDS    HTC.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1  (bases 1 to 4888)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by Medigenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project.
            Pongo pygmaeus (orangutan)
            This clone (DKFZp469P1116) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
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http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469P1116
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
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                     /db_xref="taxon:9600"
                     /clone="DKFZp469P1116"
                     /tissue_type="kidney"
                     /clone_lib="469 (synonym: pkidl). Vector pSport1_Sfi; host
                     DH10B; sites SfiIA + SfiIB"
                     /dev_stage="adult"
                     /note="similar to 5-methyltetrahydrofolate--homocysteine
                     methyltransferase (Homo sapiens)"
     gene            1..4888
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     CDS             595..2754
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                     REAMQGVFLYHAIKSGMDMGIVNAGNLPVYDDIHKELLQLCEDLIWNKDPEATEKLLR
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Query Match        21.4%;    Score 839;  DB 4;  Length 4888;
Best Local Similarity  98.9%;    Pred. No. 0;
Matches 1789;    Conservative  0;    Mismatches  19;  Indels  0;  Gaps  0;
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Qy  1747 AAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTGTCC 1806
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Db   640 AAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTGTCC  699

Qy  1807 TTCTCCTTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCAGGGAGTTTTCCTTTACCAT 1866
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Db   700 TTCTCCTTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCAGGGAGTTTTCCTTTACCAT  759

Qy  1867 GCAATCAAGTCTGGCATGGACATGGGAATAGTGAGATAGTAGATGAATGCTGAAACCTCC 1926
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Db   760 GCAATCAAGTCTGGCATGGACATGGGAATAGTGAGATAGTAGATGAATGCTGAAACCTCC  819

Qy  1927 GATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAG 1986
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Db   820 GATATCCATAAGGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCTGAG  879

Qy  1987 GCCACTGAGAAAGCTCTTACGTTACGTTACGGAGCACAGGAGCACAGGAGGAAGAAAGTCATT 2046
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   880 GCCACTGAGAAAGCTCTTACGTTACGTTACGGAGCACAGGAGCACAGGAGGAAGAAAGTCATT  939

Qy  2047 CAGACTGAGTGGAGAAATGGCCTGTCGAGAAGACGCCTTGAGCATGCCCTTGTCGTAAG 2106
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Db   940 CAGACTGAGTGGAGAAATGGCCTGTCGAGAAGACGCCTTGAGCATGCCCTTGTCGTAAG  999

Qy  2107 GGCATTGAAAAAACATATTATTGAGGATTGAGAAGCCAGGTTAAACCAAAAAAATAT 2166
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Db  1000 GGCATTGAAAAAACATATTATTGAGGATTGAGAAGCCAGGTTAAACCAAGAAAATAT 1059

Qy  2167 CCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGGAATGAAAATTGTTGGTGAT 2226
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1060 CCCTGACCTCTCAATATAATTGAAGACCCCTGATGAATGGAATGAAAATTGTTGGTGAT 1119
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Qy  2227 CTTTTTGGAGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAAAGAAAGTCAGCCCGGGTTATGAAG 2286
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1120 CTTTTTGGAGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAAAGAAAGTCAGCCCGGGTTATGAAG 1179

Qy  2287 AAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAAAGAAAGAAAACCAGAGTGCTT 2346
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Db  1180 AAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAAAGAAAGAAAACCAGAGTGCTT 1239

Qy  2347 AACGGCACAGTAGAAGAGGACCCTTACCAGGGCACCATCGTCGGCCACTGTTAAA 2406
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Db  1240 AACGGCACAGTAGAAGAGGACCCTTACCAGGGCACCATCGTCGGCCACTGTTAAA 1299

Qy  2407 GGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTC 2466
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Db  1300 GGGGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTC 1359

Qy  2467 CGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGAC 2526
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Db  1360 CGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGAC 1419

Qy  2527 CACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCTCCCTGATGAAATGATT 2586
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Db  1420 CACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCTCCCTGATGAAATGATT 1479

Qy  2587 TTTGTTGCCAAGAAATGGAGAGATTAGCTATAGAGGATTCCATTGTTGATTGGAGGAGCA 2646
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Qy  2647 ACACTTCAAAAACCCACACAGCAGTTAAAAATAGCTCCGAGATACAGTGCACCTGTAATC 2706
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Qy  2707 CATGTCCTGGACGGTCCAAGAGTGTGGTGGTGGTGGTGTTCCCAGCTGTTAGATGAAAATCTA 2766
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Qy  2767 AAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGATATTAGACAGGACCATTAT 2826
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Qy  2827 GAGTCTCTCAAGGAGAGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGTTTCCAA 2886
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Qy  3127 AGTCAAAGAAACTCCGGGCGTGGTTCGGCCAGCACAGAGTATCCAA 3186
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Db  2020 AGTCAAAGAAACTCCGGCCAGCACAGAGTATCCAA 2079

Qy  3187 GACGACATTCACCTTGTACGGCAAGGCTGCCTCGCCCAGGCTGCAGAGGCCCATAGCCACT 3246
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Db   2380 CATGAAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGTGAGCAGTCGACCGTCGCA 2439

Qy   3547 GACCTGCG 3554
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Db   2440 GACCTGCG 2447

RESULT 3
BM450887
LOCUS   BM450887   863 bp   mRNA   linear   EST 05-FEB-2002
DEFINITION AGENCOURT_6387311 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5490921
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ACCESSION   BM450887
VERSION   BM450887.1 GI:18499927
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 863)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAMI2110 row: j column: 10
            High quality sequence stop: 748.
FEATURES   Location/Qualifiers
     source   1..863
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                     /db_xref="taxon:9606"
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_67"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.75 kb. Library constructed by Life
                     Technologies."
ORIGIN

Query Match   17.4%; Score 681; DB 3; Length 863;
Best Local Similarity   99.7%; Pred. No. 0;
Matches   781; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   285 GCCTGATGTCATTTACCAAATCCATAAGGAATACTTGCTCGGGGCAGATATCATTGA 344
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   13 GCCTGATGTCATTTACCAAATCCATAAGGAATACTTGCTCGGGGCAGATATCATTGA 72

Qy   345 AACAAATACTTTAGCAGCACTAGTATTGCCCAAGCTGACTGAACACTTGGC 404

Db   73 AACAAATACTTTAGCAGCACTAGTATTGCCCAAGCTGACTGAACACTTGGC 132
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Qy   405 CTACCGGATGAACATGTGCTCTGCAGAGAGTGCCAGAAAAGTGCCGAGGAGTAACTCT 464
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Db   133 CTACCGGATGAACATGTGCTCTGCAGAGAGTGCCAGAAAAGTGCCGAGGAGTAACTCT 192

Qy   465 CCAGACAGGAATTAAGAGGTTGTGGCAGAGGGCTGTCGGGTCCGACTAATAAGACACTCTC 524
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   193 CCAGACAGGAATTAAGAGGTTGTGGCAGAGGGCTGTCGGGTCCGACTAATAAGACACTCTC 252

Qy   525 TGTGTCCCATCTGTGGAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGA 584
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   253 TGTGTCCCATCTGTGGAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGA 312

Qy   585 AGCATACCAAGAGCAGCCAAGGACTTCTGATGGGGGGTGATATCTTACTCATTGA 644
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 AGCATACCAAGAGCAGCCAAGGACTTCTGATGGGGGGTGATATCTTACTCATTGA 372

Qy   645 AACTATTTTGATACTGCCAATGCCAAGGCAGCCTTGTTTGCACTCAAAATCTTTTTGA 704
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   373 AACTATTTTTGATACTGCCAATGCCAAGGCAGCCTTGTTTGCACTCAAAATCTTTTTGA 432

Qy   705 GGAGAAATATGCTCCCGGCCTATCTTTATTTCAGGGACGATCGTTGATAAAGTGGGCG 764
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   433 GGAGAAATATGCTCCCGGCCTATCTTTATTTCAGGGACGATCGTTGATAAAGTGGGCG 492

Qy   765 GACTCTTTCCGACAGACAGAGAGGATTTGTCATCAGCGTGTCTCATCAGCGTGGAACCACT 824
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Db   493 GACTCTTTCCGACAGACAGAGAGGATTTGTCATCAGCGTGTCTCATCAGCGTGGAACCACT 552

Qy   825 CTGCATTGGATTAAATTGTGCTTGGGTGCAGTCAGCAGTGAGATGAGACCTTTTATTGAAATAAT 884
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Db   553 CTGCATTGGATTAAATTGTGCTTGGGTGCAGTCAGCAGTGAATGAGACCCTTTATTGAAATAAT 612

Qy   885 TGGAAAATGTACAACAGCCTATGTCCTCGTTATCCCAATGCAGGTCTTCCCAACACCTT 944
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Db   613 TGGAAAATGTACAACAGCCTATGTCCTCGTTATCCCAATGCAGGTCTTCCCAACACCTT 672

Qy   945 TGGTGACTATGATGAAACGCCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGA 1004
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   673 TGGTGACTATGATGAAACGCCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGA 732

Qy   1005 TGGCTTGGTCAATATAGTTGGAGGATGCGTGGGTCAACACCAGATCATATCAGGGAAAT 1064
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Db   733 TGGCTTGGTCAATATAGTTGGAGGATGCGTGGGTCAACACCAGATCATATCAGGGAAAT 792

Qy   1065 TGC 1067
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Db   793 TGC 795

RESULT 4
AL598311
LOCUS   AL598311   721 bp   mRNA   linear   EST 04-SEP-2003
DEFINITION DKFZp313F151_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
            DKFZp313F151 5', mRNA sequence.
ACCESSION   AL598311
VERSION   AL598311.1 GI:15161002
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 721)
  AUTHORS   Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
  TITLE   EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and
            Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ) (German Cancer Research Center,
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp313F151) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..721
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313F151"
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/lab_host="DH10B"
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cDNA-collection";

ORIGIN

Query Match   16.8%;   Score 660;   DB 1;   Length 721;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 660;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

| Qy | 1893 | GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT | 1952 |
| Db | 48 | GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT | 107 |

| Qy | 1953 | CTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGAAGCTTCTTACGTTATGC | 2012 |
| Db | 108 | CTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGAAGCTTCTTACGTTATGC | 167 |

| Qy | 2013 | CCAGACTCAAGGCACAGGAGGAAGAAGTCATTCAGACTGATGAGTGGAGAAATGCCC | 2072 |
| Db | 168 | CCAGACTCAAGGCACAGGAGGAAGAAGTCATTCAGACTGATGAGTGGAGAAATGCCC | 227 |

| Qy | 2073 | TGTCGAAGAACGCCTTGAGTATGCCCTTGTGAGTGGCATTGAAAAACATATTATTGAGGA | 2132 |
| Db | 228 | TGTCGAAGAACGCCTTGAGTATGCCCTTGTGAGTGGCATTGAAAAACATATTATTGAGGA | 287 |

| Qy | 2133 | TACTGAGGAAGCCAGGTTAAACCAAAAAAATATCCCGACCTTCAATATAATTGAAGG | 2192 |
| Db | 288 | TACTGAGGAAGCCAGGTTAAACCAAAAAAATATCCCGACCTTCAATATAATTGAAGG | 347 |

| Qy | 2193 | ACCCCTGATGAATGGAATGAAAATTGTTGGTGATCTTTTGGAGCTGGAAAAATGTTTCT | 2252 |
| Db | 348 | ACCCCTGATGAATGGAATGAAAATTGTTGGTGATCTTTTGGAGCTGGAAAAATGTTTCT | 407 |

| Qy | 2253 | ACCTCAGTTATAAAGTCAGCCCGGGTTATGGAAGAGGCTGTGTTGGCCACTGTATCCCTT | 2312 |
| Db | 408 | ACCTCAGTTATAAAGTCAGCCCGGGTTATGGAAGAGGCTGTGTTGGCCACTGTATCCCTT | 467 |

| Qy | 2313 | CATGGAAAAGAGAAGAGAGAGAGAGAGACCAGAGTGCTTAACGGACACAGTAGGAGAAGAGAGACCC | 2372 |
| Db | 468 | CATGGAAAAGAGAAGAGAGAGAGAGAGACCAGAGTGCTTAACGGACACAGTAGGAGAAGAGAGACCC | 527 |

| Qy | 2373 | TTACCAGGGCACCATCGTGCTGGCCACTGTTAAAGGCACGTGCACAGGCAGGAAGAA | 2432 |
| Db | 528 | TTACCAGGGCACCATCGTGCTGGCCACTGTTAAAGGCACGTGCACAGGCAGGAAGAA | 587 |

| Qy | 2433 | CATAGTTGGAGTAGTCCTTGGCTGCAATAATTCCGAGTTATTGATTTAGGAGTCATGAC | 2492 |
| Db | 588 | CATAGTTGGAGTAGTCCTTGGCTGCAATAATTCCGAGTTATTGATTTAGGAGTCATGAC | 647 |

| Qy | 2493 | TCCATGTGATAAGATACTGAAAGCTGCTTCTTGACCACAAAGCAGATATAATTGGCCTGTC | 2552 |
| Db | 648 | TCCATGTGATAAGATACTGAAAGCTGCTTCTTGACCACAAAGCAGATATAATTGGCCTGTC | 707 |

RESULT 5

BX390174
LOCUS   BX390174   871 bp   mRNA   linear   EST 29-APR-2004
DEFINITION   BX390174 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
               cDNA clone CS0DC010YO17 5'-PRIME, mRNA sequence.
ACCESSION   BX390174
VERSION   BX390174.2   GI:46877980
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1 (bases 1 to 871)
AUTHORS   Li,W.B., Gruber,C., Jesee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 8, 2003 this sequence version replaced gi:30463266.
               Contact: Genoscope
               Genoscope - Centre National de Sequencage
               2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
               Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
               end enriched, double-strand cDNA was digested with Not I and cloned
               into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
               was normalized. Library was constructed by Life Technologies, a
               division of Invitrogen. This sequence belongs to sequence cluster
               740.f.
               For more information about this cluster, see
               http://www.genoscope.cns.fr/cdna?s=CS0BAG0062C05_CS00515_1&c=740.f.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DC010YO17"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match   16.6%;   Score 651;   DB 5;   Length 871;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 701;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

| Qy | 671 | AGGCAGCCTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCGGCCTATCT | 730 |
| Db | 21 | AGGCAGCCTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCGGCCTATCT | 80 |

| Qy | 731 | TTATTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGGACAGGAGAGG | 790 |
| Db | 81 | TTATTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGGACAGGAGAGG | 140 |

| Qy | 791 | GATTTGTCATCAGCGGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGTGCTTTGG | 850 |
| Db | 141 | GATTTGTCATCAGCGGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGTGCTTTGG | 200 |

| Qy | 851 | GTGCAGCTGAGATGAGACCTTTATTGAAAATAATTGAAAATAATTGTACAGCAGCCTATGTCC | 910 |
| Db | 201 | GTGCAGCTGAAATGAGACCTTTATTGAAAATAATTGAAAATAATTGTACAGCAGCCTATGTCC | 260 |

| Qy | 911 | TCTGTTATCCCAATGCAGTCTTCCAACACCTTTGGTGACTATGGAGTCATGAC | 970 |
| Db | 261 | TCTGTTATCCCAATGCAGTCTTCCAACACCTTTGGTGACTATGGAGTCATGAC | 320 |

| Qy | 971 | TGATGGCCAAGCACCTAAAGGATTTTGCTGCATGATGGCTCAATATAGTTGGAGGAT | 1030 |
| Db | 321 | TGATGGCCAAGCACCTAAAGGATTTTGCTGCATGATGGCTCAATATAGTTGGAGGAT | 380 |

| Qy | 1031 | GCTGTGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATTGTAAGC | 1090 |

Db   381 GCTGTGGGTCAACACCAGATCATATCAGGGAAAATTGCTGAAGCTGTGAAAAATTGTAAGC 440
Qy 1091 CTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTCTTCAGAGCCCT 1150
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Db   441 CTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTCTTCAGAGCCCT 500
Qy 1151 TCAGGATTGGACCGTACCAACTTTGTTAACATTGGAGAGCGCGTAATGTTGCAGGAT 1210
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 TCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCGTAATGTTGCAGGAT 560
Qy 1211 CAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGTGTTGTTGCCA 1270
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Db   561 CAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTTGTGTTGTTGCCA 620
Qy 1271 AAGTGCAGGTGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGGCATGCTAG 1330
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Db   621 AAGTGCAGGTGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGGCATGCTAG 680
Qy 1331 ATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTT 1372
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Db   681 ATGGTCAAGTGCAATGACCACGATTTTGCAACTTAATTGCTT 722

RESULT 6
BU189680
LOCUS   BU189680   943 bp   mRNA   linear   EST 04-SEP-2002
DEFINITION AGENCOURT 7968068 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6170551
            5', mRNA sequence.
ACCESSION   BU189680
VERSION   BU189680.1 GI:22703664
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 943)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13537 row: h column: 08
            High quality sequence stop: 587.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6170551"
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH MGC 67"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.75 kb. Library constructed by Life
                     Technologies."
ORIGIN

Query Match   16.3%; Score 637; DB 5; Length 943;
Best Local Similarity   99.9%; Pred. No. 5.1e-308;
Matches   687; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Db   1 CAAAAAAATATCCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGGAATGAAA 60

Db 2215 ATTGTTGGTGATCTTTTTGGAGCTGGAAAAATGTTTCACCTCAGGTTATAAAGTCAGCC 2274
Qy   61 ATTGTTGGTGATCTTTTTGGAGCTGGAAAAATGTTTCACCTCAGGTTATAAAGTCAGCC 120
Qy 2275 CGGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAGAGAAGAA 2334
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Db   121 CGGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAGAGAAGAA 180
Qy 2335 ACCAGAGTGCTTAACGGCACAGTAGAGAAGAAGACCCTACCAGGGCACCATCGTGCTG 2394
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Db   181 ACCAGAGTGCTTAACGGCACAGTAGAGAAGAAGACCCTACCAGGGCACCATCGTGCTG 240
Qy 2395 GCCACTGTTAAAGGCGACGTGCACGTGCACGACATAGGCAAGAACACATAGTTGGAGTAGTCCTTGGC 2454
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Db   241 GCCACTGTTAAAGGCGACGTGCACGTGCACGACATAGGCAAGAACACATAGTTGGAGTAGTCCTTGGC 300
Qy 2455 TGCAATAATTCCGAGTTATTGATTTAGGAGTCATGAGTCCATGTGATGAAGATACTGAAA 2514
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Db   301 TGCAATAATTCCGAGTTATTGATTTAGGAGTCATGAGTCCATGTGATGAAGATACTGAAA 360
Qy 2515 GCTGCTCCTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTG 2574
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Db   361 GCTGCTCCTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTG 420
Qy 2575 GATGAAATGATTTTGTTGTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTG 2634
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GATGAAATGATTTTGTTGTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTG 480
Qy 2635 ATTGGAGAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGCTCCGAGATACAGT 2694
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ATTGGAGAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGCTCCGAGATACAGT 540
Qy 2695 GCACCTGTAATCCATGTCCTGACGCGTCCCAAGAGTGTGGTGTTCCCAGCTGTTA 2754
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Db   541 GCACCTGTAATCCATGTCCTGACGCGTCCCAAGAGTGTGGTGTTCCCAGCTGTTA 600
Qy 2755 GATGAAAATCTAAAGATGAATACTTTGAGGAAAATCATGGAAGAATATGAAGATATTAGA 2814
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Db   601 AATGAAAATCTAAAGATGAATGAATACTTTGAGGAAAATCATGGAAGAATATGAAGATATTAGA 660
Qy 2815 CAGGACCATTATGAGTCTCTCAAGGAGA 2842
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Db   661 CAGGACCATTATGAGTCTCTCAAGGAGA 688

RESULT 7
CN414972
LOCUS   CN414972   698 bp   mRNA   linear   EST 16-MAY-2004
DEFINITION 1700041800817700 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN414972
VERSION   CN414972.1 GI:47402566
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 698)
AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
TITLE   Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED   15146197
COMMENT   Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com

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                and H9 (p26) maintained in feeder-free conditions"
ORIGIN

Query Match           15.9%;   Score 623;  DB 7;  Length 698;
Best Local Similarity 99.9%;   Pred. No. 5.6e-301;
Matches 673;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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Db      25 GGCTTGGTCAATATAGTTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATT 84

Qy    1066 GCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCCACCTGCTTTTGAAGGACAT 1125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      85 GCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCCACCTGCTTTTGAAGGACAT 144

Qy    1126 ATGTTACTGTCTCGGTCTAGAGCCCCTTCAGGATTGGACCGTACCACCAACTTGTTAACATT 1185
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 ATGTTACTGTCTCGGTCTAGAGCCCCTTCAGGATTGGACCGTACCACCAACTTGTTAACATT 204

Qy    1186 GGAGAGCGCGTGTAATGTTGCAGGATCAAGGAAGTTGCTAAACTATCATCATGGCAGGAAAC 1245
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     205 GGAGAGCGCGTGTAATGTTGCAGGATCAAGGAAGTTGCTAAACTATCATCATGGCAGGAAAC 264

Qy    1246 TATGAAGAAGCCCTTGGTGTTGTGTTGCCAAAGTGCAGGTGAAATGGGAGCCCAGGTGTTGGAT 1305
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 TATGAAGAAGCCCTTGGTGTTGTGTTGCCAAAGTGCAGGTGAAATGGGAGCCCAGGTGTTGGAT 324

Qy    1306 GTCAACATGGATGATGGCATGCTAGATGTCAAGTGCAATGCACAGATTTTGCAACTTA 1365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 GTCAACATGGATGATGGCATGCTAGATGTCAAGTGCAATGCACAGATTTTGCAACTTA 384

Qy    1366 ATTGCTTCCGAGCCAGACATCGCAAAGTACCTTTGTGCATCGACTCCTCCAATTTTGCT 1425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 ATTGCTTCCGAGCCAGACATCGCAAAGTACCTTTGTGCATCGACTCCTCCAATTTTGCT 444

Qy    1426 GTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTG 1485
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 GTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTG 504

Qy    1486 AAGGAAGGAGGACGACTTCTTGGAGAGAGGCCAGGAGAGTAAAAAGTAAAGTATGGAGCTGCT 1545
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     505 AAGGAAGGAGGACGACTTCTTGGAGAGAGGCCAGGAGAGTAAAAAGTAAAGTATGGAGCTGCT 564

Qy    1546 ATGGTGGTCATGGCTTTTGATGAAGAAGGACAGCAACAGAAAACAGACACAAAAATCAGA 1605
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     565 ATGGTGGTCATGGCTTTTGATGAAGAAGGACAGCAACAGAAAACAGACACAAAAATCAGA 624

Qy    1606 GTGTGCACCCGCGGCCTACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATT 1665
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     625 GTGTGCATCCGGCGCCTACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATT 684

Qy    1666 ATTTTTGACCCTAA 1679
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Db     685 ATTTTTGACCCTAA 698

RESULT 8
BP313585
BP313585
LOCUS       BP313585    583 bp    mRNA    linear    EST 17-SEP-2004
DEFINITION  BP313585 Sugano cDNA library, mammary gland OCUB-F Homo sapiens
            cDNA clone OFRO3689, mRNA sequence.
ACCESSION   BP313585
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VERSION     BP313585.1   GI:52242560
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 583)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
  PUBMED    15342556
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
     source          1..583
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="OFRO3689"
                     /tissue_type="mammary gland"
                     /cell_line="OCUB-F"
                     /clone_lib="Sugano cDNA library, mammary gland OCUB-F"
                     /note="mammary gland tumor"
ORIGIN

Query Match           13.9%;   Score 545;  DB 3;  Length 583;
Best Local Similarity 100.0%;  Pred. No. 9.3e-262;
Matches 545;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    2290 GCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAAGAAGAAGAAAACCAGAGTGCTTAAC 2349
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 GCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAAGAAGAAGAAAACCAGAGTGCTTAAC 87

Qy    2350 GGCACAGTAGAAGAAGAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTTAAAGGC 2409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 GGCACAGTAGAAGAAGAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTTAAAGGC 147

Qy    2410 GAGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGCTGCTGCAATAATTTCCGA 2469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 GAGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGCTGCTGCAATAATTTCCGA 207

Qy    2470 GTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTCGTCTGACCAC 2529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 GTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTCGTCTGACCAC 267

Qy    2530 AAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCCTCCGGATGAAATGATTTTT 2589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 AAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCCTCCGGATGAAATGATTTTT 327

Qy    2590 GTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACC 2649
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 GTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACC 387

Qy    2650 ACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATAACAGTGCACCTGTAATCCAT 2709
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 ACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATAACAGTGCACCTGTAATCCAT 447

Qy    2710 GTCCTGGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTAGATGAAAATCTAAAG 2769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 GTCCTGGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTAGATGAAAATCTAAAG 507

Qy    2770 GATGAATACTTTGAGGAAATCATGGAAGAATATGAAGATTAGACAGGACCATTATGAG 2829
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     508 GATGAATACTTTGAGGAAATCATGGAAGAATATGAAGATTAGACAGGACCATTATGAG 567

Qy    2830 TCTCT 2834
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Db   568 TCTCT 572

RESULT 9
BP336553
LOCUS   BP336553   582 bp   mRNA   linear   EST 17-SEP-2004
DEFINITION   Homo sapiens cDNA clone SMR05967, mRNA sequence.
ACCESSION   BP336553
VERSION   BP336553.1 GI:52266128
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 582)
AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
             Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE   Sequence comparison of human and mouse genes reveals a homologous
             block structure in the promoter regions
JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED   15342556
COMMENT   Contact: Yutaka Suzuki
             Department of Virology
             Institute of Medical Science, University of Tokyo
             4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
             Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES   Location/Qualifiers
     source   1..582
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="SMR05967"
                     /tissue_type="coronary artery"
                     /cell_type="smooth muscle cell"
                     /clone_lib="Sugano cDNA library, coronary artery smooth
                     muscle cell"
ORIGIN

Query Match   13.5%; Score 529; DB 3; Length 582;
Best Local Similarity   99.8%; Pred. No. 1e-253;
Matches 579; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   680 TGTTTGCACTCCAAAATCTTTTGAGAGAAATATGCTCCCCGGCCTATCTTTATTTCAG 739
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3 TGTTTGCACTCCAAAATCTTTTGAGAGAAATATGCTCCCCGGCCTATCTTTATTTCAG 62

Qy   740 GGACGATCGTTGATAAAAGTGGGCGACTCTTTCCGACACAGACAGGAGGGATTTGTCA 799
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63 GGACGATCGTTGATAAAAGTGGGCGACTCTTTCCGACACAGACAGGAGGGATTTGTCA 122

Qy   800 TCAGCGTGTCTCATGGAGAACCACCTGCATTGGATTAAATTGTGCTTTGGGTGCAGCTG 859
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 TCAGCGTGTCTCATGGAGAACCACCTGCATTGGATTAAATTGTGCTTTGGGTGCAGCTG 182

Qy   860 AGATGAGACCTTTATTGGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCGTTATC 919
         | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   183 AAATGAGACCTTTATTGGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCGTTATC 242

Qy   920 CCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAACGCCTTCATGATGGCCA 979
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243 CCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAACGCCTTCATGATGGCCA 302

Qy   980 AGCACCTAAAGATTTTGCTATGGATGGCTGTCAATATAGTTGGAGGATGCTGTGGGGT 1039
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 AGCACCTAAAGATTTTGCTATGGATGGCTGTCAATATAGTTGGAGGATGCTGTGGGGT 362

Qy 1040 CAACACCAGATCATATCAGGGAAATTGCTGAGAGCTGTGAAAAATTGCTAGCCTAGAGTTC 1099
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 CAACACCAGATCATATCAGGGAAATTGCTGAGAGCTGTGAAAAATTGCTAGCCTAGAGTTC 422

Qy 1100 CACCTGCCACTGCTTTGAAGGACATATGTTACTGTCGTGGTCTAGAGCCCTTCAGGATTG 1159

Db   423 CACCTGCCACTGCTTTGAAGGACATATGTTACTGTCGTGGTCTAGAGCCCTTCAGGATTG 482
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 1160 GACCGTACACCAACTTTGTTAACATTGGAGAGCGCTGTAAATGTTGCAGGATCAAGGAAGT 1219
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 GACCGTACACCAACTTTGTTAACATTGGAGAGCGCTGTAAATGTTGCAGGATCAAGGAAGT 542

Qy 1220 TTGCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTT 1259
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Db   543 TTGCTAAACTCATCATGGCAGGAAACTATGAAGAAGCCTT 582

RESULT 10
BP337383
LOCUS   BP337383   583 bp   mRNA   linear   EST 17-SEP-2004
DEFINITION   Homo sapiens cDNA clone SMR08247, mRNA sequence.
ACCESSION   BP337383
VERSION   BP337383.1 GI:52266989
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 583)
AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
             Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE   Sequence comparison of human and mouse genes reveals a homologous
             block structure in the promoter regions
JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED   15342556
COMMENT   Contact: Yutaka Suzuki
             Department of Virology
             Institute of Medical Science, University of Tokyo
             4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
             Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES   Location/Qualifiers
     source   1..583
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                     /db_xref="taxon:9606"
                     /clone="SMR08247"
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                     muscle cell"
ORIGIN

Query Match   12.8%; Score 501; DB 3; Length 583;
Best Local Similarity   99.8%; Pred. No. 1.2e-239;
Matches 551; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   710 AATATGTCCCCGGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTC 769
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   32 AATATGTCCCCGGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTC 91

Qy   770 TTTCCGACAGACAGGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACCTCTGCA 829
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   92 TTTCCGACAGACAGGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACCTCTGCA 151

Qy   830 TTGGATTAAATTGTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGGAAATAATTGGAA 889
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   152 TTGGATTAAATTGTGCTTTGGGTGCAGCTGAAATGAGACCTTTATTGGAAATAATTGGAA 211

Qy   890 AATGTACAACAGCCTATGTCCTCGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTG 949
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   212 AATGTACAACAGCCTATGTCCTCGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTG 271

Qy   950 ACTATGATGAAACGCCTTCATGATGGCCAAGCACCTAAAGATTTTGCTATGGATGGCT 1009
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   272 ACTATGATGAAACGCCTTCATGATGGCCAAGCACCTAAAGATTTTGCTATGGATGGCT 331

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Qy    1010 TGGTCAATATAGTTGGAGGATGCTGTGGTCAACACCAGATCATATCAGGGAAATTGCTG 1069
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     332 TGGTCAATATAGTTGGAGGATGCTGTGGTCAACACCAGATCATATCAGGGAAATTGCTG 391

Qy    1070 AAGCTGTGAAAAATTGTAAGCCTAGAGTTCACCTGCCACTGCTTTTGAAGGACATATGT 1129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     392 AAGCTGTGAAAAATTGTAAGCCTAGAGTTCACCTGCCACTGCTTTTGAAGGACATATGT 451

Qy    1130 TACTGTCTGGTCTAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAG 1189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     452 TACTGTCTGGTCTAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAG 511

Qy    1190 AGGCTGTAATGTTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGCGCAGGAAACTATG 1249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     512 AGCGCTGTAATGTTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGCGCAGGAAACTATG 571

Qy    1250 AAGAAGCCTTGT 1261
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Db     572 AAGAAGCCTTGT 583
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RESULT 11
BP220649
LOCUS   BP220649   560 bp   mRNA   linear   EST 15-SEP-2004
DEFINITION   BP220649 Sugano cDNA library, colon Homo sapiens cDNA clone
             COL04124, mRNA sequence.
ACCESSION   BP220649
VERSION   BP220649.1 GI:52093554
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 560)
AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
             Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE   Sequence comparison of human and mouse genes reveals a homologous
             block structure in the promoter regions
JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED   15342556
COMMENT   Contact: Yutaka Suzuki
             Department of Virology
             Institute of Medical Science, University of Tokyo
             4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
             Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="COL04124"
                     /tissue_type="colon"
                     /clone_lib="Sugano cDNA library, colon"
ORIGIN

Query Match   12.7%; Score 497; DB 3; Length 560;
Best Local Similarity   99.8%; Pred. No. 1.3e-237;
Matches 547;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

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Qy    2571 CCTGGATGAAATGAATGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATTAAGGATTCCATT 2630
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13 CCTGGATGAAATGAATGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATTAAGGATTCCATT 72

Qy    2631 GTTGATTGGAGGAGCAACCACTTCAAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATA 2690
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 GTTGATTGGAGGAGCAACCACTTCAAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATA 132

Qy    2691 CAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCT 2750
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     133 CAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCT 192

Qy    2751 GTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAGATAT 2810
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Db     193 GTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAGAGGAGAGATCATGGAAGAATATGAAGAGATAT

Qy    2811 TAGACAGGACCATTATGAGTCTCTCAAGGAGAGGAGAGACTTACCCTTAAGTCAAGCCAG 2870
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     253 TAGACAGGACCATTATGAGTCTCTCAAGGAGAGGAGAGACTTACCCTTAAGTCAAGCCAG 312

Qy    2871 AAAAGTTGGTTCCAAATGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTAT 2930
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     313 AAAAGTTGGTTCCAAATGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTAT 372

Qy    2931 TGGGACCCAGGTCTTTGAAGACTATGACCTGCGAGAAGCTGGTGGACTACATTGACTGAAG 2990
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     373 TGGGACCCAGGTCTTTGAAGACTATGACCTGCGAGAAGCTGGTGGACTACATTGACTGAA 432

Qy    2991 GCCTTCTTTGATGTCTGGCAGCTCCGGGCAAGTACCCGAATCGAAGCTTCCCCAAGAT 3050
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     433 GCCTTCTTTGATGTCTGGCAGCTCCGGGCAAGTACCCGAATCGAAGCTTCCCCAAGAT 492

Qy    3051 ATTTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGTTCTACGATGATGCCCACAATAT 3110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     493 ATTTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGTTCTACGATGATGCCCACAATAT 552

Qy    3111 GCTGAACA 3118
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Db     553 GCTGAACA 560
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RESULT 12
AL041796
LOCUS   AL041796   490 bp   mRNA   linear   EST 04-SEP-2003
DEFINITION   DKFZp434B1618_r1 434 (synonym: htes3) Homo sapiens cDNA clone
             DKFZp434B1618 5', mRNA sequence.
ACCESSION   AL041796
VERSION   AL041796.1 GI:5421143
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 490)
AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
             Wiemann,S.
TITLE   EST (Ottenwaelder, et al.)
JOURNAL   Unpublished (1999)
COMMENT   Contact: MIPS
             MIPS
             Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
             This is the 5' sequence of the clone insert
             Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
             Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
             sequenced by MediGenomix (Martinsried/Germany) within the cDNA
             sequencing consortium of the German Genome Project. No s1 sequence
             available.
             This clone (DKFZp434B1618) is available at the RZPD in Berlin.
             Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
             Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES   Location/Qualifiers
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                     /clone="DKFZp434B1618"
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                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="434 (synonym: htes3)"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN

Query Match   12.5%; Score 490; DB 1; Length 490;
Best Local Similarity 100.0%; Pred. No. 4.2e-234;

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Matches  490;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   2487 CATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGACCACAAAGCAGATATAATTGG 2546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGACCACAAAGCAGATATAATTGG 60

Qy   2547 CCTGTGTCAGGACTCATCACTCCTTCCCTGATGAAATGATTTTTGTTGCCAAGGAAATGGA 2606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTGTGTCAGGACTCATCACTCCTTCCCTGATGAAATGATTTTTGTTGCCAAGGAAATGGA 120

Qy   2607 GAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACAC 2666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACAC 180

Qy   2667 AGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAA 2726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAA 240

Qy   2727 GAGTGTGTGGTGGTGTGTTCCCAGCTGTGTAGATGAAAATCTAAAGGATGAATACTTTGAGGA 2786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GAGTGTGTGGTGGTGTGTTCCCAGCTGTGTAGATGAAAATCTAAAGGATGAATACTTTGAGGA 300

Qy   2787 AATCATGGAAGAATATGAAGATATTAGACAGACCATTATGAGTCTCTCAAGGAGGAGGAG 2846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AATCATGGAAGAATATGAAGATATTAGACAGACCATTATGAGTCTCTCAAGGAGGAGGAG 360

Qy   2847 ATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGCTGTCTGGACC 2906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGCTGTCTGGACC 420

Qy   2907 TCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAA 2966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAA 480

Qy   2967 GCTGGTGGAC 2976
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Db    481 GCTGGTGGAC 490
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RESULT 13
DQ037676
LOCUS       DQ037676    3677 bp    DNA    linear    GSS 02-JUN-2005
DEFINITION  Pan troglodytes MTR gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ037676
VERSION     DQ037676.1  GI:66888885
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 3677)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 3677)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment. Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1..3677
                     /organism="Pan troglodytes"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
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                     /gene="MTR"
                     /locus_tag="HC7587"

ORIGIN

Query Match             12.5%;  Score 490;  DB 11;  Length 3677;
Best Local Similarity   99.4%;  Pred. No. 4.5e-234;
Matches  690;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy   2537 ATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGATGAAATGATTTTTGTTGCCA 2596
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 ATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGATGAAATGATTTTTGTTGCCA 2499

Qy   2597 AGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAA 2656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAA 2559

Qy   2657 AAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGG 2716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 AAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGG 2619

Qy   2717 ACGCGTCCAAGAGTGTGTGGTGGTGTGTTCCCAGCTGTGTTAGATGAAAATCTAAAGGATGAAT 2776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2620 ACGCGTCCAAGAGTGTGTGGTGGTGTGTTCCCAGCTGTGTTAGATGAAAATCTAAAGGATGAAT 2679

Qy   2777 ACTTTGAGGAAATCATGGAAGAATATGAAGATATTAGACAGACCATTATGAGTCTCTCA 2836
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ACTTTGAGGAAATCATGGAAGAATATGAAGATATTAGACAGACCATTATGAGTCTCTCA 2739

Qy   2837 AGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGTGGC 2896
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 AGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGTGGC 2799

Qy   2897 TGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATG 2956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 TGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATG 2859

Qy   2957 ACCTGCAGAAGCTGGTGGACTACATTGACTCGGAAGCCTTCTTTGATGTCTGCAGCTCC 3016
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 ACCTGCAGAAGCTGGTGGACTACATTGACTCGGAAGCCTTCTTTGATGTCTGCAGCTCC 2919

Qy   3017 GGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACAAAACAGTAGGTGGAG 3076
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2920 GGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACAAAACAGTAGGTGGAG 2979

Qy   3077 AGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACACTGATTAGTCAAAAGA 3136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2980 AGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACACTGATTAGTCAAAAGA 3039

Qy   3137 AACTCCGGGCCCGGGGTGTGGTTGGGTTCGGCACGACAGTATCCAAGACGACAATTC 3196
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3040 AACTCCGGGCCCGGGGTGTGGTTGGGTTCTGCGGCACGACAGTATCCAAGACGACAATTC 3099

Qy   3197 ACCTGTACGCAGAGGCTGCTGCTGCCCAGGCTGC 3230
          ||||||||||||||||||||||||||||||||||
Db   3100 ACCTGTACGCAGAGGCTGCTGCTGCCCAGGCTGC 3133
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RESULT 14
BP336015
LOCUS       BP336015    582 bp    mRNA    linear    EST 17-SEP-2004
DEFINITION  Homo sapiens cDNA library, coronary artery smooth muscle cell
            Sugano cDNA clone SMR04476, mRNA sequence.
ACCESSION   BP336015
VERSION     BP336015.1  GI:52265574
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
```

REFERENCE   1 (bases 1 to 582)
AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE   Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED   15342556
COMMENT   Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES   Location/Qualifiers
     source   1..582
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="SMR04476"
                     /tissue_type="coronary artery"
                     /cell_type="smooth muscle cell"
                     /clone_lib="Sugano cDNA library, coronary artery smooth
                     muscle cell"

ORIGIN

Query Match   12.2%; Score 480; DB 3; Length 582;
Best Local Similarity   99.7%; Pred. No. 4.5e-229;
Matches 580; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   678 CTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGGCCTATCTTTATTTC 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGGCCTATCTTTATTTC 60

Qy   738 AGGGACGATCGTTGATAAAGTGGGCGGACTCTTTCCGACACAGCAGGAGAGGATTTGT 797
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGGGACGATCGTTGATAAAGTGGGCGGACTCTTTCCGACACAGCAGGAGAGGATTTGT 120

Qy   798 CATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGTGCTTTGGGTGCAGC 857
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATTGTGCTTTGGGTGCAGC 180

Qy   858 TGAGATGAGACCTTTATTGAAATAATTGAAAATGTACAACAGCCTATGTCCTCTGTTA 917
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGAAATGAGACCTTTATTGAAATAATTGAAAATGTACAACAGCCTATGTCCTCTGTTA 240

Qy   918 TCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAACGCCTTCTATGATGGC 977
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   241 TCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGACGAAACGCCTTCTATGATGGC 300

Qy   978 CAAGCACCTAAAGAGATTTTGCTATGGATGGCTTGGTCAATATAGTTGGAGGATGCTGTGG 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CAAGCACCTAAAGAGATTTTGCTATGGATGGCTTGGTCAATATAGTTGGAGGATGCTGTGG 360

Qy   1038 GTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATTGTAAGCCTAGAGT 1097
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAATTGTAAGCCTAGAGT 420

Qy   1098 TCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCGTCGGTCTAGAGCCCTTCAGGAT 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCGTCGGTCTAGAGCCCTTCAGGAT 480

Qy   1158 TGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATGTTGCAGGATCAAGGAA 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATGTTGCAGGATCAAGGAA 540

Qy   1218 GTTTGCTAAACTCATCGGCAGGAAACTATGAAGAAGCCTT 1259
          ||||||||||||||||||||||||||||||||||||||||
Db   541 GTTTGCTAAACTCATCGGCAGGAAACTATGAAGAAGCCTT 582

RESULT 15
BQ062840
LOCUS   BQ062840   1043 bp   mRNA   linear   EST 02-APR-2002
DEFINITION AGENCOURT_6826659 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924378

ACCESSION   BQ062840
VERSION   BQ062840.1 GI:19890017
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1043)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2094 row: g column: 03
            High quality sequence start: 242
            High quality sequence stop: 479.
FEATURES   Location/Qualifiers
     source   1..1043
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5924378"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_9"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."

ORIGIN

Query Match   11.4%; Score 448; DB 3; Length 1043;
Best Local Similarity   99.6%; Pred. No. 5.7e-213;
Matches 668; Conservative   0; Mismatches   2; Indels   1; Gaps   1;

Qy   2483 GAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCCTGACCACAAAGCAGATATAA 2542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118 GAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTCCTGACCACAAAGCAGATATAA 177

Qy   2543 TTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAATGATTTTGTTGCCAAGGAAA 2602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 TTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAATGATTTTGTTGCCAAGGAAA 237

Qy   2603 TGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTCAAAAACCC 2662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 TGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTCAAAAACCC 297

Qy   2663 ACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGT 2722
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 ACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGT 357

Qy   2723 CCAAGAGTGGTGGTGTGTTCCCAGCTGTTCCCAGCTGTTAGATGAAGATATTAGACAGGA 2782
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   358 CCAAGAGTGGTGGTGTGTTCCCAGCTGTTCCCAGCTGTTAGATGAAGATATTAGACAGGA 417

Qy   2783 AGGAAATCATGGAAGAATGAGAAGATATTAGACAGGACCATTATGAGTCTCTCAAG-GAG 2841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   418 AGGAAATCATGGAAGAATGAGAAGATATTAGACAGGACCATTATGAGTCTCTCAAGAGAG 477

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Qy   1219  TTTGCTAAACTCATCATGCAGGAGAAGCCTTGTGTGTTGCCAAAGTGCAG  1278
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  TTTGCTAAACTCATCATGCAGGAGAAGCCTTGTGTGTTGCCAAAGTGCAG    60

Qy   1279  GTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGGCATGGTAGTCCA  1338
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGGCATGGTAGTCCA   120

Qy   1339  AGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGACATCGCAAAGGTACCT  1398
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  AGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGACATCGCAAAGGTACCT   180

Qy   1399  TTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTAAAGTGCTGCCAAGGG  1458
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTAAAGTGCTGCCAAGGG   240

Qy   1459  AAGTGCATTGTCAATAGCATATCGTGAAGGAGGAGGAGGAGCACTTCTTGGAAGAAGCC  1518
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  AAGTGCATTGTCAATAGCATATCGTGAAGGAGGAGGAGGAGCACTTCTTGGAAGAAGCC   300

Qy   1519  AGGAAGATTAAAAGTATGGAGCTGCTATGGTGGTCATGGCTTTTGATGAAGAAGGACAG  1578
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AGGAAGATTAAAAGTATGGAGCTGCTATGGTGGTCATGGCTTTTGATGAAGAAGGACAG   360

Qy   1579  GCAACACGAAACAGCACACAAAAATCAGAGTGTGCACCCGGGCCTACCATCTGCTTGTGAAA  1638
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GCAACACGAAACAGCACACAAAAATCAGAGTGTGCACCCGGGCCTACCATCTGCTTGTGAA   420

Qy   1639  AAACTGGGCTTTAATCCAA  1658
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Db    421  AAACTGGGCTTTAATCCAA   440
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RESULT 17
CV334327
LOCUS       CV334327                                     404 bp    mRNA       linear     EST 24-SEP-2004
DEFINITION  IL3-NT0280-250101-421-E07 NT0280 Homo sapiens cDNA, mRNA sequence.
ACCESSION   CV334327
VERSION     CV334327.1   GI:52657541
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
    TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
  COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. http://www.ludwig.org.br.
FEATURES             Location/Qualifiers
     source          1..404
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
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Qy   2842  AGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGCTTCCAAATGGATTGGCTGTCT  2901
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Db    478  AGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGCTTCCAAATGGATTGGCTGTCT   537

Qy   2902  GAACCTCACCCAGTGAAGCCCACGTTTATTGGACCCAGGTCTTTGAAGACTGAGACCTG  2961
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    538  GAACCTCACCCAGTGAAGCCCACGTTTATTGGACCCAGGTCTTTGAAGACTGAGACCTG   597

Qy   2962  CAGAAGCTGGTGACTACATTGACTGGAAGCCTTCTTCTTGATGTCTGGCAGTCCGGGGC  3021
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    598  CAGAAGCTGGTGACTACATTGACTGGAAGCCTTCTTCTTGATGTCTGGCAGTCCGGGGC   657

Qy   3022  AAGTACCCGAATCGAGGCTTCCCAGATATTTAACGACAAAACAGTAGGTGGAGAGGCC  3081
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    658  AAGTACCCGAATCGAGGCTTCCCAGATATTTAACGACAAAACAGTAGGTGGAGAGGCC   717

Qy   3082  AGGAAGGTCTACGATGATGCCCACAATATGCTGAACACACTGATTAGTAGTCAAAAGAAACTC  3141
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    718  AGGAAGGTCTACGATGATGCCCACAATATGCTGAACACACTGATTAGTAGTCAAAAGAAACTC   777

Qy   3142  CGGGCCCGGGG  3152
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Db    778  CGGGCCCGGGG   788
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RESULT 16
BX485695
LOCUS       BX485695                                     626 bp    mRNA       linear     EST 04-SEP-2003
DEFINITION  DKFZp686C08248_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686C08248 5', mRNA sequence.
ACCESSION   BX485695
VERSION     BX485695.1   GI:31948689
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 626)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W.,
            Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
    TITLE   EST (Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W.,
            et al.)
  JOURNAL   Unpublished (2003)
  COMMENT   Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by MediGenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project. No s1 sequence
            available.
            This clone (DKFZp686C08248) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686C08248"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN
Query Match     11.2%;  Score 440;  DB 5;  Length 626;
Best Local Similarity   100.0%;  Pred. No. 5.9e-209;
Matches  440;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6462473"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match   9.3%;   Score 363;   DB 5;   Length 937;
Best Local Similarity   99.4%;   Pred. No. 3.2e-170;
Matches   513;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

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Qy  3361 TTTGCCGTTGCCTGCTTTGGGGTAGAGAGCTCATGAGGATGGATGATGGTGAC 3420
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     1 TTTGCCGTTGCCTGCTTTGGGGTAGAGAGCTGAGCAAGGCTATGAGGATGGATGATGGTGAC 60

Qy  3421 GACTACAGCAGCATCATGGTCAAGGCGCTGGGGGGACCGGCTGGCAGAGGCCTTTGCAGAA 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GACTACAGCAGCATCATGGTCAAGGCGCTGGGGGGACCGGCTGGCAGAGGCCTTTGCAGAA 120

Qy  3481 GAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGAC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GAGTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGAC 180

Qy  3541 GTCGCAGACCTGCGGAAGGTTGCGGTACAAGGGCATCCCGCCGCTCCTGGCGTACCCCAGC 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTCGCAGACCTGCGGCAGGCTGCGGTACAAGGGCATCCCGCCGCTCCTGGCGTACCCCAGC 240

Qy  3601 CAGCCCGACCACACCGAGAAGCTCACCATGTGGACTCGCAGACATCGAGCACTCACA 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGCCCGACCACACCGAGAAGCTCACCATGTGGACTCGCAGACATCGAGCACTCACA 300

Qy  3661 GGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTTCAGGCCTCTAC 3720
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Db   301 GGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTTCAGGCCTCTAC 360

Qy  3721 TTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAGATTCCAAGGATCAGGTTGCAG 3780
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Db   361 TTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAGATTCCAAGGATCAGGTTGAG 420

Qy  3781 GATTATGCATTGAGGAAGAACATATCTCGTGGCTGAGGTTGAGAAATGGCTTGGACCCATT 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GATTATGCATTGAGGAAGAACATATCTCGTGGCTGAGGTTGAGAAATGGCTTGGACCCATT 480

Qy  3841 TTGGGATATGATACAGACTAACTTTTTTTTTTTTTTT 3876
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Db   481 TTGGGATATGATACAGACTAACTTTTTTTTTTTTTTTT 516
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RESULT 19
BB879762
LOCUS   BB879762   874 bp   mRNA   linear   EST 20-OCT-2000
DEFINITION   601491666F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893729 5', mRNA sequence.
ACCESSION   BB879762
VERSION   BB879762.1   GI:10328538
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1   (bases 1 to 874)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)

/note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match   10.3%;   Score 404;   DB 7;   Length 404;
Best Local Similarity   100.0%;   Pred. No. 7.4e-191;
Matches   404;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy  2508 ACTGAAAGCTGCTTGACCACAAAGCAGAGATATAATTGGCCTGTCAGGACTCATCACTCC 2567
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ACTGAAAGCTGCTTGACCACAAAGCAGAGATATAATTGGCCTGTCAGGACTCATCACTCC 60

Qy  2568 TTCCCTGGATGAAAATGATTTTTGTTGCCAAGGAAATGGAAATGGAAGATTAGCTATAAGGATTCC 2627
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Db    61 TTCCCTGGATGAAAATGATTTTTGTTGCCAAGGAAATGGAAATGGAAGATTAGCTATAAGGATTCC 120

Qy  2628 ATTGTTGATTGGAGGAGCAACCACTTCAAAAACCACACAGCAGTTAAAATAGCTCCGAG 2687
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAG 180

Qy  2688 ATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTGTTCCCA 2747
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Db   181 ATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTGTTCCCA 240

Qy  2748 GCTGTTAGATGATGAAAATCTAAAGGATGAATACTTTGAGGAAAATCATGAAGAATATGAAGA 2807
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Db   241 GCTGTTAGATGATGAAAATCTAAAGGATGAATACTTTGAGGAAAATCATGAAGAATATGAAGA 300

Qy  2808 TATTAGACAGGACCATTATGAGTCTTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGC 2867
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Db   301 TATTAGACAGGACCATTATGAGTCTTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGC 360

Qy  2868 CAGAAAAAGTGGTTTCCAAATGGCTGTTCTGAACCTCACC 2911
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Db   361 CAGAAAAAGTGGTTTCCAAATGGCTGTTCTGAACCTCACC 404
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RESULT 18
BQ960377
LOCUS   BQ960377   937 bp   mRNA   linear   EST 21-AUG-2002
DEFINITION   AGENCOURT_8946185 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6462473 5', mRNA sequence.
ACCESSION   BQ960377
VERSION   BQ960377.1   GI:22375855
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1   (bases 1 to 937)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Rubin Laboratory
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLCM2652 row: g column: 18
  High quality sequence stop: 568.
FEATURES   Location/Qualifiers
  source   1..937
     /organism="Homo sapiens"

Left column:

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JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: DCTD/DTP/Gazdar
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM9682 row: d column: 18
          High quality sequence stop: 561.
FEATURES  Location/Qualifiers
  source  1..874
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          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="IMAGE:3893729"
          /tissue_type="large cell carcinoma, undifferentiated"
          /lab_host="DH10B (phage-resistant)"
          /clone_lib="NIH_MGC_69"
          /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
          Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
          Average insert size 1.1 kb.  Library constructed by Life
          Technologies."
ORIGIN

Query Match     8.9%;  Score 350; DB 2; Length 874;
Best Local Similarity   99.6%; Pred. No. 1.1e-163;
Matches 450; Conservative  0; Mismatches  2; Indels  0; Gaps  0;

Qy  3377 TTGGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGGTGACGACTACAGCAGCATCA 3436
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    77 TTGGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGGTGACGACTACAGCAGCATCA 136

Qy  3437 TGGTCAAGGCGCTGGGGGACCGCTCGCAGAGAGCTCCTTTGCAGAAGAGCTCCATGAAAGAG 3496
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Db   137 TGGTCAAGGCGCTGGGGGACCGCTCGCAGAGAGCTCCTTTGCAGAAGAGCTCCATGAAAGAG 196

Qy  3497 TTCGCCGAGAACTGTGGGCCTACTGTGCAGTGAGCAGTCGCAGACCTGCGAA 3556
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   197 TTCGCCGAGAACTGTGGGCCTACTGTGCAGTGAGCAGTCGCAGACCTGCGAA 256

Qy  3557 GGTTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGCCGCACCACCG 3616
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   257 GGCTGCGGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGCCGCACCACCG 316

Qy  3617 AGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACAGGCATTAGGTTAACAG 3676
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Db   317 AGAAGCTCACCATGTGAGACTTGCGAGACATCGAGCAGTCTACAGGCATTAGGTTAACAG 376

Qy  3677 AATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACTTCTCCAATTTGAAGT 3736
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Db   377 AATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACTTCTCCAATTTGAAGT 436

Qy  3737 CCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGATTATGCATTGAGGA 3796
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Db   437 CCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGATTATGCATTGAGGA 496

Qy  3797 AGAACATATCTGTGGCTGAGGTTGAGAAATGG 3828
         ||||||||||||||||||||||||||||||||
Db   497 AGAACATATCTGTGGCTGAGGTTGAGAAATGG 528

RESULT 20
BP268350
LOCUS       BP268350   579 bp  mRNA  linear  EST 16-SEP-2004
DEFINITION  BP268350 Sugano cDNA library, thyroid JTH Homo sapiens cDNA clone
            JTH09813, mRNA sequence.
ACCESSION   BP268350
VERSION     BP268350.1  GI:52183582
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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Right column:

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ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1  (bases 1 to 579)
AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
          Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE     Sequence comparison of human and mouse genes reveals a homologous
          block structure in the promoter regions
JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED    15342556
COMMENT   Contact: Yutaka Suzuki
          Institute of Medical Science, University of Tokyo
          Department of Virology
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES  Location/Qualifiers
  source  1..579
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="JTH09813"
          /tissue_type="thyroid"
          /cell_line="JTH"
          /clone_lib="Sugano cDNA library, thyroid JTH"
          /note="thyroid tumor"
ORIGIN

Query Match     8.5%;  Score 332; DB 3; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.2e-154;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  525 TGTGTCCCATCTGTGGAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGA 584
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db   16 TGTGTCCCATCTGTGGAAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGA 75

Qy  585 AGCATACCAAGACAGCAGGCCAAAGGACTTCTGGATGGCGGGGGTTGATATCTTACTCATTGA 644
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Db   76 AGCATACCAAGACAGCAGGCCAAAGGACTTCTGGATGGCGGGGGTTGATATCTTACTCATTGA 135

Qy  645 AACTATTTTGATACTGCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGA 704
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  136 AACTATTTTGATACTGCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGA 195

Qy  705 GGAGAAATATGCTCCCCGGCCTATCTTATTTCAGGGACGATCGTTGATAAAGTGGGGG 764
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Db  196 GGAGAAATATGCTCCCCGGCCTATCTTATTTCAGGGACGATCGTTGATAAAGTGGGGG 255

Qy  765 GACTCTTTCCGACAGACAGGAGAGGATTTGTCATCAGCGTGTCTCATGGGAAGAACCACT 824
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  256 GACTCTTTCCGACAGACAGGAGAGGATTTGTCATCAGCGTGTCTCATGGGAAGAACCACT 315

Qy  825 CTGCATTGGATTAAATTGTGCTTTGGGTGCAG 856
        ||||||||||||||||||||||||||||||||
Db  316 CTGCATTGGATTAAATTGTGCTTTGGGTGCAG 347

RESULT 21
BX470290
LOCUS       BX470290   527 bp  mRNA  linear  EST 04-SEP-2003
DEFINITION  DKFZp779J129_r1 779 (synonym: hncc1) Homo sapiens cDNA clone
            DKFZp779J129 5', mRNA sequence.
ACCESSION   BX470290
VERSION     BX470290.1  GI:32023018
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 527)
AUTHORS     Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
```

```
TITLE       EST (Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL     Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp779J129) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES       Location/Qualifiers
   source      1..527
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="DKFZp779J129"
               /tissue_type="liver"
               /dev_stage="fetal"
               /lab_host="DH10B"
               /clone_lib="779 (synonym: hnccl)"
               /note="Vector: pSport1_SfiI; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Query Match             8.2%;    Score 323;  DB 5;  Length 527;
Best Local Similarity  99.2%;    Pred. No. 4e-150;
Matches  523;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy  2878  GGTTTCCAAATGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCAGTTTATTGGGACC  2937
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Db     1  GGTTTCCAAATGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCAGTTTATTGGGACC    60

Qy  2938  CAGGTCTTTGAAGACTATGACCTGGCAGAAGCTTGGTGGACTACATTGACTGGAAGCCTTC  2997
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Db    61  CAGGTCTTTGAAGACTATGACCTGGCAGAAGCTTGGTGGACTACATTGACTGGAAGCCTTC   120

Qy  2998  TTTGATGTCTGGCAGCTCCGGGGCCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAAC  3057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  TTTGATGTCTGGCAGCTCCGGGGCCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAAC   180

Qy  3058  GACAAAACAGTAGGTGGAGAGGTCCAGGAAGGTCTACGGAAGGTCTCCACCAATATGCTGAAC  3117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GACAAAACAGTAGGTGGAGAGGTCCAGGAAGGTCTACGGAAGGTCTCCACCAATATGCTGAAC   240

Qy  3118  ACACTGATTAGTCAAAAGAAAACTCCGGGCCCGGGGTGTGGTTCTGGCCAGCACAG  3177
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Db   241  ACACTGATTAGTCAAAAGAAAACTCCGGGCCCGGGGTGTGGTTCTGGCCAGCACAG   300

Qy  3178  AGTATCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCAGGCTGCAGAGCCC  3237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AGTATCCAAGACGACATTCACCTGTACGCGAGGCTGCTGTGCCCCAGGCTGCAGAGCCC   360

Qy  3238  ATAGCCACTTTCTATGGGTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCA  3297
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Db   361  ATAGCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCA   420

Qy  3298  TACTACTGGCCTCTCAGACTTCCCTTCATCGCTCCCTTGCATTCCGTGACTACCTCGGGC  3357
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Db   421  TACTACTGGCCTCTCAGACTTCATCGCTCCCTTGCATTCCGTGACTACCTCGGGC   480

Qy  3358  CTGTTTGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTA  3404
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Db   481  CTGTTTGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTA   527
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ACCESSION   AW277117
VERSION     AW277117.1  GI:6664147
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,
            Michael R. Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: David B. Krizman, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Possible reversed clone: polyT not found
            Seq primer: -40UP from Gibco
            High quality sequence stop: 421.
FEATURES       Location/Qualifiers
   source      1..523
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               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:2745018"
               /sex="female"
               /tissue_type="papillary serous ovarian metastasis"
               /lab_host="DH10B"
               /clone_lib="NCI_CGAP_Ov39"
               /note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dT
               priming. Non-directionally cloned into the UDG sites of
               pAMP10.  Size-selected on agarose gel, average insert
               size 500 bp.  Primary library; non-amplified.  cDNA
               Library Preparation: David B. Krizman, Ph.D (NCI).
               Reference: Krizman et al. (1996) Cancer Research
               56:5380-5383."

ORIGIN

Query Match             8.2%;    Score 321;  DB 1;  Length 523;
Best Local Similarity  99.5%;    Pred. No. 4.1e-149;
Matches  421;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy  1328  TAGATGGTCCAAGTGCAATGACCAGATTTGCAACTAATTGCTTCCGAGCCAGACATCG  1387
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Db   432  TAGATGGTCCAAGTGCAATGACCAGATTTGCAACTAATTGCTTCCGAGCCAGACATCG   373

Qy  1388  CAAAGGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTTAAAGT  1447
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Db   372  CAAAGGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTTAAAGT   313

Qy  1448  GCTGCCAAGGAGTCATTGTCAATAGCATTAGTCTGAAGGAGGAGGAGGACGACTTCT  1507
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Db   312  GCTGCCAAGGAGTCATTGTCAATAGCATTAGTCTGAAGGAGGAGGAGGACGACTTCT   253

Qy  1508  TGGAGAAGGCCAGGAAGATTAAAAGTATGGAGCTGCTATGGTGGTGCATGGCTTTTGATG  1567
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   252  TGGAGAAGGCCAGGAAGATTAAAAGTATGGAGCTGCTATGGTGGTGCATGGCTTTTGATG   193

Qy  1568  AAGAAGGACAGGCAACAGAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCTACCATC  1627
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Db   192  AAGAAGGACAGGCAACAGAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCTACCATC   133
```

```
RESULT 22
AW277117/c  AW277117
LOCUS       xp63a10.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745018 3'
DEFINITION                  523 bp    mRNA    linear    EST 03-JAN-2000
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```
similar to SW:METH_HUMAN Q99707
5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE ;, mRNA
sequence.
```

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Qy    1628 TGCTTGTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATATCCTAA 1687
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132 TGCTTGTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATATCCTAA   73

Qy    1688 CCATTCGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTTATCCATGCAACAA 1747
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 CCATTCGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTTATCCATGCAACAA   13

Qy    1748 AAG 1750
           |||
Db      12 AAG   10
```

RESULT 23
BQ364647
LOCUS   BQ364647   506 bp   mRNA   linear   EST 20-MAY-2002
DEFINITION MR2-SN0005-150500-002-d12 SN0005 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ364647
VERSION   BQ364647.1 GI:21037237
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 506)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=SN0005-
            150500-002-d12&t3=2000-05-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 20
            High quality sequence stop: 505.
FEATURES   Location/Qualifiers
     source   1..506
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="SN0005"
                     /note="Organ: stomach normal; Vector: puc18; Site 1: SmaI;
                     Site 2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Query Match   8.0%; Score 315; DB 3; Length 506;
Best Local Similarity 99.5%; Pred. No. 4.2e-146;
Matches 415; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy     877 GAAATAATTGGAAAATGTACACAGCCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCC 936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      55 GAAATAATTGGAAAATGTACACAGCCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCC 114
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     937 AACACCTTGGTGACTATGATGAAACGCCTTCTATGATGGCCAAGCACCTAAAGGATTT 996
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     115 AACACCTTGGTGACTATGATGAAACGCCTTCTATGATGGCCAAGCACCTAAAGGATTT 174

Qy     997 GCTATGATGGCTTGGTCAATATAGTTGGAGGATGCTGTGGGTCAACACCAGATCATATC 1056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 GCTATGATGGCTTGGTCAATATAGTTGGAGGATGCTGTGGGTCAACACCAGATCATATC 234

Qy    1057 AGGGAAATTGCTGAAGCTGTGAAAAATTGTAAGCCTTCCACCTGCCCACTGCCTTT 1116
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 AGGGAAATTGCTGAAGCTGTGAAAAATTGTAAGCCTTCCACCTGCCCACTGCCTTT 294

Qy    1117 GAAGGACATATGTTACTGTCTGGTCTCAGAGCCCTTCAGGATTGGACCGTACACCAACTT 1176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 GAAGGACATATGTTACTGTCTGGTCTCAGAGCCCTTCAGGATTGGACCGTACACCAACTA 354

Qy    1177 GTTAACATTGGAGAGCGCCTGTAATGTTGCAGGATCAAGGAAGTTTGCTAAACTCATCATG 1236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 GTTAACATTGGAGAGCGCCTGTAATGTTGCAGGATCAAGGAAGTTTGCTAAACTCATCATG 414

Qy    1237 GCAGGAAACTATGAAGAAGCCTTGTCGTTGCCAAAGTGCAGTGGAAATGGGAGCC 1293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 GCAGGAAACTATGAAGAAGCCTTGTCGTTGCCAAAGTGCAGTGGAAATGGGAGCC 471
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RESULT 24
BG258321
LOCUS   BG258321   997 bp   mRNA   linear   EST 13-FEB-2001
DEFINITION 602379766F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4510409 5',
            mRNA sequence.
ACCESSION   BG258321
VERSION   BG258321.1 GI:12768137
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 997)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10392 row: c column: 18
            High quality sequence stop: 640.
FEATURES   Location/Qualifiers
     source   1..997
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4510409"
                     /tissue_type="embryonal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_92"
                     /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 2.5 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

Query Match   8.0%; Score 315; DB 2; Length 997;
Best Local Similarity 100.0%; Pred. No. 4.4e-146;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  2229 TTTTGGAGCTGGAAAAATGTTTCTACCTCAGTTATAAAGTCAGCCCGGGTTATGAAGAA 2288
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78 TTTTGGAGCTGGAAAAATGTTTCTACCTCAGTTATAAAGTCAGCCCGGGTTATGAAGAA  137

Qy  2289 GGCTGTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAGAAGAAACCAGAGTGCTTAA 2348
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 GGCTGTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAGAAGAAACCAGAGTGCTTAA  197

Qy  2349 CGGCACAGTAGAAGAAGGACCCTTACCAGGGCACCATCGTGCTGCCACTGTTAAAGG 2408
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 CGGCACAGTAGAAGAAGGACCCTTACCAGGGCACCATCGTGCTGCCACTGTTAAAGG  257

Qy  2409 CGACGTGCACGGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTCCG 2468
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   258 CGACGTGCACGGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTCCG  317

Qy  2469 AGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGTGCTCTTGACCA 2528
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   318 AGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGTGCTCTTGACCA  377

Qy  2529 CAAAGCAGATATAAT 2543
         |||||||||||||||
Db   378 CAAAGCAGATATAAT  392
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RESULT 25
BX332266
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LOCUS       BX332266                 961 bp    mRNA    linear   EST 08-APR-2004
DEFINITION  BX332266 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC010YO17 5-PRIME, mRNA sequence.
ACCESSION   BX332266
VERSION     BX332266.2  GI:46280008
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 961)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On May 2, 2003 this sequence version replaced gi:30343109.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            740.f.
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DC010AH09QP1&c=740.f.
FEATURES             Location/Qualifiers
     source          1..961
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DC010YO17"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

Query Match   8.0%; Score 314; DB 5; Length 961;
Best Local Similarity 100.0%; Pred. No. 1.4e-145;

Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   389 GCCTTGAACACTTGGCCTACCGGATGAACATGTGCTCTGCAGGAGTGGCCAGAAAAGCTG 448
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   526 GCCTTGAACACTTGGCCTACCGGATGAACATGTGCTCTGCAGGAGTGGCCAGAAAAGCTG 585

Qy   449 CCGGAGGAGTAACTCTCCAGACAGGAATTAAGAGGTTGTGGCAGGGGCTCTGGGTCCGA 508
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   586 CCGGAGGAGTAACTCTCCAGACAGGAATTAAGAGGTTGTGGCAGGGGCTCTGGGTCCGA 645

Qy   509 CTAATAAGACACTCTCTGTGTCCCATCGTGTGAAAAGCCGATTATAGGAACATCACAT 568
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   646 CTAATAAGACACTCTCTGTGTCCCATCGTGTGAAAAGCCGATTATAGGAACATCACAT 705

Qy   569 TTGATGAGCTTGTTGAAGCATACCAAGAGCAGCAGGACTTCTGATGGCGGGGGTTG 628
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   706 TTGATGAGCTTGTTGAAGCATACCAAGAGCAGCAGGACTTCTGATGGCGGGGGTTG 765

Qy   629 ATATCTTACTCATTGAAACTATTTTGATACTGCCAAGCAGCGCCTTGTTTTGCAC 688
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   766 ATATCTTACTCATTGAAACTATTTTGATACTGCCAAGCAGCGCCTTGTTTTGCAC 825

Qy   689 TCCAAAATCTTTTT 702
         ||||||||||||||
Db   826 TCCAAAATCTTTTT 839
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RESULT 26
CV344680/c
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LOCUS       CV344680                 574 bp    mRNA    linear   EST 24-SEP-2004
DEFINITION  MR1-HN0069-020101-013-h11 HN0069 Homo sapiens cDNA, mRNA sequence.
ACCESSION   CV344680
VERSION     CV344680.1  GI:52667894
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 574)
AUTHORS     Dias Neto,E., Garcia Correa.R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED      10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. http://www.ludwig.org.br.
FEATURES             Location/Qualifiers
     source          1..574
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HN0069"
                     /note="Organ: head_normal; Vector: puc18; Site 1: SmaI;
                     Site 2: SmaI; A mini-library was made by cloning products
                     derived from ORSTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
```

ORIGIN
          low stringency conditions."

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Query Match      7.6%;  Score 298;  DB 7;  Length 574;
Best Local Similarity  99.7%;  Pred. No. 1.5e-137;
Matches 348;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  2367 GGACCCTTACCAGGGCACCATCGTGCTGCGGCCACTGTTAAAGGCGACGTGCACGACATAGG 2426
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   393 GGACCCTTACCAGGGCACCATCGTGCTGCGGCCACTGTTAAAGGCGACGTGCACGACATAGG  334

Qy  2427 CAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCCGAGTTATTGATTTAGGAGT 2486
         |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   333 CAAGAACATAGTTGGAGTAGTCCTTGGCTGCCATAATTTCCGAGTTATTGATTTAGGAGT  274

Qy  2487 CATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGACCACAAAGCAGATATAATTGG 2546
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   273 CATGACTCCATGTGATAAGATACTGAAAGCTGCTCTTGACCACAAAGCAGATATAATTGG  214

Qy  2547 CCTGTCAGGACGACTCATCACTCCCTCCCTGGATGAAATGATTTTGTTGCCAAGGAAATGGA 2606
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   213 CCTGTCAGGACGACTCATCACTCCCTCCCTGGATGAAATGATTTTGTTGCCAAGGAAATGGA  154

Qy  2607 GAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACACTTCAAAAACCCACAC 2666
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   153 GAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACACTTCAAAAACCCACAC   94

Qy  2667 AGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTG 2715
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db    93 AGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTG   45
```

RESULT 27
BP336596
LOCUS   BP336596   581 bp   mRNA   linear   EST 17-SEP-2004
DEFINITION BP336596 Sugano cDNA library, coronary artery smooth muscle cell
            Homo sapiens cDNA clone SMR06067, mRNA sequence.
ACCESSION   BP336596
VERSION   BP336596.1 GI:52266175
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 581)
AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE   Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED   15342556
COMMENT   Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES   Location/Qualifiers
     source   1..581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="SMR06067"
                     /tissue_type="coronary artery"
                     /cell_type="smooth muscle cell"
                     /clone_lib="Sugano cDNA library, coronary artery smooth
                     muscle cell"
ORIGIN

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Query Match      7.3%;  Score 287;  DB 3;  Length 581;
Best Local Similarity  99.5%;  Pred. No. 5.1e-132;
Matches 387;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy   697 CTTTTTGAGGAGGAAAATGCTCCCCGGCCTATCTTTATTTCAGGGACGAGATCGTTGATAAA 756
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19 CTTTTTGAGGAGGAAAATGCTCCCCGGCCTATCTTTATTTCAGGGACGAGATCGTTGATAAA  78

Qy   757 AGTGGGCGGACTCTTTCCGGACAGACAGGAGAGGGATTTGTCATCAGCGTGTCATGGA 816
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    79 AGTGGGCGGACTCTTTCCGGACAGACAGGAGAGGGATTTGTCATCAGCGTGTCATGGA  138

Qy   817 GAACCACTCGCATGGATTAAATTGTGCTTGGTGCAGCTGAGATGAGACCTTTTATT 876
         |||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   139 GAACCACTCGCATGGATTAAATTGTGCTTGGTGCAGCTGAAATGAGACCTTTTATT  198

Qy   877 GAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCCAATGCAGTCTCCC 936
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199 GAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCCAATGCAGTCTCCC  258

Qy   937 AACACCTTGGTGACATGATGAGAAACGCCTTCTATGATGGCCAAGCACCTAAAGGATTTT 996
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259 AACACCTTGGTGACATGATGAGAAACGCCTTCTATGATGGCCAAGCACCTAAAGGATTTT  318

Qy   997 GCTATGGATGGCTTGGTCAATATAGTTGGAGGATGCGTGTGGGTCAACACCAGATCATATC 1056
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   319 GCTATGGATGGCTTGGTCAATATAGTTGGAGGATGCGTGTGGGTCAACACCAGATCATATC  378

Qy  1057 AGGGAAATTGCTGAAGCTGTGAAAAATTG 1085
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Db   379 AGGGAAATTGCTGAAGCTGTGAAAAATTG  407
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RESULT 28
BX498595
LOCUS   BX498595   587 bp   mRNA   linear   EST 04-SEP-2003
DEFINITION DKFZp779G0140_r1 779 (synonym: hncc1) Homo sapiens cDNA clone
            DKFZp779G0140 5', mRNA sequence.
ACCESSION   BX498595
VERSION   BX498595.1 GI:32016249
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 587)
AUTHORS   Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
TITLE   EST (Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL   Unpublished (2003)
COMMENT   Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No sl sequence available.
            This clone (DKFZp779G0140) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES   Location/Qualifiers
     source   1..587
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp779G0140"
                     /tissue_type="liver"
                     /dev_stage="fetal"
                     /lab_host="DH10B"
                     /clone_lib="779 (synonym: hncc1)"
                     /note="Vector: pSport1_sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN

Query Match   6.8%;   Score 267;   DB 7;   Length 623;
Best Local Similarity   99.3%;   Pred. No. 5.9e-122;
Matches 417;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

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Qy   2622 GATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGC 2681
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 GATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGC 130

Qy   2682 TCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGTGGTGTG 2741
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 TCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGTGGTGTG 190

Qy   2742 TTCCCAGCTGTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATA 2801
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 TTCTCAGCTGTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATA 250

Qy   2802 TGAAGATATTAGACAGGACCATTATGAGTCTCTCAAGGAGAGAGGAGATACTTACCCTTAAG 2861
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 TGAAGATATTAGACAGGACCATTATGAGTCTCTCAAGGAGAGAGGAGATACTTACCCTTAAG 310

Qy   2862 TCAAGCCAGAAAAGTGGTTCCAAATGAATTGGCTGTCTGAACCTCACCCAGTGAGCC 2921
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 TCAAGCCAGAAAAGTGGTTCCAAATGAATTGGCTGTCTGAACCTCACCCAGTGAGCC 370

Qy   2922 CACGTTTATTGGGACCACCCAGGTCTTTGAAGACTATGACCTGCGAGAAGCTGGTGGACTACAT 2981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CACGTTTATTGGGACCACCCAGGTCTTTGAAGACTATGACCTGCGAGAAGCTGGTGGACTACAT 430

Qy   2982 TGACTGGAAGCCTTTCTTTGATGTCTGCAGCTCCGGGCAAGTACCCGAATCGAGGCTT 3041
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 TGACTGGAAGCCTTTCTTTGATGTCTGCAGCTCCGGGCAAGTACCCGAATCGAGGCTT 490
```

RESULT 30
BP332632
LOCUS   BP332632   583 bp   mRNA   linear   EST 17-SEP-2004
DEFINITION   BP332632 Sugano cDNA library, renal proximal tubule primary
             epithelial cell Homo sapiens cDNA clone RPR09337, mRNA sequence.
ACCESSION   BP332632
VERSION   BP332632.1 GI:52262069
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 583)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
             Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE   Sequence comparison of human and mouse genes reveals a homologous
             block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
   PUBMED   15342556
COMMENT   Contact: Yutaka Suzuki
             Department of Virology
             Institute of Medical Science, University of Tokyo
             4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
             Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES   Location/Qualifiers
     source   1..583
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="RPR09337"
                     /tissue_type="renal proximal tubule"
                     /cell_type="primary epithelial cell"
                     /clone_lib="Sugano cDNA library, renal proximal tubule
                     primary epithelial cell"
ORIGIN

Query Match   6.4%;   Score 251;   DB 3;   Length 583;
Best Local Similarity   100.0%;   Pred. No. 6.5e-114;
Matches 251;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Query Match   6.8%;   Score 267;   DB 5;   Length 587;
Best Local Similarity   99.7%;   Pred. No. 5.9e-122;
Matches 317;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   0;

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Qy   3560 TGCGGTACAAGGGCATCGGCGCCTCCTGGCTACCCCAGCCAGCCAGCCCGACCACCACGAGA 3619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 TGCGGTACAAGGGCATCGGCGCCTCCTGGCTACCCCAGCCAGCCAGCCCGACCACCACGAGA 199

Qy   3620 AGCTCACCATGTGGAGACTCGCAGAGATCGAGCAGTCTACAGGCAGTTAGGTTAAACAGAAT 3679
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200 AGCTCACCATGTGGAGACTCGCAGAGATCGAGCAGTCTACAGGCAGTTAGGTTAAACAGAAT 259

Qy   3680 CATTAGCAAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACTTCTCCAATTGAAGTCCA 3739
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260 CATTAGCAAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACTTCTCCAATTGAAGTCCA 319

Qy   3740 AATATTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGATTATGCATTGAGGAAGA 3799
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    320 AATATTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGATTATGCATTGAGGAAGA 379

Qy   3800 ACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCCATTTTGGGATATGATACAGACT 3859
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    380 ACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCCATTTTGGGATATGATACAGACT 439

Qy   3860 AACTTTTTTTTTTTTTTT 3877
          ||||||||||||||||
Db    440 AACTTTTTTTTTTTTTTT 457
```

RESULT 29
CR629973
LOCUS   CR629973   623 bp   mRNA   linear   EST 11-AUG-2004
DEFINITION   DKFZp469I0922_r1 469 (synonym: pkidl) Pongo pygmaeus cDNA clone
             DKFZp469I0922 5', mRNA sequence.
ACCESSION   CR629973
VERSION   CR629973.1 GI:51126053
KEYWORDS   EST.
SOURCE   Pongo pygmaeus (orangutan)
  ORGANISM   Pongo pygmaeus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Pongo.
REFERENCE   1 (bases 1 to 623)
  AUTHORS   Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
             Fobo,G., Han,M. and Wiemann,S.
  TITLE   Pongo pygmaeus mRNA (Bahr,A., Lauber,J., Mewes,H.W., et al.)
  JOURNAL   Unpublished (2004)
COMMENT   Contact: MIPS
             MIPS
             Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
             This is the 5' sequence of the clone insert clone from S. Wiemann,
             Molecular Genome Analysis, German Cancer Research Center (DKFZ);
             Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
             (Hilden/Germany) within the cDNA sequencing consortium of the
             German Genome Project. This clone (DKFZp469I0922) is available at
             the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
             Berlin, Germany. Please contact RZPD for ordering:
             http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469I0922
             Further information about the clone and the sequencing project is
             available at http://mips.gsf.de/projects/cdna/.
FEATURES   Location/Qualifiers
     source   1..623
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp469I0922"
                     /tissue_type="kidney"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="469 (synonym: pkidl)"
                     /note="Vector: pSport1_sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN
```

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Qy      2  GTCACCTGTGGAGGAGCACGTCTTCTCTGCCGCGGCCCTCTGGCCAAGAGGAGACTCGACA    61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    333  GTCACCTGTGGAGGAGCACGTCTTCTCTGCCGCGGCCCTCTGGCCAAGAGGAGACTCGACA   392

Qy     62  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCTGCCAACCCGAAGGTCTGAAGAAACCCCTGCGGG   121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCTGCCAACCCGAAGGTCTGAAGAAACCCCTGCGGG   452

Qy    122  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGATGGAGGATGGGGACCA   181
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGATGGAGGATGGGGACCA   512

Qy    182  TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG   241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513  TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG   572

Qy    242  CCAGGCCGCTG   252
           |||||||||||
Db    573  CCAGGCCGCTG   583
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RESULT 31
BX484356
LOCUS   BX484356   466 bp   mRNA   linear   EST 04-SEP-2003
DEFINITION DKFZp686H23242_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686H23242_5', mRNA sequence.
ACCESSION   BX484356
VERSION   BX484356.1 GI:31946072
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 466)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W.,
            Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
  TITLE   EST (Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W.,
            et al.)
  JOURNAL   Unpublished (2003)
COMMENT   Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
            sequenced by MediGenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project. 81 sequence
            also available.
            This clone (DKFZp686H23242) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg.6, 14059
            Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES   Location/Qualifiers
     source   1..466
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686H23242"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

Query Match   6.0%; Score 236; DB 5; Length 466;
Best Local Similarity   100.0%; Pred. No. 2.3e-106;
Matches 236; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    964  CCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAGTT  1023
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    116  CCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAGTT   175

Qy   1024  GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT  1083
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176  GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT   235

Qy   1084  TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGG  1139
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    236  TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGG   291
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RESULT 32
BP348983
LOCUS   BP348983   581 bp   mRNA   linear   EST 17-SEP-2004
DEFINITION BP348983 Sugano cDNA library, brain Homo sapiens cDNA clone
            SZR02673, mRNA sequence.
ACCESSION   BP348983
VERSION   BP348983.1 GI:52278968
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 581)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE   Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
   PUBMED   15342556
COMMENT   Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES   Location/Qualifiers
     source   1..581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="SZR02673"
                     /tissue_type="brain"
                     /clone_lib="Sugano cDNA library, brain"
ORIGIN

Query Match   5.9%; Score 232; DB 3; Length 581;
Best Local Similarity   100.0%; Pred. No. 2.3e-104;
Matches 232; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      2  GTCACCTGTGGAGGAGCACGTCTTCTCTGCCGCGGCCCTCTGGCCAAGAGGAGACTCGACA    61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    350  GTCACCTGTGGAGGAGCACGTCTTCTCTGCCGCGGCCCTCTGGCCAAGAGGAGACTCGACA   409

Qy     62  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCTGCCAACCCGAAGGTCTGAAGAAACCCCTGCGGG   121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    410  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCTGCCAACCCGAAGGTCTGAAGAAACCCCTGCGGG   469

Qy    122  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGAAGAGGATGGGGACCA   181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    470  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGAAGAGGATGGGGACCA   529

Qy    182  TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAA   233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    530  TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAA   581
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Qy    904  TATGTCCTCTGTTATCCCAATGCAGTGTCTTCCAACACCTTTGGTGACTATGATGAAACG   963
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     56  TATGTCCTCTGTTATCCCAATGCAGTGTCTTCCAACACCTTTGGTGACTATGATGAAACG   115
```

RESULT 33
BP249465
LOCUS   BP249465   592 bp   mRNA   linear   EST 15-SEP-2004

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DEFINITION   BP249465 Sugano cDNA library, embryo kidney Homo sapiens cDNA clone
             HKR13611, mRNA sequence.
ACCESSION    BP249465
VERSION      BP249465.1  GI:52131744
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1 (bases 1 to 592)
AUTHORS      Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
             Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE        Sequence comparison of human and mouse genes reveals a homologous
             block structure in the promoter regions
JOURNAL      Genome Res. 14 (9), 1711-1718 (2004)
PUBMED       15342556
COMMENT      Contact: Yutaka Suzuki
             Department of Virology
             Institute of Medical Science, University of Tokyo
             4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
             Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
     source          1..592
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HKR13611"
                     /tissue_type="kidney"
                     /cell_line="293"
                     /dev_stage="embryo"
                     /clone_lib="Sugano cDNA library, embryo kidney"
ORIGIN

Query Match             5.9%;  Score 231; DB 3; Length 592;
Best Local Similarity 100.0%;  Pred. No. 7.5e-104;
         Matches  231;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      2 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGGCCCCTCGCCAAGGAGGAGACTCGACA 61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGGCCCCTCGCCAAGGAGGAGACTCGACA 421

Qy     62 ACATGTCACCCGGCTCCAAGACCTGTCGCAACCGAAGGTCTGAAGAAAACCCTGCGGG 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 ACATGTCACCCGGCTCCAAGACCTGTCGCAACCGAAGGTCTGAAGAAAACCCTGCGGG 481

Qy    122 ATGAGATCAATGCCATTCGCAGAAGAGGATTATGGTGCTGCTAGTGGTGCTGAGGAGGATGGGGACCA 181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 ATGAGATCAATGCCATTCGCAGAAGAGGATTATGGTGCTGCTAGTGGTGCTGAGGAGGATGGGGACCA 541

Qy    182 TGATCCAGCGGGAGAAGCTAAACGAAGACACTTCCGAGGTCAGGAATTTA 232
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 TGATCCAGCGGGAGAAGCTAAACGAAGACACTTCCGAGGTCAGGAGAATTTA 592

RESULT 34
BU429497
LOCUS        BU429497              496 bp    mRNA    linear    EST 09-SEP-2002
DEFINITION   UI-HF-BN0-aem-h-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
             IMAGE:3064927 5', mRNA sequence.
ACCESSION    BU429497
VERSION      BU429497.1  GI:22767984
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1 (bases 1 to 496)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
```

```
             Email: cgapbs-r@mail.nih.gov
             Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1..496
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3064927"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LITI)"
                     /clone_lib="NIH_MGC_50"
                     /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (3.5-4.4kb).  Directionally cloned. Cells provided by
                     Louis M. Staudt, Ph.D.  Library preparation by Maria de
                     Fatima Bonaldo, Ph.D. and  M. Bento Soares, Ph.D. "
ORIGIN

Query Match             5.5%;  Score 216; DB 5; Length 496;
Best Local Similarity  99.2%;  Pred. No. 2.6e-96;
         Matches  366;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy   3165 CTGGCCAGCACAGAGTATCCAAGACGACATTCACCTGTACGCAGAGCTGCTGCTGCCCCA 3224
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8 CTGGCCAGCACAGAGTATCCAAGACGACATTCACCTGTACGCAGAGCTGCTGCTGCCCCA 67

Qy   3225 GGCTGCAGAGCCCATAGCCACTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGC 3284
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     68 GGCTGCAGAGCCCATAGCCACTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGC 127

Qy   3285 CAGCACGGAGCCATACTACTGCCTCTCAGACTTCATCGGTCATCGTCCCTTGCATTCTGGCATCCG 3344
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    128 CAGCACGGAGCCATACTACTGCCTCTCAGACTTCATCGTCCCTTGCATTCTGGCATCCG 187

Qy   3345 TGACTACCTGGGCCGTGTTGACGACTACAGCAGCACAGCAGCATCATGGTCAAGGCGCTGGCTGGC 3404
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    188 TGACTACCTGGGCCGTGTTGACGACTACAGCAGCACAGCAGCATCATGGTANAAGAGCTGGGGTANAAGAGCTGGGGAT 247

Qy   3405 TGAGGATGATGGTGACGACTACAGCAGCACAGCAGCATCATGTGGGGACCGGCTGGC 3464
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 TGAGGATGATGGTGACGACTACAGCAGCACAGCAGCATCATGTGGGGACCGGCTGGC 307

Qy   3465 AGAGGCCTTTGCAGAAGAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGG 3524
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 AAAGGCCTTTGCAGAAGAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGG 367

Qy   3525 CAGTGAGCA 3533
          |||||||||
Db    368 CAGTGAGCA 376

RESULT 35
CV356711
LOCUS        CV356711              618 bp    mRNA    linear    EST 27-SEP-2004
DEFINITION   MR4-RT0026-050201-301-h10 RT0026 Homo sapiens cDNA, mRNA sequence.
ACCESSION    CV356711
VERSION      CV356711.1  GI:5706766
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
```

REFERENCE   1 (bases 1 to 618)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
             O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
             Laboratory of Cancer Genetics
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. http://www.ludwig.org.br.
FEATURES   Location/Qualifiers
     source   1..618
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="RT0026"
                     /note="Organ: kidney tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Query Match   5.4%; Score 212; DB 7; Length 618;
Best Local Similarity 99.6%; Pred. No. 2.7e-94;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1420 TTTGCTGTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATT 1479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   117 TTTGCTGTGATTGAAGCTGGGTTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATT 176

Qy   1480 AGTCTGAAGGAGGAGGAGGAGGACGACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGA 1539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   177 AGTCTGAAGGAGGAGGAGGAGGACGACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGA 236

Qy   1540 GCTGCTATGGTGGTCATGGCTTTTGATGAAGAAGGACAACAGCAAGAAACAGACACAAAA 1599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   237 GCTGCTATGGTGGTCATGGCTTTTGATGAAGAAGGACAACAGCAAGAAACAGACACACAAAA 296

Qy   1600 ATCAGAGTGTGCACCCGGCCTACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAAT 1659
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   297 ATCAGAGTGTGCACCCGGCNTACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAAT 356

Qy   1660 GACATTATTTTTGACCCTAATAT 1682
            ||||||||||||||||||||||||
Db   357 GACATTATTTTTTGACCCTAATAT 379

RESULT 36
AA356439
LOCUS   AA356439   292 bp   mRNA   linear   EST 21-APR-1997
DEFINITION EST64989 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
            similar to 5-methyltetrahydrofolate-homocysteine methyltransferase,
            mRNA sequence.
ACCESSION   AA356439
VERSION   AA356439.1 GI:2008758
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 292)
AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
             Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
             White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
             Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
             Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
             Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
             Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
             Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
             Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
             Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
             Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
             Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
             He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,J., Kim,A.K.,
             Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
             Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
             Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
             Fraser,C.M. and Venter,J.C.
TITLE   Initial assessment of human gene diversity and expression patterns
             based upon 83 million nucleotides of cDNA sequence
JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
PUBMED   7566098
COMMENT   Contact: Kerlavage, AR
             Bioinformatics
             The Institute for Genomic Research
             9712 Medical Center Drive, Rockville, MD 20850 USA
             Tel: 3018699056
             Fax: 3018699423
             Email: arkerlav@tigr.org
             For clone availability, additional sequence and expression
             information related to this EST, please check the TIGR Human Gene
             Index (http://www.tigr.org/tdb/hgi/hgi.html)
             Seq primer: M13 Reverse.
FEATURES   Location/Qualifiers
     source   1..292
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):158577"
                     /db_xref="taxon:9606"
                     /cell_type="T-lymphocyte"
                     /clone_lib="Jurkat T-cells VI"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

Query Match   5.2%; Score 205; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 8.6e-91;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3270 TGAGAAGGACTTCGCCAGCACGGACCATACTACTGCCTTCAGACTTCATCGCCTCCCTT 3329
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 TGAGAAGGACTTCGCCAGCACGGACCATACTACTGCCTTCAGACTTCATCGCCTCCCTT 121

Qy   3330 GCATTCTGGCATCCGTGACTACCTGGGCCTGTTGCCGTTGCCGCTGCCTTTGGGGTAGAAGA 3389
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122 GCATTCTGGCATCCGTGACTACCTGGGCCTGTTGCCGTTGCCGCTGCCTTTGGGGTAGAAGA 181

Qy   3390 GCTGAGCAAGGCCTATGAGGATGATGTGAGCGACTACAGCAGCATCATGGTCAAGGCGCT 3449
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182 GCTGAGCAAGGCCTATGAGGATGATGTGAGCGACTACAGCAGCATCATGGTCAAGGCGCT 241

Qy   3450 GGGGGACCGGCTGGCCAGAGGCTTT 3474
            ||||||||||||||||||||||||||
Db   242 GGGGGACCGGCTGGCAGAGGCCTTT 266

RESULT 37
BX955050/c
LOCUS   BX955050   356 bp   mRNA   linear   EST 01-MAR-2004
DEFINITION DKFZp781F1761_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone

REFERENCE   1 (bases 1 to 581)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
             Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE   Sequence comparison of human and mouse genes reveals a homologous
             block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
   PUBMED   15342556
  COMMENT   Contact: Yutaka Suzuki
             Department of Virology
             Institute of Medical Science, University of Tokyo
             4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
             Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES   Location/Qualifiers
     source   1..581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HKR11133"
                     /tissue_type="kidney"
                     /cell_line="293"
                     /dev_stage="embryo"
                     /clone_lib="Sugano cDNA library, embryo kidney"
ORIGIN

Query Match   4.6%; Score 180; DB 3; Length 581;
Best Local Similarity 99.6%; Pred. No. 3.3e-78;
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   2 GTCACCTGTGGAGCACGTCTTCTCTGCCGCGGCCCTCGCCAAGGAGGAGACTCGACA 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   351 GTCACCTGTGGAGCACGTCTTCTCTGCCGCGGCCCTCGCCAAGGAGGAGACTCGACA 410

Qy   62 ACATGTCACCCGCCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCTGCGGG 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   411 ACATGTCACCCGCCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCTGCGGG 470

Qy   122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGATGGGACCA 181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   471 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGATGGGACCA 530

Qy   182 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTA 232
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   531 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTA 581

RESULT 39
BU184298
LOCUS   BU184298   996 bp   mRNA   linear   EST 04-SEP-2002
DEFINITION AGENCOURT_7858169 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6168654
            5', mRNA sequence.
ACCESSION   BU184298
VERSION   BU184298.1 GI:22698282
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 996)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/, Mammalian Gene Collection (MGC)
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13532 row: i column: 07
            High quality sequence stop: 181.

ACCESSION   DKFZp781F1761 5', mRNA sequence.
BX955050
VERSION   BX955050.1 GI:43436899
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 356)
  AUTHORS   Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE   EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.)
  JOURNAL   Unpublished (2003)
  COMMENT   Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp781F1761) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES   Location/Qualifiers
     source   1..356
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp781F1761"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="781 (synonym: hlcc4)"
                     /note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

Query Match   5.1%; Score 201; DB 5; Length 356;
Best Local Similarity 100.0%; Pred. No. 8.9e-89;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   518 CACTCTCTGTGTCCCCATCTGTGGAAAGGCCGGATTATAGGAAACATCACATTTGATGAGC 577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 CACTCTCTGTGTCCCCATCTGTGGAAAGGCCGGATTATAGGAAACATCACATTTGATGAGC 142

Qy   578 TTGTTGAAGCATACCAAGAGCAGGCAGGCCAAAGGACTTCTCGGATGGCGCGGGTTGATATCTTAC 637
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 TTGTTGAAGCATACCAAGAGCAGGCAGGCCAAAGGACTTCTCGGATGGCGCGGGTTGATATCTTAC 82

Qy   638 TCATTGAAACTATTTTTGATACTGCCAATGCCAAGGCAGCCCTTGTTTGCACTCCAAAATC 697
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 TCATTGAAACTATTTTTGATACTGCCAATGCCAAGGCAGCCCTTGTTTGCACTCCAAAATC 22

Qy   698 TTTTTGAGGAGAAATATGCTC 718
          |||||||||||||||||||||
Db   21 TTTTTGAGGAGAAATATGCTC 1

RESULT 38
BP248483
LOCUS   BP248483   581 bp   mRNA   linear   EST 15-SEP-2004
DEFINITION BP248483 Sugano cDNA library, embryo kidney Homo sapiens cDNA clone
            HKR11133, mRNA sequence.
ACCESSION   BP248483
VERSION   BP248483.1 GI:52130762
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

FEATURES
source   Location/Qualifiers
                1..996
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6168654"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_72"
                /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 2 kb. Library constructed by Life
                Technologies."

ORIGIN

Query Match   4.0%;   Score 158; DB 5;   Length 996;
Best Local Similarity   99.5%;   Pred. No. 3.9e-67;
Matches 208;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   2675 AAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGG 2734
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AAATAGCTCCGAGATACAGTGCACCTGTAATCCATGTCCTGGACGCGTCCAAGAGTGTGG 60

Qy   2735 TGGTGTGTTCCCAGCTGTTAGATGAAGAAATCTAAAGGATGAAATCATGG 2794
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGGTGTGTTCCCAGCTGTTAGATGAAGAAATCTAAAGGATGAAATCATGG 120

Qy   2795 AAGAATATGAAGAATATTAGACAGGACCATTATGAGTCTCTCAAGGAGAGAGATACTTAC 2854
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAGAATATGAAGAATATTAGACAGGACCATTATGAGTCTCTCAAGGAGAGAGATACTTAC 180

Qy   2855 CCTTAAGTCAAGCCAGAAAAAAGTGGTTTC 2883
          ||||||||||||||||||||||||||||||
Db   181 CCTTAAGTCAAGCCAGAAAAAAGTGGTTTC 209

RESULT 40
AI872333/c
LOCUS   AI872333   668 bp   mRNA   linear   EST 07-MAR-2000
DEFINITION wm57h11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2440101 3'
            similar to SW:METH_HUMAN Q99707
            5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE ;, mRNA
            sequence.
ACCESSION   AI872333
VERSION   AI872333.1 GI:5546382
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 668)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
            Insert Length: 2769   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 404.
FEATURES   Location/Qualifiers
     source   1..668
                     /organism="Homo sapiens"
                     /mol_type="mRNA"

                     /db_xref="taxon:9606"
                     /clone="IMAGE:2440101"
                     /tissue_type="moderately-differentiated endometrial
                     adenocarcinoma, 3 pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut2"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.85 kb. Life Technologies catalog #:
                     11539-012"

ORIGIN

Query Match   3.9%;   Score 154;   DB 1;   Length 668;
Best Local Similarity   100.0%;   Pred. No. 4e-65;
Matches 154;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3724 TCCAATTTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT 3783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   252 TCCAATTTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT 193

Qy   3784 TATGCATTGAGGAAGAAGACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTTG 3843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192 TATGCATTGAGGAAGAAGACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTTG 133

Qy   3844 GGATATGATACAGACTAACTTTTTTTTTTTTTTT 3877
          ||||||||||||||||||||||||||||||||||
Db   132 GGATATGATACAGACTAACTTTTTTTTTTTTTTT 99

RESULT 41
CV363529
LOCUS   CV363529   477 bp   mRNA   linear   EST 27-SEP-2004
DEFINITION PM1-CN0098-110101-009-a05 CN0098 Homo sapiens cDNA, mRNA sequence.
ACCESSION   CV363529
VERSION   CV363529.1 GI:52713584
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 477)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. http://www.ludwig.org.br.
FEATURES   Location/Qualifiers
     source   1..477
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="CN0098"
                     /note="Organ: colon normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)

ORIGIN

　　　　profiles into the pUC 18 vector. Reverse transcription of
　　　　tissue mRNA and cDNA amplification were performed under
　　　　low stringency conditions."

Query Match　　3.6%; Score 142; DB 7; Length 477;
Best Local Similarity 99.5%; Pred. No. 4.2e-59;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy　　3366 CGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGAGTGACGACTA 3425
　　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　 152 CGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGAGTGACGACTA 211

Qy　　3426 CAGCAGCATCATGTGGTCAAGGCGCTCGGGGGGACCCGCTGGCAGAGGCCTTGCAGAAGAGCT 3485
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　 212 CGGCAGCACATCATGTCAAGGCGCTCGGGGGGACCCGCTGGCAGAGGCCTTGCAGAAGAGCT 271

Qy　　3486 CCATGAAAGAGTTCGCCGAGAACTGTGTGGGCCTACTGTGGCAGCTGGACGTGACGTCGC 3545
　　　　　　||||||||||||||||||||||
Db　　 272 CCATGAAAGAGTTCGCCGAGAACTGTGTGGGCCTACTGTGGCAGCTGGACGTGACGTCGC 331

Qy　　.3546 AGACCTGCGAAGG 3558
　　　　　　 |||||||||||||
Db　　 332 AGACCTGCGAAGG 344

RESULT 42
LOCUS　　　　CR767594
DEFINITION　DKFZp469O148_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
　　　　　　　DKFZp469O148 5'; mRNA sequence.
ACCESSION　　CR767594
VERSION　　　CR767594.1　GI:52609891
KEYWORDS　　EST.
SOURCE　　　Pongo pygmaeus (orangutan)
ORGANISM　　Pongo pygmaeus
　　　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　　Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
　　　　　　　Hominidae; Pongo.
REFERENCE　　1 (bases 1 to 552)
AUTHORS　　　Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
　　　　　　　Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
　　　　　　　Wiemann,S.
TITLE　　　　Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,
　　　　　　　Deutschenbaur,S., et al.)
JOURNAL　　　Unpublished (2004)
COMMENT　　　Contact: MIPS
　　　　　　　MIPS
　　　　　　　Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
　　　　　　　This is the 5' sequence of the clone insert. Clone from S. Wiemann,
　　　　　　　Molecular Genome Analysis, German Cancer Research Center (DKFZ);
　　　　　　　Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
　　　　　　　(Martinsried/Germany) within the cDNA sequencing consortium of the
　　　　　　　German Genome Project. This clone (DKFZp469O148) is available at
　　　　　　　the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
　　　　　　　Berlin, Germany. Please contact RZPD for ordering;
　　　　　　　http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469O148
　　　　　　　Further information about the clone and the sequencing project is
　　　　　　　available at http://mips.gsf.de/projects/cdna/.
FEATURES　　　Location/Qualifiers
　source　　　1..552
　　　　　　　/organism="Pongo pygmaeus"
　　　　　　　/mol_type="mRNA"
　　　　　　　/db_xref="taxon:9600"
　　　　　　　/clone="DKFZp469O148"
　　　　　　　/tissue_type="kidney"
　　　　　　　/dev_stage="adult"
　　　　　　　/lab_host="DH10B"
　　　　　　　/clone_lib="469 (synonym: pkid1)"
　　　　　　　/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN

Query Match　　3.5%; Score 136; DB 7; Length 552;

───

Best Local Similarity　99.2%; Pred. No. 4.4e-56;
Matches 236; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy　　1391 AGGTACCTTTGTGCATCGACTCCTCCAATTTTCGTGTGATTGATTGAAGCTGGTTAAAGTGCT 1450
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　 95 AGGTACCTTTGTGCATCGACTCCTCCAATTTCGTGTGATTGATTGAAGCTGGTTAAAGTGCT 154

Qy　　1451 GCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAACGAAGGAAGGAGAGAGACGACTTCTTGG 1510
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　 155 GCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAACGAAGGAAGGAGAGAGACGACTTCTTGG 214

Qy　　1511 AGAAGGGCCAGGAAGATTAAAAAGTATGAGCTGCTATGGTGCTCATGGTGTCATGGTGTCATGATGAAG 1570
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　 215 AGAAGGGCCGGAAGATTAAAAAGTATGAGCTGCTATGGTGCTCATGGTGTCATGATGAAG 274

Qy　　1571 AAGGACAGGCAACAGAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCTACCATCT 1628
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　 275 AAGGACAGGCAACAGAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCTACCATCT 332

RESULT 43
BF749082/c
LOCUS　　　　BF749082　　　　　　　　　226 bp　　mRNA　　　linear　　　EST 10-JAN-2001
DEFINITION　MR2-BN0386-051000-014-f10 BN0386 Homo sapiens cDNA, mRNA sequence.
ACCESSION　　BF749082
VERSION　　　BF749082.1　GI:12075758
KEYWORDS　　EST.
SOURCE　　　Homo sapiens (human)
ORGANISM　　Homo sapiens
　　　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　　Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
　　　　　　　Hominidae; Homo.
REFERENCE　　1 (bases 1 to 226)
AUTHORS　　　Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
　　　　　　　Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
　　　　　　　Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
　　　　　　　Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
　　　　　　　O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
　　　　　　　Simpson,A.J.
TITLE　　　　Shotgun sequencing of the human transcriptome with ORF expressed
　　　　　　　sequence tags
JOURNAL　　　Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED　　　10737800
COMMENT　　　Contact: Simpson A.J.G.
　　　　　　　Laboratory of Cancer Genetics
　　　　　　　Ludwig Institute for Cancer Research
　　　　　　　Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
　　　　　　　Brazil
　　　　　　　Tel: +55-11-2704922
　　　　　　　Fax: +55-11-2707001
　　　　　　　Email: asimpson@ludwig.org.br
　　　　　　　This sequence was derived from the FAPESP/LICR Human Cancer Genome
　　　　　　　Project. This entry can be seen in the following URL
　　　　　　　(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=BN0386-
　　　　　　　051000-014-f10&t3=2000-10-05&t4=1)
　　　　　　　Seq primer: puc 18 forward
　　　　　　　High quality sequence stop: 226.
FEATURES　　　Location/Qualifiers
　source　　　1..226
　　　　　　　/organism="Homo sapiens"
　　　　　　　/mol_type="mRNA"
　　　　　　　/db_xref="taxon:9606"
　　　　　　　/dev_stage="Adult"
　　　　　　　/clone_lib="BN0386"
　　　　　　　/note="Organ: breast normal; Vector: puc18; Site_1: SmaI;
　　　　　　　Site_2: SmaI; A mini-library was made by cloning products
　　　　　　　derived from ORESTES PCR (U.S. Letters Patent application
　　　　　　　No. 196,716 - Ludwig Institute for Cancer Research)
　　　　　　　profiles into the pUC 18 vector. Reverse transcription of
　　　　　　　tissue mRNA and cDNA amplification were performed under
　　　　　　　low stringency conditions."

ORIGIN

```
Query Match       3.4%;  Score 134;  DB 2;  Length 226;
Best Local Similarity  100.0%;  Pred. No. 4.3e-55;
Matches  134;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1446  GTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACGACTT 1505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225  GTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACGACTT 166

Qy  1506  CTTGGGAGAAGGCCAGGAAGCCAGGAAGATTAAAAAGTATGGCGTCTGCTGGTCATGGCTTTTGA 1565
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165  CTTGGGAGAAGGCCAGGAAGCCAGGAAGATTAAAAAGTATGGCGTCTGCTGGTCATGGCTTTTGA 106

Qy  1566  TGAAGAAGGACAGG 1579
          ||||||||||||||
Db   105  TGAAGAAGGACAGG 92


RESULT 44
CR773515
LOCUS       CR773515                486 bp    mRNA    linear   EST 23-SEP-2004
DEFINITION  DKFZp459D0754_r1 459 (synonym: pcor1) Pongo pygmaeus cDNA clone
            DKFZp459D0754 5', mRNA sequence.
ACCESSION   CR773515
VERSION     CR773515.1  GI:52616788
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
ORGANISM    Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1  (bases 1 to 486)
AUTHORS     Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
TITLE       Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
JOURNAL     Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
            Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp459D0754
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1..486
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp459D0754"
                     /tissue_type="cortex"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="459 (synonym: pcor1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN

Query Match       3.3%;  Score 129;  DB 7;  Pred. No. 1.5e-52;  Length 486;
Best Local Similarity  100.0%;
Matches  129;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  2913  AGTGAAGCCCACGTTATTGGGACCCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGT 2972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255  AGTGAAGCCCACGTTATTGGGACCCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGT 314

Qy  2973  GGACTACATTGACTGGAAGCCTTTCTTTGATGTCTGGCAGCTCCGGGGCCAAGTACCCGAA 3032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315  GGACTACATTGACTGGAAGCCTTTCTTTGATGTCTGGCAGCTCCGGGGCCAAGTACCCGAA 374

Qy  3033  TCGAGGGCTT 3041
          ||||||||||
Db   375  TCGAGGGCTT 383


RESULT 45
CR751928
LOCUS       CR751928                444 bp    mRNA    linear   EST 30-AUG-2004
DEFINITION  DKFZp469P1116_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
            DKFZp469P1116 5', mRNA sequence.
ACCESSION   CR751928
VERSION     CR751928.1  GI:51670967
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
ORGANISM    Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1  (bases 1 to 444)
AUTHORS     Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
TITLE       Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,
            Deutschenbaur,S., et al.)
JOURNAL     Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
            (Martinsried/Germany) within the cDNA sequencing consortium of the
            German Genome Project. This clone (DKFZp469P1116) is available at
            the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
            Berlin, Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469P1116
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1..444
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp469P1116"
                     /tissue_type="kidney"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="469 (synonym: pkid1)"
                     /note="Vector: pSport1_sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN

Query Match       3.3%;  Score 128;  DB 7;  Pred. No. 4.6e-52;  Length 444;
Best Local Similarity  100.0%;
Matches  128;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1391  AGTGTACCTTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGTTAAAGTGCT 1450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131  AGTGTACCTTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGTTAAAGTGCT 190

Qy  1451  GCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGAGGACGACTCTTGG 1510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191  GCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGAGGACGACTCTTGG 250

Qy  1511  AGAAGGCC 1518
          ||||||||
Db   251  AGAAGGCC 258


RESULT 46
BQ960236
LOCUS       BQ960236               1168 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT 8945812 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6459642
            5', mRNA sequence.
ACCESSION   BQ960236
VERSION     BQ960236.1  GI:22375714
KEYWORDS    EST.
```

SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1168)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2645 row: a column: 19
            High quality sequence stop: 131.
FEATURES   Location/Qualifiers
     source 1..1168
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6459642"
            /tissue_type="epidermoid carcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC 101"
            /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
            XhoI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G).Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
ORIGIN

Query Match   3.2%; Score 127; DB 5; Length 1168;
Best Local Similarity   100.0%; Pred. No. 1.5e-51;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3361 TTTGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGAC 3420
            ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   1 TTTGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCCATGAGGATGATGGTGAC 60

Qy   3421 GACTACAGCAGCATCATGGTCAAGGCCGCTCGGGGGACCGGGGGGGCCTTTGCAGAA 3480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GACTACAGCAGCATCATGGTCAAGGCCGCTCGGGGGACCGGGGGGGCCTTTGCAGAA 120

Qy   3481 GAGCTCC 3487
            |||||||
Db   121 GAGCTCC 127

RESULT 47
CR853354
LOCUS   CR853354   269 bp   mRNA   linear   EST 22-OCT-2004
DEFINITION DKFZp469J177_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
            DKFZp469J177 5', mRNA sequence.
ACCESSION   CR853354
VERSION   CR853354.1 GI:54568166
KEYWORDS   EST.
SOURCE   Pongo pygmaeus (orangutan)
ORGANISM   Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1 (bases 1 to 269)
AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.

TITLE   Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,
            Deutschenbaur,S., et al.)
JOURNAL   Unpublished (2004)
COMMENT   Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de, sequenced by Medigenomix
            (Martinsried/Germany) within the cDNA sequencing consortium of the
            German Genome Project. This clone (DKFZp469J177) is available at
            the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
            Berlin, Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469J177
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES   Location/Qualifiers
     source 1..269
            /organism="Pongo pygmaeus"
            /mol_type="mRNA"
            /db_xref="taxon:9600"
            /clone="DKFZp469J177"
            /tissue_type="kidney"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="469 (synonym: pkid1)"
            /note="Vector: pSport1_sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN

Query Match   3.2%; Score 124; DB 7; Length 269;
Best Local Similarity   100.0%; Pred. No. 4.7e-50;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1391 AGGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTTAAAGTGCT 1450
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   146 AGGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTTAAAGTGCT 205

Qy   1451 GCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAACGAAGGAAGGAGGAGGACGACTTCTTGG 1510
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   206 GCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAACGAAGGAAGGAGGAGGACGACTTCTTGG 265

Qy   1511 AGAA 1514
            ||||
Db   266 AGAA 269

RESULT 48
AQ744889
LOCUS   AQ744889   857 bp   DNA   linear   GSS 16-JUL-1999
DEFINITION HS_5507_A1_D02_SP6 RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=1083 Col=3 Row=G, genomic survey sequence.
ACCESSION   AQ744889
VERSION   AQ744889.1 GI:5522411
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 857)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE   Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED   10449764
COMMENT   Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1083 row: G column: 3
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 857.

FEATURES
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            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="Plate=1083 Col=3 Row=G"
            /sex="male"
            /clone_lib="RPCI-11 Human Male BAC Library"
            /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
            Male blood DNA was isolated from one randomly chosen donor
            and partially digested with a combination of EcoRI and
            EcoRI Methylase. Size selected DNA was cloned into the
            pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match   3.0%; Score 117; DB 9; Length 857;
Best Local Similarity   100.0%; Pred. No. 1.6e-46;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  1759 GAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTGTCCTTCTCCTTCCGA 1818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 GAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTGTCCTTCTCCTTCCGA 340

Qy  1819 GGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTTACCATGCAATCAAG 1875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 GGAATGGAAGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTTACCATGCAATCAAG 397
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RESULT 49
AG092782
LOCUS   AG092782   735 bp   DNA   linear   GSS 03-NOV-2001
DEFINITION   Pan troglodytes DNA, clone: PTB-093A19.R, genomic survey sequence.
ACCESSION   AG092782
VERSION   AG092782.1 GI:16644584
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE   BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 735)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT   Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
PRIMERS
            Sequencing: M13Rev
LIBRARY
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            R.Site 1 : SacI

R.Site 2 : SacI.
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ORIGIN

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Qy  2315 TGGAAAAAGAAAGAAGAAGAAGAAACCAGAGTGCTTAACGGACACAGTAGAAGAAGAGAGG 2368
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RESULT 50
CF135946
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DEFINITION   UI-HF-BN0-amo-c-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
            IMAGE:3090794 5', mRNA sequence.
ACCESSION   CF135946
VERSION   CF135946.1 GI:33251390
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 153)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE   Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  PUBMED   8889548
COMMENT   Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156   MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Louis Staudt
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/humanfl.html
            Seq primer: pYX-5.

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            (3.5-4.4kb). Directionally cloned. Cells provided by
            Louis M. Staudt, Ph.D. Library preparation by Maria de

ORIGIN

Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "

Query Match   2.5%; Score 98; DB 6; Length 153;
Best Local Similarity   99.3%; Pred. No. 5.4e-37;
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Qy   3458 GGCTGGCAGAGGCCTTTGCAGAAGAGCTCCATGAAAGAGTTCGCCCAGAAACTGTGGGCCT 3517
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Qy   3518 ACTGTGGCAGTGAGCAGCTGGACGTCGCA 3546
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Db   125 ACTGTGGCAGTGAGCAGCTGGACGTCGCA 153

Search completed: March 7, 2006, 10:54:49
Job time : 13647 secs

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              GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:     March 7, 2006, 01:43:57 ; Search time 18876 Seconds
                                       (without alignments)
                                       11801.732 Million cell updates/sec

Title:          US-10-607-712-1
Perfect score:  3919
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Scoring table:  OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched:       5883141 segs, 2842172553 residues

Word size :     18   Oy more - this ne ounch includes oligomers 18-60.

Total number of hits satisfying chosen parameters:  196778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :  GenEmbl:*
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           13:  gb_vi:*
           14:  gb_htg:*
           15:  gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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7	3517	89.7	7122	8	AX069340	AX069340 Sequence
8	3517	89.7	7122	8	HSU75743	U75743 Human methi
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17	714	18.2	1835	6	CQ721809	CQ721809 Sequence
18	308	7.9	4172	6	CQ850206	CQ850206 Sequence
19	308	7.9	4172	8	AK127317	AK127317 Homo sapi
20	297	7.6	435	8	AY429553	AY429553 Homo sapi
21	222	5.7	305	6	BD060282	BD060282 Secreted
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23	217	5.5	183166	14	AL357554	AL357554 Homo sapi
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28 c	189	4.8	183166	14	AL357554	AL357554 Homo sapi
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30 c	182	4.6	73656	14	AC016512	AC016512 Homo sapi
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36 c	96	2.4	732	6	CQ750107	CQ750107 Sequence
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38 c	93	2.4	758	10	BV597233	BV597233 S216P6112
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40	65	1.7	4498	9	AF034214	AF034214 Rattus no
41	63	1.6	63	6	AX611831	AX611831 Sequence
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49 c	54	1.4	268715	14	AC121488	AC121488 Rattus no
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69	26	0.7	26	6	AR482301	AR482301 Sequence
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72	26	0.7	26	6	AR482316	AR482316 Sequence
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74 c	26	0.7	2051	8	X14048	X14048 Canis famil
75 c	26	0.7	7387	8	AC109519	AC109519 Homo sapi
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77	26	0.7	64848	8	AL603746	AL603746 Human DNA
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87	26	0.7	154747	14	AB113354	AB113354 Sus scrof
88	26	0.7	158432	14	AC105438	AC105438 Sus scrof
89 c	26	0.7	164287	9	AL691422	AL691422 Mouse DNA
90 c	26	0.7	169246	14	AC135840	AC135840 Sus scrof
91 c	26	0.7	171329	4	CR956646	CR956646 Pig DNA s

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	96	26	0.7	178594	AC139455	14	AC139455	AC139455 Homo sapi
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	98	26	0.7	181256	AC150611	14	AC150611	AC150611 Callithri
	99	26	0.7	181432	AC134962	14	AC134962	AC134962 Sus scrof
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c	101	26	0.7	184056	AC141857	14	AC141857	AC141857 Sus scrof
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c	103	26	0.7	191122	AL359769	8	AL359769	AL359769 Homo sapi
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	109	26	0.7	223708	AC133607	8	AC133607	AC133607 Mus muscu
	110	26	0.7	226568	AC148012	9	AC148012	AC148012 Mus muscu
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	112	26	0.7	236536	AC139941	9	AC139941	AC139941 Mus muscu
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	125	25	0.6	25	AR482313	25	AR482313	AR482313 Sequence
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	127	25	0.6	25	AR482315	25	AR482315	AR482315 Sequence
	128	25	0.6	25	AR482318	25	AR482318	AR482318 Sequence
	129	25	0.6	237	CQ529205	237	CQ529205	CQ529205 Sequence
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	132	25	0.6	412	AF298347	15	AF298347	AF298347 Gastrolob
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	134	25	0.6	789	BD145240	6	BD145240	BD145240 Primer fo
	135	25	0.6	789	AX865178	8	AX865178	AX865178 Sequence
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	140	25	0.6	1838	BC074656	5	BC074656	BC074656 Xenopus t
	141	25	0.6	1895	AY332500S2	4	AY332500S2	AY332500S2 Sus scrof
	142	25	0.6	1974	BC050075	8	BC050075	BC050075 Homo sapi
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	144	25	0.6	2049	BC028304	8	BC028304	BC028304 Homo sapi
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	146	25	0.6	7215	DMPI3K68D	2	DMPI3K68D	X92892 D.melanogas
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c	163	25	0.6	137083	AP007630	14	AP007630	AP007630 Lotus cor
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	185	25	0.6	164808	HSDJ293L8	4	HSDJ293L8	AL078594 Human DNA
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	187	25	0.6	166014	AC022538	8	AC022538	AC022538 Homo sapi
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	195	25	0.6	172816	AC123981	8	AC123981	AC123981 Pan trogl
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c	201	25	0.6	177068	AC021504	8	AC021504	AC021504 Homo sapi
	202	25	0.6	177352	AC146673	14	AC146673	AC146673 Otolemur
c	203	25	0.6	178315	AC122688	8	AC122688	AC122688 Homo sapi
c	204	25	0.6	178413	AP001370	14	AP001370	AP001370 Homo sapi
c	205	25	0.6	182133	AC151102	14	AC151102	AC151102 Bos tauru
	206	25	0.6	182503	AL672195	8	AL672195	AL672195 Mouse DNA
	207	25	0.6	183149	AC130353	14	AC130353	AC130353 Homo sapi
	208	25	0.6	184370	AC136887	14	AC136887	AC136887 Sus scrof
	209	25	0.6	184864	AC013553	14	AC013553	AC013553 Homo sapi
c	210	25	0.6	185081	CT009693	14	CT009693	CT009693 Homo sapi
	211	25	0.6	185824	AC156317	14	AC156317	AC156317 Bos tauru
	212	25	0.6	187186	CR392353	14	CR392353	CR392353 Danio rer
	213	25	0.6	187377	CR933822	5	CR933822	CR933822 Zebrafish
	214	25	0.6	187856	AC146933	14	AC146933	AC146933 Sus scrof
	215	25	0.6	188517	AC136513	14	AC136513	AC136513 Mus muscu
	216	25	0.6	188853	AC102105	9	AC102105	AC102105 Mus muscu
	217	25	0.6	189091	AC112263	9	AC112263	AC112263 Mus muscu
	218	25	0.6	189985	AC140099	14	AC140099	AC140099 Sus scrof
	219	25	0.6	190275	AC138042	14	AC138042	AC138042 Sus scrof
	220	25	0.6	192063	AC099665	8	AC099665	AC099665 Homo sapi
	221	25	0.6	193342	AC009120	8	AC009120	AC009120 Homo sapi
	222	25	0.6	196195	AC122383	9	AC122383	AC122383 Mus muscu
c	223	25	0.6	196311	CNS01DVP	8	CNS01DVP	CNS01DVP Human chr
c	224	25	0.6	196357	AC163960	14	AC163960	AC163960 Sus scrof
	225	25	0.6	196567	AL928855	9	AL928855	AL928855 Mouse DNA
	226	25	0.6	196724	AL590963	9	AL590963	AL590963 Mouse DNA
	227	25	0.6	196782	AL390956	14	AL390956	AL390956 Homo sapi
c	228	25	0.6	198515	RN323M7	14	RN323M7	CR937049 Rattus no
	229	25	0.6	198784	AC154888	14	AC154888	AC154888 Bos tauru
	230	25	0.6	198935	AC068573	14	AC068573	AC068573 Homo sapi
	231	25	0.6	200598	AC012505	14	AC012505	AC012505 Homo sapi
	232	25	0.6	202377	AC109165	9	AC109165	AC109165 Mus muscu
	233	25	0.6	202381	AC166026	4	AC166026	AC166026 Oryctolag
c	234	25	0.6	204138	SSC427478	4	SSC427478	AJ427478 Sus scrof
c	235	25	0.6	204177	AC124494	9	AC124494	AC124494 Mus muscu
c	236	25	0.6	206119	AL392168	9	AL392168	AL392168 Mus muscu
	237	25	0.6	206513	AL928728	5	AL928728	AL928728 Zebrafish

c	No.	E	Len	Pos	Score	Accession	Match	Description
c	238	0.6	25	206533	8	CNS01RH1	AL160237	Human chr
c	239	0.6	25	206774	14	CR956436	CR956436	Sus scrof
c	240	0.6	25	208992	14	CR956415	CR956415	Sus scrof
c	241	0.6	25	210464	14	AC162828	AC162828	Bos tauru
c	242	0.6	25	211025	9	AC126796	AC126796	Mus muscu
c	243	0.6	25	211659	14	CR956360	CR956360	Sus scrof
c	244	0.6	25	212667	9	AL672180	AL672180	Mouse DNA
c	245	0.6	25	212885	15	AC152071	AC152071	Bos tauru
c	246	0.6	25	213808	9	RN139I21	CR937048	Rattus no
c	247	0.6	25	214261	14	AL935117	AL935117	Zebrafish
c	248	0.6	25	215397	8	AL354497	AL355346	Human DNA
c	249	0.6	25	220832	14	AC164224	AC164224	Bos tauru
c	250	0.6	25	222059	14	AC129158	AC129158	Rattus no
c	251	0.6	25	223477	14	CR854966	CR854966	Danio rer
c	252	0.6	25	225310	14	AC150170	AC150170	Gallus ga
c	253	0.6	25	226763	5	BX649352	BX649352	Zebrafish
c	254	0.6	25	226857	14	CT009542	CT009542	Sus scrof
c	255	0.6	25	229155	8	AC018755	AC018755	Homo sapi
c	256	0.6	25	230400	14	BX248506	BX248506	Zebrafish
c	257	0.6	25	238494	14	AC095717	AC095717	Rattus no
c	258	0.6	25	239439	9	AC117573	AC117573	Mus muscu
c	259	0.6	25	240288	14	AC132298	AC132298	Mus muscu
c	260	0.6	25	242670	14	AC151187	AC151187	Bos tauru
c	261	0.6	25	245394	14	AC125756	AC125756	Rattus no
c	262	0.6	25	246542	14	AC125601	AC125601	Rattus no
c	263	0.6	25	247765	14	BX927092	BX927092	Danio rer
c	264	0.6	25	248717	14	BX470107	BX470107	Danio rer
c	265	0.6	25	251199	6	AX658289	AX658289	Sequence
c	266	0.6	25	251199	8	HUAE000659	AE000659	Homo sapi
c	267	0.6	25	254530	14	AC157170	AC157170	Bos tauru
c	268	0.6	25	264033	14	AC160449	AC160449	Bos tauru
c	269	0.6	25	271025	14	AC111564	AC111564	Rattus no
c	270	0.6	25	271975	14	AC111856	AC111856	Rattus no
c	271	0.6	25	275067	14	CR792438	CR792438	Danio rer
c	272	0.6	25	285749	14	AC106055	AC106055	Rattus no
c	273	0.6	25	343050	2	PFA929353	AL929353	Plasmodiu
c	274	0.6	24	24	6	CQ785841	CQ785841	Sequence
c	275	0.6	24	24	6	CQ785843	CQ785843	Sequence
c	276	0.6	24	24	6	AR482289	AR482289	Sequence
c	277	0.6	24	24	6	AR482290	AR482290	Sequence
c	278	0.6	24	24	6	AR482291	AR482291	Sequence
c	279	0.6	24	24	6	AR482293	AR482293	Sequence
c	280	0.6	24	24	6	AR482295	AR482295	Sequence
c	281	0.6	24	24	6	AR482303	AR482303	Sequence
c	282	0.6	24	24	6	AR482305	AR482305	Sequence
c	283	0.6	24	24	6	AR482307	AR482307	Sequence
c	284	0.6	24	24	6	AR482309	AR482309	Sequence
c	285	0.6	24	24	6	AR482317	AR482317	Sequence
c	286	0.6	24	24	6	AR482319	AR482319	Sequence
c	287	0.6	24	24	6	CQ466406	CQ466406	Sequence
c	288	0.6	24	199	6	CQ468002	CQ468002	Sequence
c	289	0.6	24	199	6	AB132097	AB132097	Homo sapi
c	290	0.6	24	341	10	CQ522431	CQ522431	Sequence
c	291	0.6	24	374	6	AF501663	AF501663	Epinephel
c	292	0.6	24	467	5	BC048542	BC048542	Mus muscu
c	293	0.6	24	513	6	BV559670	BV559670	qsb23b11.
c	294	0.6	24	559	10	BV329768	BV329768	S241P687F
c	295	0.6	24	577	10	BV288237	BV288237	S232P6229
c	296	0.6	24	640	8	BC015849	BC015849	Homo sapi
c	297	0.6	24	719	8	BD107994	BD107994	EST and e
c	298	0.6	24	793	6	AR412441	AR412441	Sequence
c	299	0.6	24	793	6	AX969275	AX969275	Sequence
c	300	0.6	24	793	6	BV564981	BV564981	rak56a09.
c	301	0.6	24	804	10	BV575296	BV575296	GS91P6076
c	302	0.6	24	857	6	BD101491	BD101491	Novel gen
c	303	0.6	24	891	6	BD021553	BD021553	Novel gen
c	304	0.6	24	891	6	BC062675	BC062675	Homo sapi
c	305	0.6	24	1434	4	BC092772	BC092772	Danio rer
c	306	0.6	24	1438	5	BC047881	BC047881	Homo sapi
c	307	0.6	24	1553	8	AK024764	AK024764	Human DNA
c	308	0.6	24	1652	6	CS033673	CS033673	Sequence
c	309	0.6	24	1977	6	CS042625	CS042625	Sequence
c	310	0.6	24	1977	6	CS042625	CS042625	Sequence

c	No.	E	Len	Pos	Score	Accession	Match	Description
c	311	0.6	24	2009	9	BC027202	BC027202	Mus muscu
c	312	0.6	24	2139	9	F333472S14	AF333485	Mus muscu
c	313	0.6	24	2191	9	BC004000	BC004000	Mus muscu
c	314	0.6	24	2586	8	BC041958	BC041958	Homo sapi
c	315	0.6	24	2813	9	HSM804479	AL833168	Homo sapi
c	316	0.6	24	3053	5	BC045212	AB045212	Oreochrom
c	317	0.6	24	4001	5	BC084325	BC084325	Xenopus l
c	318	0.6	24	4936	15	AK121600	AK121600	Oryza sat
c	319	0.6	24	9417	6	A80967	A80967	Sequence 19
c	320	0.6	24	9417	6	A95346	A95346	Sequence 19
c	321	0.6	24	9417	8	HSAJ3112	AJ003112	Homo sapi
c	322	0.6	24	19796	8	AB035346	AB035346	Homo sapi
c	323	0.6	24	31211	14	AC017253	AC017253	Drosophil
c	324	0.6	24	34575	4	AB079894	AB079894	Sus scrof
c	325	0.6	24	34754	4	SSC494748	AJ494748	Sus scrof
c	326	0.6	24	40014	4	AC091538	AC091538	Sus scrof
c	327	0.6	24	40704	8	L48038	L48038	Structure o
c	328	0.6	24	43952	8	HSU105G4	Z92846	Human DNA s
c	329	0.6	24	49480	8	AL450269	AL450269	Human DNA
c	330	0.6	24	62964	14	AC104959	AC104959	Homo sapi
c	331	0.6	24	65389	8	AY497017	AY497017	Pongo pyg
c	332	0.6	24	65878	14	AC084777	AC084777	Homo sapi
c	333	0.6	24	66069	8	AY497016	AY497016	Pan trogl
c	334	0.6	24	66091	8	AY497014	AY497014	Gorilla g
c	335	0.6	24	66319	14	AC069376	AC069376	Homo sapi
c	336	0.6	24	66380	14	AC136771	AC136771	Homo sapi
c	337	0.6	24	66318	14	AC130321	AC130321	Homo sapi
c	338	0.6	24	68318	8	AC151408	AC151408	Pan trogl
c	339	0.6	24	70244	14	AC090836	AC090836	Homo sapi
c	340	0.6	24	72456	5	BX248387	BX248387	Zebrafish
c	341	0.6	24	72690	14	AC140527_3		Continuation (4 of
c	342	0.6	24	73220	14	AY663398	AY663398	Homo sapi
c	343	0.6	24	74719	14	AC139688	AC139688	Homo sapi
c	344	0.6	24	75199	5	CR545472	CR545472	Zebrafish
c	345	0.6	24	76815	14	AC166660	AC166660	Bos tauru
c	346	0.6	24	78546	8	AY663393	AY663393	Homo sapi
c	347	0.6	24	80601	14	AC134755	AC134755	Rattus no
c	348	0.6	24	80743	14	AL162402	AL162402	Human DNA
c	349	0.6	24	81466	14	AC139852	AC139852	Medicago
c	350	0.6	24	86057	8	AC092112	AC092112	Homo sapi
c	351	0.6	24	87738	8	BX296568	BX296568	Human DNA
c	352	0.6	24	93240	14	AC007586	AC007586	Drosophil
c	353	0.6	24	95642	8	AL137064	AL137064	Human DNA
c	354	0.6	24	101064	8	CR753835	CR753835	Human DNA
c	355	0.6	24	101385	5	CNS099BW	BX629356	Tetraodon
c	356	0.6	24	103940	14	AP007687	AP007687	Lotus cor
c	357	0.6	24	107436	15	AC006068	AC006068	Arabidops
c	358	0.6	24	107898	8	CR753309	CR753309	Human DNA
c	359	0.6	24	108736	8	CNS01RGR	AL159179	Human chr
c	360	0.6	24	109757	9	AL162379	AL162379	Human DNA
c	361	0.6	24	109929	9	AC093922	AC093922	Genomic s
c	362	0.6	24	110000	1	HSAC001237		Continuation (4 of
c	363	0.6	24	110000	1	AE017243_3		Continuation (4 of
c	364	0.6	24	110000	1	AE017332_4		Continuation (5 of
c	365	0.6	24	110000	14	AC130665_1		Continuation (2 of
c	366	0.6	24	110000	14	AC151717_1		Continuation (2 of
c	367	0.6	24	110000	15	AP008210_050		Continuation (51 o
c	368	0.6	24	110000	15	AP008210_051		Continuation (52 o
c	369	0.6	24	110625	8	CR753901	CR753901	Human DNA
c	370	0.6	24	111035	8	AC022405	AC022405	Homo sapi
c	371	0.6	24	111437	8	AY663401	AY663401	Pan trogl
c	372	0.6	24	111862	14	AC001237	HSAC001237	Homo sapi
c	373	0.6	24	113075	8	AL512363	AL512363	Human DNA
c	374	0.6	24	117916	4	AC095024	AC095024	Sus scrof
c	375	0.6	24	118869	14	AC140573	AC140573	Macaca mu
c	376	0.6	24	120070	8	AC092929	AC092929	Homo sapi
c	377	0.6	24	120938	15	AC007017	AC007017	Arabidops
c	378	0.6	24	121483	4	BX323833	BX323833	Pig DNA s
c	379	0.6	24	121909	8	HSJ492P14	AL121977	Human DNA
c	380	0.6	24	122742	14	HS167P19	Z93014	Homo sapien
c	381	0.6	24	122921	8	AP005790	AP005790	Homo sapi
c	382	0.6	24	123414	14	AC164019	AC164019	Bos tauru
c	383	0.6	24	124787	8	BX248406	BX248406	Human DNA

	#	Accession	ct	Position			Description
	384	AC000026	8	126312	0.6	24	AC000026 Homo sapi
	385	AY263454	14	126784	0.6	24	AY263454 Sus scrof
	386	AC161722	14	131804	0.6	24	AC161722 Loxodonta
	387	AC025218	8	132202	0.6	24	AC025218 Homo sapi
c	388	CT009611	14	132636	0.6	24	CT009611 Homo sapi
	389	AC112907	8	132875	0.6	24	AC112907 Homo sapi
	390	AC123788	8	133129	0.6	24	AC123788 Homo sapi
	391	HSDJ315G1	8	133391	0.6	24	AL121601 Human DNA
	392	AC159804	14	133786	0.6	24	AC159804 Glycine m
c	393	HSDJ78N10	8	136377	0.6	24	AL121959 Human DNA
c	394	BX571700	5	137898	0.6	24	BX571700 Zebrafish
c	395	AC090820	8	138021	0.6	24	AC090820 Homo sapi
c	396	AC162298	9	138146	0.6	24	AC162298 Mus muscu
	397	CR956369	14	140279	0.6	24	CR956369 Sus scrof
c	398	CR956416	4	141597	0.6	24	CR956416 Pig DNA s
	399	OSJN00239	15	144144	0.6	24	AL731589 Oryza sat
	400	AC115534	14	144235	0.6	24	AC115534 Sus scrof
c	401	AC145762	9	145577	0.6	24	AC145762 Sus scrof
	402	AC125140	9	146052	0.6	24	AC125140 Mus muscu
	403	AC069039	14	146517	0.6	24	AC069039 Homo sapi
	404	AC162751	14	146543	0.6	24	AC162751 Loxodonta
	405	AC087309	8	146667	0.6	24	AC087309 Homo sapi
c	406	AJ410870	4	147663	0.6	24	AJ410870 Sus scrof
	407	AC025917	8	149091	0.6	24	AC025917 Homo sapi
c	408	AC152859	13	149113	0.6	24	AC152859 Sus scrof
	409	AC117191	9	149461	0.6	24	AC117191 Mus muscu
	410	AC093767	8	149505	0.6	24	AC093767 Homo sapi
c	411	AC119516	14	149848	0.6	24	AC119516 Rattus no
	412	RN45C15	8	150638	0.6	24	AP000874 Rattus no
	413	CR956388	4	151277	0.6	24	CR956388 Pig DNA s
	414	CR853291	14	151383	0.6	24	CR853291 Danio rer
	415	AC154271	14	151420	0.6	24	AC154271 Mus muscu
	416	AP003117	8	152095	0.6	24	AP003117 Homo sapi
	417	AP003117	8	152176	0.6	24	AP003117 Homo sapi
	418	AC148863	14	152577	0.6	24	AC148863 Sus scrof
	419	AC136886	14	152605	0.6	24	AC136886 Sus scrof
	420	AC148432	14	153125	0.6	24	AC148432 Sorex ara
	421	AC146761	8	153907	0.6	24	AC146761 Pan trogl
	422	AC161048	14	154222	0.6	24	AC161048 Mus muscu
c	423	AP006300	8	154336	0.6	24	AP006300 Homo sapi
c	424	AL669826	9	154338	0.6	24	AL669826 Mouse DNA
c	425	AC129961	8	154348	0.6	24	AC129961 Sus scrof
	426	HS914P14	8	155375	0.6	24	AL031117 Human DNA
	427	AC009682	8	155428	0.6	24	AC009682 Homo sapi
	428	AL353809	8	155892	0.6	24	AL353809 Human DNA
	429	BX072531	5	156372	0.6	24	BX072531 Zebrafish
c	430	AC138043	14	156471	0.6	24	AC138043 Sus scrof
	431	AC015830	14	156550	0.6	24	AC015830 Homo sapi
c	432	AC026957	14	156879	0.6	24	AC026957 Homo sapi
c	433	AC140666	14	157107	0.6	24	AC140666 Sus scrof
	434	AC110897	9	157916	0.6	24	AC110897 Mus muscu
	435	SSC251914	4	158063	0.6	24	AJ251914 Sus scrof
c	436	AC132361	9	158837	0.6	24	AC132361 Mus muscu
c	437	AP005857	9	158971	0.6	24	AP005857 Homo sapi
c	438	AC026085	14	159322	0.6	24	AC026085 Homo sapi
	439	AL954768	5	159442	0.6	24	AL954768 Zebrafish
c	440	AC151306	14	159671	0.6	24	AC151306 Xenopus t
c	441	AC013701	8	160275	0.6	24	AC013701 Homo sapi
	442	AC092903	8	161141	0.6	24	AC092903 Homo sapi
	443	AC073174	14	161551	0.6	24	AC073174 Homo sapi
c	444	AC011572	14	162112	0.6	24	AC011572 Homo sapi
	445	AC115535	14	162335	0.6	24	AC115535 Sus scrof
	446	AJ928958	9	163351	0.6	24	AJ928958 Mouse DNA
c	447	AC117927	14	163355	0.6	24	AC117927 Mus muscu
	448	AC122016	9	163943	0.6	24	AC122016 Mus muscu
	449	AC016254	4	164331	0.6	24	AC016254 Homo sapi
	450	AC092874	4	164404	0.6	24	AC092874 Sus scrof
	451	AP003716	8	165187	0.6	24	AP003716 Homo sapi
c	452	AC136301	14	165288	0.6	24	AC136301 Homo sapi
c	453	AC136301	14	165288	0.6	24	AC136301 Homo sapi
c	454	AC087233	14	165330	0.6	24	AC087233 Mus Muscu
c	455	AC152462	19	166002	0.6	24	AC152462 Papio anu
c	456	AC087237	8	166380	0.6	24	AC087237 Homo sapi
c	457	AC084737	14	166458	0.6	24	AC084737 Homo sapi
	458	AC012594	8	166702	0.6	24	AC012594 Homo sapi
c	459	AC157922	14	167053	0.6	24	AC157922 Mus muscu
c	460	AY016023	5	167215	0.6	24	AY016023 Sphaeroid
c	461	AC007556	8	167358	0.6	24	AC007556 Homo sapi
c	462	AC009915	2	167368	0.6	24	AC009915 Drosophil
	463	AC011505	8	167417	0.6	24	AC011505 Homo sapi
c	464	CR627494	14	167611	0.6	24	CR627494 Danio rer
c	465	AC166031	14	167886	0.6	24	AC166031 Sus scrof
c	466	CR956391	4	168012	0.6	24	CR956391 Pig DNA s
	467	AC152885	14	168506	0.6	24	AC152885 Glycine m
	468	AC126929	14	168712	0.6	24	AC126929 Mus muscu
	469	AC146181	14	168845	0.6	24	AC146181 Pan trogl
	470	AC161828	14	169461	0.6	24	AC161828 Mus muscu
c	471	AC008043	8	169581	0.6	24	AC008043 Drosophil
	472	AC146251	14	169687	0.6	24	AC146251 Pan trogl
	473	CT009670	14	170156	0.6	24	CT009670 Sus scrof
	474	AC138167	14	170451	0.6	24	AC138167 Sus scrof
	475	AL589745	14	170765	0.6	24	AL589745 Human DNA
	476	AC142352	8	171165	0.6	24	AC142352 Pan trogl
	477	AC132872	8	171569	0.6	24	AC132872 Homo sapi
	478	AJ928790	5	171673	0.6	24	AJ928790 Zebrafish
	479	BX296548	4	172252	0.6	24	BX296548 Pig DNA s
c	480	AC103941	8	172685	0.6	24	AC103941 Mus muscu
c	481	AC103725	8	172945	0.6	24	AC103725 Homo sapi
	482	AC002059	8	173029	0.6	24	AC002059 Homo sapi
	483	AC092810	8	173917	0.6	24	AC092810 Homo sapi
c	484	AC144119	14	173982	0.6	24	AC144119 Macaca mu
c	485	AC121781	9	174187	0.6	24	AC121781 Mus muscu
	486	AC025344	14	174700	0.6	24	AC025344 Homo sapi
	487	AC145778	14	174987	0.6	24	AC145778 Sus scrof
	488	AC137657	14	175005	0.6	24	AC137657 Sus scrof
	489	AC137657	14	175005	0.6	24	AC137657 Sus scrof
	490	AC069021	8	175464	0.6	24	AC069021 Homo sapi
	491	AC009863	14	175550	0.6	24	AC009863 Homo sapi
	492	AC012149	14	176155	0.6	24	AC012149 Homo sapi
	493	AC092053	8	176593	0.6	24	AC092053 Homo sapi
	494	AC016732	8	176741	0.6	24	AC016732 Homo sapi
	495	AC138562	14	177051	0.6	24	AC138562 Sus scrof
	496	BX470219	5	177086	0.6	24	BX470219 Zebrafish
	497	AC166881	14	177675	0.6	24	AC166881 Oryctolag
	498	AC104330	9	178219	0.6	24	AC104330 Homo sapi
	499	AC114629	9	178437	0.6	24	AC114629 Mus muscu
	500	CR376771	5	178445	0.6	24	CR376771 Zebrafish
c	501	CR956370	14	178648	0.6	24	CR956370 Sus scrof
c	502	CR956370	14	178648	0.6	24	CR956370 Sus scrof
	503	AC140968	14	179158	0.6	24	AC140968 Sus scrof
	504	AC026871	14	179237	0.6	24	AC026871 Homo sapi
	505	AC150168	14	180146	0.6	24	AC150168 Gallus ga
	506	AC154595	9	180529	0.6	24	AC154595 Mus muscu
c	507	AC145073	9	180689	0.6	24	AC145073 Homo sapi
c	508	AC160467	9	181197	0.6	24	AC160467 Mus muscu
c	509	AC146968	14	181244	0.6	24	AC146968 Sus scrof
c	510	BX088591	5	181336	0.6	24	BX088591 Zebrafish
c	511	AC021420	14	181605	0.6	24	AC021420 Homo sapi
c	512	AC107068	8	181804	0.6	24	AC107068 Homo sapi
	513	AC151395	14	181922	0.6	24	AC151395 Sus scrof
c	514	AC122156	14	181922	0.6	24	AC122156 Sus scrof
	515	AC160777	14	183163	0.6	24	AC160777 Bos tauru
	516	AC098815	14	183521	0.6	24	AC098815 Sus scrof
	517	AC073438	14	183567	0.6	24	AC073438 Homo sapi
c	518	CT932062	14	184157	0.6	24	CT932062 Danio rer
	519	CT009693	14	184995	0.6	24	CT009693 Sus scrof
	520	AC021975	14	185081	0.6	24	AC021975 Homo sapi
	521	AC097352	14	185954	0.6	24	AC097352 Canis fam
c	522	AC166221	14	186090	0.6	24	AC166221 Sus scrof
	523	AC138066	14	186393	0.6	24	AC138066 Pan trogl
	524	AC097589	14	186605	0.6	24	AC097589 Sus scrof
	525	AC155643	14	186730	0.6	24	AC155643 Mus muscu
c	526	CNS0000E	8	187480	0.6	24	AL049835 Human chr
c	527	CR956427	14	187564	0.6	24	CR956427 Sus scrof
c	528	CR974434	14	187800	0.6	24	CR974434 Sus scrof
c	529	CR974434	14	188449	0.6	24	CR974434 Sus scrof

Flag	No.	Count	Position	Score	Len	Accession	Organism
c	530	14	188515	0.6	24	AC102531	Mus muscu
c	531	8	188725	0.6	24	AC148700	Macaca mu
c	532	14	189501	0.6	24	AC105436	Sus scrof
c	533	14	190799	0.6	24	CT025537	Mus muscu
c	534	9	191726	0.6	24	AC115026	Mus muscu
c	535	8	191916	0.6	24	AC092139	Homo sapi
c	536	14	191932	0.6	24	AC095027	Canis fam
c	537	9	192952	0.6	24	AC158623	Mus muscu
c	538	14	192952	0.6	24	AC118028	Mus muscu
c	539	14	193317	0.6	24	AC026966	Homo sapi
c	540	8	193908	0.6	24	AC098645	Papio anu
c	541	14	193988	0.6	24	AC151182	Rattus no
c	542	14	194130	0.6	24	AC153101	Sus scrof
c	543	14	194183	0.6	24	AC026010	Homo sapi
c	544	8	194995	0.6	24	AC146428	Pan trogl
c	545	14	195159	0.6	24	AC102500	Mus muscu
c	546	14	195323	0.6	24	AC026612	Homo sapi
c	547	9	195413	0.6	24	AC068912	Mus muscu
c	548	14	196798	0.6	24	AC152196	Bos tauru
c	549	8	196859	0.6	24	AC087277	Homo sapi
c	550	8	197019	0.6	24	AC104435	Homo sapi
c	551	14	197210	0.6	24	AC012270	Homo sapi
c	552	9	197310	0.6	24	BX005240	Mouse DNA
c	553	8	197425	0.6	24	AC016776	Homo sapi
c	554	8	197621	0.6	24	AC092809	Homo sapi
c	555	14	198568	0.6	24	AC016754	Homo sapi
c	556	14	198572	0.6	24	AC161895	Bos tauru
c	557	9	198752	0.6	24	BX957279	Zebrafish
c	558	9	199694	0.6	24	AC154401	Mus muscu
c	559	8	199914	0.6	24	BS000009	Pan trogl
c	560	14	200248	0.6	24	AC145063	Pan trogl
c	561	9	201051	0.6	24	AC126426	Mus muscu
c	562	14	201375	0.6	24	AC139789	Homo sapi
c	563	14	201676	0.6	24	AC105367	Sus scrof
c	564	14	201680	0.6	24	AC163943	Bos tauru
c	565	9	202735	0.6	24	AC147107	Mus muscu
c	566	14	202735	0.6	24	AC159225	Mus muscu
c	567	14	202998	0.6	24	AC072058	Homo sapi
c	568	9	203402	0.6	24	AC159911	Mus muscu
c	569	14	204193	0.6	24	AC136884	Sus scrof
c	570	9	204251	0.6	24	AC108430	Mus muscu
c	571	14	204331	0.6	24	CR974477	Sus scrof
c	572	5	205265	0.6	24	AC146621	Otolemur
c	573	9	206042	0.6	24	BX005225	Zebrafish
c	574	9	206275	0.6	24	AC148004	Mus muscu
c	575	14	206778	0.6	24	CT009690	Sus scrof
c	576	9	207791	0.6	24	AC102501	Mus muscu
c	577	8	208067	0.6	24	AC146508	Pan trogl
c	578	14	208430	0.6	24	AC027641	Homo sapi
c	579	8	210791	0.6	24	CNS01DV7	Human chr
c	580	8	211735	0.6	24	AC091564	Homo sapi
c	581	14	214578	0.6	24	AC102217	Mus muscu
c	582	14	214581	0.6	24	AC162042	Bos tauru
c	583	4	215342	0.6	24	AC149292	Sus scrof
c	584	14	215987	0.6	24	AC134464	Mus muscu
c	585	14	216824	0.6	24	AC163705	Gallus ga
c	586	14	218379	0.6	24	AC110703	Rattus no
c	587	14	221701	0.6	24	AC152603	Bos tauru
c	588	14	221771	0.6	24	AC162998	Bos tauru
c	589	14	222623	0.6	24	AC097872	Rattus no
c	590	14	223478	0.6	24	AC106224	Rattus no
c	591	9	223552	0.6	24	AC124316	Mus muscu
c	592	9	223728	0.6	24	AC135443	Rattus no
c	593	14	224735	0.6	24	AC132661	Rattus no
c	594	9	226857	0.6	24	CT009542	Sus scrof
c	595	14	226904	0.6	24	AC111606	Rattus no
c	596	5	227420	0.6	24	CR788254	Zebrafish
c	597	14	228327	0.6	24	AL844514	Zebrafish
c	598	9	228925	0.6	24	AC162604	Bos tauru
c	599	14	229020	0.6	24	CR974572	Sus scrof
c	600	9	230409	0.6	24	AL772187	Mouse DNA
c	601	14	230632	0.6	24	AC111363	Rattus no
c	602	14	230936	0.6	24	AC099285	Rattus no

Flag	No.	Count	Position	Score	Len	Accession	Organism
c	603	14	231718	0.6	24	AC109552	Rattus no
c	604	14	231785	0.6	24	AC094057	Rattus no
	605	9	232275	0.6	24	AC129544	Mus muscu
c	606	14	233407	0.6	24	AC129452	Rattus no
c	607	14	233576	0.6	24	AC113797	Rattus no
	608	9	233924	0.6	24	AC134579	Mus muscu
c	609	14	235407	0.6	24	AC094280	Rattus no
c	610	14	235783	0.6	24	AC134202	Rattus no
c	611	14	238079	0.6	24	AC096000	Rattus no
c	612	14	238113	0.6	24	AC094216	Rattus no
	613	9	239053	0.6	24	AC102568	Mus muscu
c	614	14	240364	0.6	24	AC114875	Rattus no
c	615	14	241006	0.6	24	AC152096	Bos tauru
c	616	14	241531	0.6	24	AC122959	Rattus no
c	617	14	241765	0.6	24	AC132557	Rattus no
c	618	14	244538	0.6	24	AC105696	Rattus no
c	619	14	245004	0.6	24	AC119106	Rattus no
c	620	14	245565	0.6	24	AC157232	Bos tauru
c	621	14	246654	0.6	24	AC151223	Bos tauru
c	622	14	246746	0.6	24	AC121627	Rattus no
	623	9	247089	0.6	24	AC073947	Mus muscu
c	624	14	247271	0.6	24	AC163918	Bos tauru
c	625	14	247786	0.6	24	AC098752	Rattus no
c	626	14	248888	0.6	24	AC152225	Bos tauru
c	627	14	249287	0.6	24	AC142252	Mus muscu
c	628	14	250189	0.6	24	AC118814	Rattus no
	629	2	253394	0.6	24	AE014833	Plasmodiu
c	630	14	255998	0.6	24	AC125769	Rattus no
c	631	14	256715	0.6	24	AC117146	Rattus no
c	632	14	260809	0.6	24	AC126820	Rattus no
c	633	14	261632	0.6	24	AC111591	Rattus no
c	634	14	265185	0.6	24	AC117637	Mus muscu
c	635	14	268715	0.6	24	AC121488	Rattus no
c	636	14	269794	0.6	24	AC127082	Rattus no
c	637	14	270706	0.6	24	AC128862	Rattus no
c	638	14	270991	0.6	24	AC136210	Gallus ga
c	639	14	272655	0.6	24	AC160731	Bos tauru
c	640	14	272655	0.6	24	CR974460	Sus scrof
	641	2	287397	0.6	24	AE003738	Drosophil
c	642	14	294682	0.6	24	AC151287	Mus muscu
c	643	14	296131	0.6	24	AL928718	Mus muscu
c	644	14	328252	0.6	24	AC096000	Rattus no
c	645	6	23	0.6	23	CQ785842	Sequence
	646	6	23	0.6	23	AR482299	Sequence
	647	6	23	0.6	23	AR482308	Sequence
	648	6	23	0.6	23	AX203605	Sequence
	649	6	23	0.6	23	AX613835	Sequence
c	650	10	201	0.6	23	BV199973	sqnm20284
c	651	10	292	0.6	23	BV208193	sqnm22575
	652	10	301	0.6	23	BV364106	S231P673R
	653	10	358	0.6	23	AB152615	Homo sapi
	654	8	421	0.6	23	AB007148	Homo sapi
	655	6	421	0.6	23	AX401155	Sequence
	656	6	458	0.6	23	AX827297	Sequence
	657	10	460	0.6	23	AL159264	STS from HSJ09A7
c	658	6	481	0.6	23	CQ524582	Sequence
	659	6	505	0.6	23	BD132668	Secreted
	660	10	512	0.6	23	BV394135	S243P6220
	661	2	512	0.6	23	AF457562	Anopheles
	662	10	561	0.6	23	BV215769	S233P6418
	663	10	584	0.6	23	G84464	S208P6561RH
	664	10	610	0.6	23	BV426869	S237P6238
	665	10	640	0.6	23	BV065314	S212P6583
	666	10	658	0.6	23	BV356785	S231P6137
	667	10	662	0.6	23	BV316293	S236P6395
	668	10	676	0.6	23	BV023951	S212P6643
	669	10	686	0.6	23	BV222331	S233P6276
	670	4	688	0.6	23	AY285260	Sus scrof
	671	10	697	0.6	23	BV578115	G591P6112
	672	10	718	0.6	23	BV272954	S235P682R
c	673	15		0.6	23	AF310871	Betula pe
c	674	10		0.6	23	BV055221	S212P6024
c	675	10		0.6	23	BV077076	S212P6796

Row		23	0.6	Pos	N	Accession	Description
676		23	0.6	740	10	BV609693	BV609693 S215P6131
677	c	23	0.6	749	10	BV646875	BV646875 S217P6017
678	c	23	0.6	749	10	BV102732	BV102732 MARC 2331
679		23	0.6	756	10	BV365552	BV365552 S231P6338
680	c	23	0.6	776	4	SSCKIIB	X56503 Porcine CKI
681		23	0.6	796	10	BV588904	BV588904 G591P6386
682	c	23	0.6	801	9	BC027529	BC027529 Mus muscu
683	c	23	0.6	804	9	BC038674	BC038674 Mus muscu
684		23	0.6	835	9	AF097438	AF097438 Mus muscu
685		23	0.6	838	10	BV571202	BV571202 G591P6210
686	c	23	0.6	854	9	BV567881	BV567881 qdn91a10.
687		23	0.6	889	9	BC089464	BC089464 Rattus no
688	c	23	0.6	890	9	BC088027	BC088027 Xenopus t
689	c	23	0.6	925	5	BV474932	BV474932 G591P6292
690		23	0.6	937	10	BC027755	BC027755 Mus muscu
691		23	0.6	965	9	BC024400	BC024400 Mus muscu
692	c	23	0.6	1023	9	AY058495	AY058495 Drosophil
693		23	0.6	1046	2	AY065275	AY065275 Arabidops
694		23	0.6	1061	15	AK115293	AK115293 Ciona int
695		23	0.6	1205	9	BC058805	BC058805 Mus muscu
696	c	23	0.6	1229	8	BC032031	BC032031 Homo sapi
697		23	0.6	1319	9	BC100465	BC100465 Mus muscu
698	c	23	0.6	1320	5	BC094397	BC094397 Xenopus l
699		23	0.6	1342	9	AF180805	AF180805 Mus muscu
700		23	0.6	1421	9	AB056757	AB056757 Macaca fa
701	c	23	0.6	1460	8	CQ976593	CQ976593 Sequence
702		23	0.6	1492	6	AY547296	AY547296 Homo sapi
703		23	0.6	1492	8	AF247788	AF247788 Homo sapi
704	c	23	0.6	1566	4	AY48494S9	AY48494S9 Sus scrof
705		23	0.6	1567	8	BC007548	BC007548 Homo sapi
706	c	23	0.6	1610	8	BC033123	BC033123 Homo sapi
707		23	0.6	1610	8	BC015353	BC015353 Homo sapi
708		23	0.6	1642	15	BT002864	BT002864 Arabidops
709		23	0.6	1666	4	AY864618	AY864618 Sus scrof
710	c	23	0.6	1684	9	BC062053	BC062053 Rattus no
711		23	0.6	1780	9	BC027238	BC027238 Mus muscu
712		23	0.6	1821	9	AB116526	AB116526 Rattus no
713	c	23	0.6	1947	8	BX537781	BX537781 Homo sapi
714	c	23	0.6	1977	8	HSM805868	HSM805868 Homo sapi
715	c	23	0.6	1980	9	BC004042	BC004042 Mus muscu
716		23	0.6	1983	8	BC003063	BC003063 Homo sapi
717		23	0.6	1985	9	BC079044	BC079044 Rattus no
718		23	0.6	1991	8	AK128768	AK128768 Homo sapi
719		23	0.6	2015	8	AB051127	AB051127 Macaca fa
720		23	0.6	2052	9	BC079996	BC079996 Rattus no
721	c	23	0.6	2337	9	AY061276	AY061276 Drosophil
722		23	0.6	2424	4	HSU60669	U60669 Human 1 alp
723		23	0.6	2433	9	BC022143	BC022143 Mus muscu
724	c	23	0.6	2458	8	BC026615	BC026615 Homo sapi
725	c	23	0.6	2472	9	BC013552	BC013552 Mus muscu
726		23	0.6	2479	5	BC091060	BC091060 Xenopus t
727		23	0.6	2543	8	BC010144	BC010144 Homo sapi
728	c	23	0.6	2645	9	AB107226	AB107226 Cricetulu
729		23	0.6	2654	9	BC051254	BC051254 Mus muscu
730		23	0.6	2681	8	BC062011	BC062011 Rattus no
731	c	23	0.6	2723	9	AB178966	AB178966 Macaca fa
732		23	0.6	2778	13	MMU401376	MMU401376 Mus muscu
733	c	23	0.6	2790	8	LFDPL3	D10830 La France d
734		23	0.6	2798	8	BC038220	BC038220 Homo sapi
735	c	23	0.6	2843	9	BT011496	BT011496 Drosophil
736		23	0.6	3145	9	BC062011	BC062011 Rattus no
737	c	23	0.6	3197	9	AF041431	AF041431 Mus muscu
738		23	0.6	3382	5	RATCIARCPT	L14617 Rattus norv
739	c	23	0.6	3456	15	AK120832	AK120832 Oryza sat
740		23	0.6	3501	15	AK121669	AK121669 Oryza sat
741		23	0.6	3510	5	AJ719395	AJ719395 Gallus ga
742	c	23	0.6	3741	5	AB185847	AB185847 Oryzias l
743		23	0.6	3802	8	BC096750	BC096750 Homo sapi
744	c	23	0.6	3894	9	BC053925	BC053925 Mus muscu
745		23	0.6	4117	9	BC063078	BC063078 Mus muscu
746	c	23	0.6	4399	15	AK120928	AK120928 Oryza sat
747		23	0.6	5107	8	HS283334	Z83334 H.sapiens R
748		23	0.6	5529	8	HSRPS3AGE	X87373 Homo sapien

Row		23	0.6	Pos	N	Accession	Description
749	c	23	0.6	5565	6	AX345165	AX345165 Sequence
750	c	23	0.6	9235	9	MMU32107	U32107 Mus muscu
751	c	23	0.6	9371	2	AY600247	AY600247 Physarum
752		23	0.6	10480	6	AX347103	AX347103 Sequence
753		23	0.6	11012	4	AY044189	AY044189 Sus scrof
754	c	23	0.6	12486	8	AC073439	AC073439 Homo sapi
755		23	0.6	12779	2	AE001381	AE001381 Plasmodiu
756		23	0.6	14117	6	AX331935	AX331935 Sequence
757		23	0.6	14117	8	HSHHA2GEN	X90761 Homo sapien
758	c	23	0.6	20486	6	AX281500	AX281500 Sequence
759		23	0.6	23369	4	BX548168	BX548168 Pig DNA s
760	c	23	0.6	28160	15	SSCRCRXR1	Z49778 S.scrofa ge
761		23	0.6	32196	8	AP006092	AP006092 Lotus cor
762	c	23	0.6	34245	8	AC110797	AC110797 Homo sapi
763		23	0.6	35376	6	CQ869707	CQ869707 Sequence
764		23	0.6	41613	5	BX890563	BX890563 Zebrafish
765		23	0.6	42210	8	AC004790	AC004790 Homo sapi
766	c	23	0.6	45154	8	AC112724	AC112724 Homo sapi
767		23	0.6	45653	14	AC164871	AC164871 Sorex ara
768		23	0.6	48042	5	BX323016	BX323016 Zebrafish
769		23	0.6	49705	9	AC020217	AC020217 Drosophil
770		23	0.6	50768	8	AC087750	AC087750 Homo sapi
771	c	23	0.6	53301	8	BS000149	BS000149 Pan trogl
772		23	0.6	54710	14	AC164791	AC164791 Bos tauru
773		23	0.6	58864	9	AL928833	AL928833 Mouse DNA
774	c	23	0.6	60079	15	AP000371	AP000371 Arabidops
775		23	0.6	61697	8	AL596284	AL596284 Mouse DNA
776		23	0.6	62102	8	AL354933	AL354933 Human DNA
777	c	23	0.6	62868	4	CR974593	CR974593 Pig DNA s
778		23	0.6	62918	8	AC016799	AC016799 Homo sapi
779	c	23	0.6	63761	14	AL160289	AL160289 Human DNA
780	c	23	0.6	64477	14	AC117737	AC117737 Mus muscu
781		23	0.6	67124	14	AC117564	AC117564 Mus muscu
782	c	23	0.6	67718	8	AC026415	AC026415 Homo sapi
783		23	0.6	69060	14	AC100706	AC100706 Mus muscu
784		23	0.6	69699	8	AC005196	AC005196 Homo sapi
785	c	23	0.6	69784	4	SSC504726	SSC504726 Sus scrof
786		23	0.6	72382	5	BX537312	BX537312 Zebrafish
787		23	0.6	72354	8	AC110082	AC110082 Homo sapi
788		23	0.6	77162	4	AL773521	AL773521 Pig DNA s
789		23	0.6	77190	8	AC112694	AC112694 Homo sapi
790		23	0.6	78592	14	AL161427	AL161427 Human DNA
791		23	0.6	79003	14	AC026589	AC026589 Homo sapi
792		23	0.6	80015	9	BX119960	BX119960 Mouse DNA
793		23	0.6	80696	8	AC110085	AC110085 Homo sapi
794		23	0.6	81357	8	HS384021	Z85995 Human DNA s
795		23	0.6	81971	8	AC005792	AC005792 Homo sapi
796	c	23	0.6	82771	14	HS593C16	HS593C16 Homo sapi
797		23	0.6	83029	14	AC011953	AC011953 Homo sapi
798		23	0.6	84495	8	AC022127	AC022127 Homo sapi
799		23	0.6	84984	9	BX537352	BX537352 Mouse DNA
800	c	23	0.6	85712	14	AC165468	AC165468 Bos tauru
801	c	23	0.6	90877	8	AC141556	AC141556 Homo sapi
802	c	23	0.6	91912	8	AC069436	AC069436 Homo sapi
803	c	23	0.6	92245	15	AL589935	AL589935 Human DNA
804	c	23	0.6	93578	8	AC073968	AC073968 Homo sapi
805	c	23	0.6	93800	8	HSAC000055	HSAC000055 Human PAC
806		23	0.6	94387	8	HSJ37O21	HSJ37O21 Human DNA
807		23	0.6	94647	8	AL136532	AL136532 Human DNA
808		23	0.6	94656	15	AC145372	AC145372 Medicago
809		23	0.6	94893	15	AC138579	AC138579 Medicago
810		23	0.6	95356	8	AC064860	AC064860 Homo sapi
811		23	0.6	95555	14	AL139112	AL139112 Human DNA
812		23	0.6	96206	8	AL117351	AL117351 Human Chr
813		23	0.6	96792	8	AC000379	AC000379 Human Chr
814		23	0.6	97325	8	AC013283	AC013283 Homo sapi
815		23	0.6	98765	9	U95741	U95741 Human chrom
816		23	0.6	101224	14	AL928836	AL928836 Mouse DNA
817	c	23	0.6	102298	14	AC165807	AC165807 Bos tauru
818		23	0.6	103004	9	AC106750	AC106750 Mouse DNA
819		23	0.6	103510	9	AL671671	AL671671 Mouse DNA
820	c	23	0.6	104492	14	AL031315	AL031315 Human DNA
821		23	0.6	104492	14	HS171H20	AP007944 Lotus cor

#	c	score	eval	len	n	id	description
822		23	0.6	104799	14	AC161817_8	Continuation (9 of / Homo sapi
823		23	0.6	105171	8	AY663410	AY663410 Homo sapi
824		23	0.6	106857	15	AC157777	AC157777 Medicago
825		23	0.6	107044	14	AC142570	AC142570 Gallus ga
826		23	0.6	107132	14	AC312914	AF312914 Homo sapi
827	c	23	0.6	107593	14	AC107484	AC107484 Human DNA
828	c	23	0.6	107910	6	CS086315	CS086315 Sequence
829	c	23	0.6	107910	8	HUAC002394	AC002394 Human Chr
830	c	23	0.6	109441	8	AY663404	AY663404 Homo sapi
831		23	0.6	110000	1	AE017244_06	Continuation (7 of
832		23	0.6	110000	8	BA000037_30	Continuation (31 o
833		23	0.6	110000	8	AB128049_03	Continuation (4 of
834		23	0.6	110000	8	AB128049_04	Continuation (5 of
835		23	0.6	110000	8	AB128049_05	Continuation (6 of
836		23	0.6	110000	14	AC109710_3	Continuation (4 of
837		23	0.6	110000	14	AC140148_1	Continuation (2 of
838		23	0.6	110000	14	AC145312_2	Continuation (3 of
839		23	0.6	110000	14	BX119990_1	Continuation (2 of
840		23	0.6	110000	14	CR974431_0	CR974431 Sus scrof
841		23	0.6	110000	14	CR974431_3	Continuation (4 of
842		23	0.6	110000	15	AP008217_007	Continuation (8 of
843		23	0.6	110000	15	AP008217_218	Continuation (219
844		23	0.6	110000	15	AP008207_062	Continuation (63 o
845		23	0.6	110000	15	AP008209_217	Continuation (218
846		23	0.6	110000	15	AP008213_219	Continuation (220
847		23	0.6	110541	8	AC107061	AC107061 Homo sapi
848		23	0.6	112259	14	AC026579	AC026579 Homo sapi
849		23	0.6	112259	14	AC026579	AC026579 Homo sapi
850		23	0.6	112568	8	AC073886	AC073886 Homo sapi
851		23	0.6	113114	8	AC079400	AC079400 Homo sapi
852		23	0.6	114156	5	AL590390	AL590390 Mouse DNA
853		23	0.6	114180	5	CR936359	CR936359 Zebrafish
854		23	0.6	116609	5	BX511244	BX511244 Zebrafish
855		23	0.6	117872	8	AL162396	AL162396 Human DNA
856		23	0.6	118276	8	AC004148	AC004148 Homo sapi
857		23	0.6	118404	4	AL773591	AL773591 Pig DNA s
858		23	0.6	120180	5	BX323592	BX323592 Zebrafish
859	c	23	0.6	120989	14	AC156746	AC156746 Bos tauru
860	c	23	0.6	121223	15	AC123514	AC123514 Oryza sat
861	c	23	0.6	121780	14	HS774I24	AL031290 Human DNA
862		23	0.6	121936	9	AL691513	AL691513 Mouse DNA
863		23	0.6	122167	5	BX511009	BX511009 Zebrafish
864		23	0.6	122825	8	AC108067	AC108067 Homo sapi
865		23	0.6	123782	8	HSDJ756N5	AL132825 Human DNA
866		23	0.6	125042	14	AC164944	AC164944 Sus scrof
867	c	23	0.6	126867	8	AC022443	AC022443 Homo sapi
868	c	23	0.6	126933	14	AC148351	AC148351 Sorex ara
869		23	0.6	127234	4	AB206998	AB206998 Sus scrof
870		23	0.6	128073	9	AL772151	AL772151 Mouse DNA
871		23	0.6	128150	14	AC148748	AC148748 Sorex ara
872		23	0.6	128243	14	AC162129	AC162129 Loxodonta
873		23	0.6	128990	9	AC113344	AC113344 Homo sapi
874	c	23	0.6	129264	4	CR956409	CR956409 Pig DNA s
875		23	0.6	129624	14	BX296540	BX296540 Sus scrof
876	c	23	0.6	130117	9	RN394C12	CR937051 Rattus no
877		23	0.6	130267	14	AC010597	AC010597 Homo sapi
878		23	0.6	130988	8	HS364I22	AL031012 Human DNA
879		23	0.6	131005	14	AC150890	AC150890 Medicago
880		23	0.6	131621	14	AC166224	AC166224 Sorex ara
881		23	0.6	131860	9	AC133163	AC133163 Mus muscu
882		23	0.6	132150	8	AC005586	AC005586 Homo sapi
883		23	0.6	132421	9	AC116569	AC116569 Mus muscu
884		23	0.6	133508	14	AC160877	AC160877 Atelerix
885		23	0.6	133836	8	AC010343	AC010343 Homo sapi
886		23	0.6	133838	8	AC105410	AC105410 Homo sapi
887		23	0.6	134926	8	AP001347	AP001347 Homo sapi
888		23	0.6	135412	14	AC148279	AC148279 Sorex ara
889		23	0.6	135508	14	AC120215	AC120215 Sus scrof
890		23	0.6	135756	14	AC158274	AC158274 Atelerix
891		23	0.6	136646	14	AC135220	AC135220 Sus scrof
892		23	0.6	137001	8	AP001005	AP001005 Homo sapi
893	c	23	0.6	137001	14	AC104678	AC104678 Sus scrof
894		23	0.6	137371	9	AC115124	AC115124 Mus muscu

#	c	score	eval	len	n	id	description
895	c	23	0.6	137520	4	ECA459965	AJ459965 Equus cab
896	c	23	0.6	137737	8	AC010378	AC010378 Homo sapi
897		23	0.6	138783	8	HS564M11	AL035409 Human DNA
898	c	23	0.6	139771	15	AC135564	AC135564 Oryza sat
899	c	23	0.6	140112	14	AC148127	AC148127 Otolemur
900	c	23	0.6	140773	14	HSDJ012208	AL096678 Human DNA
901		23	0.6	141200	14	AC012227	AC012227 Homo sapi
902		23	0.6	141293	14	AC104563	AC104563 Homo sapi
903		23	0.6	141380	14	AP004337	AP004337 Oryza sat
904		23	0.6	141620	14	AC163972	AC163972 Homo sapi
905		23	0.6	142446	15	AC142444	AC142444 Homo sapi
906		23	0.6	142730	14	AP005126	AP005126 Oryza sat
907		23	0.6	142759	14	AC108186	AC108186 Felis cat
908	c	23	0.6	142790	14	AC163267	AC163267 Rhinoloph
909	c	23	0.6	142903	14	AC009616	AC009616 Homo sapi
910	c	23	0.6	142971	9	AC117253	AC117253 Mus muscu
911	c	23	0.6	143644	8	AC020629	AC020629 Homo sapi
912	c	23	0.6	143750	14	AC149903	AC149903 Strongylo
913		23	0.6	143947	8	AC109999	AC109999 Homo sapi
914		23	0.6	144026	14	AC012462	AC012462 Homo sapi
915		23	0.6	144034	14	AC165403	AC165403 Callicebu
916		23	0.6	144446	14	AC069244	AC069244 Homo sapi
917		23	0.6	144500	8	AC146219	AC146219 Pan trogl
918		23	0.6	145417	14	AC010231	AC010231 Homo sapi
919		23	0.6	145633	14	AC138169	AC138169 Sus scrof
920		23	0.6	146455	8	BS000107	BS000107 Pan trogl
921		23	0.6	147021	8	AC127512	AC127512 Homo sapi
922		23	0.6	147288	14	AC006501	AC006501 Homo sapi
923		23	0.6	147601	8	AL355812	AL355812 Human DNA
924		23	0.6	147854	14	AC012655	AC012655 Homo sapi
925		23	0.6	147862	8	AC021422	AC021422 Homo sapi
926		23	0.6	147978	8	AC108922	AC108922 Homo sapi
927		23	0.6	148468	8	AL137781	AL137781 Human DNA
928		23	0.6	148620	14	AL355882	AL355882 Homo sapi
929		23	0.6	149180	9	BX890605	BX890605 Mouse DNA
930		23	0.6	149188	8	AL035688	HS173A13 Human DNA
931		23	0.6	149494	8	AC148701	AC148701 Macaca mu
932	c	23	0.6	149562	14	AC114781	AC114781 Homo sapi
933	c	23	0.6	149602	14	AC161411	AC161411 Mus muscu
934		23	0.6	149859	14	AC143353	AC143353 Homo sapi
935		23	0.6	150005	14	AC148356	AC148356 Sorex ara
936		23	0.6	150022	8	AC110667	AC110667 Canis fam
937		23	0.6	150122	8	AL450344	AL450344 Human DNA
938		23	0.6	150128	9	AC122536	AC122536 Mus muscu
939		23	0.6	150159	9	BX088567	BX088567 Mouse DNA
940		23	0.6	150400	14	AC166227	AC166227 Sorex ara
941	c	23	0.6	150649	4	AB192510	AB192510 Sus scrof
942	c	23	0.6	151194	9	AC122911	AC122911 Mus muscu
943	c	23	0.6	151383	9	AC102918	AC102918 Mus muscu
944		23	0.6	151405	4	AC112988	AC112988 Pig DNA s
945		23	0.6	151523	15	CR956388	CR956388 Oryza sat
946		23	0.6	151858	14	AP004261	AP004261 Oryza sat
947	c	23	0.6	152058	5	AC147901	AC147901 Xenopus t
948		23	0.6	152211	9	AC091756	AC091756 Sus scrof
949		23	0.6	152279	4	AJ251829	SSC251829 Sus scrof
950	c	23	0.6	153745	9	AC155915	AC155915 Mus muscu
951	c	23	0.6	153745	4	AC117959	AC117959 Rattus no
952		23	0.6	153745	4	AY587061	AY587061 Sus scrof
953		23	0.6	153745	4	AY587061	AY587061 Sus scrof
954		23	0.6	153857	14	AC022451	AC022451 Homo sapi
955		23	0.6	153866	8	AC022507	AC022507 Homo sapi
956		23	0.6	154101	14	AF336380	AF336380 Mus muscu
957		23	0.6	154513	8	AC009307	AC009307 Homo sapi
958		23	0.6	154775	14	AC136885	AC136885 Sus scrof
959		23	0.6	154954	14	AC145047	AC145047 Sus scrof
960		23	0.6	155263	14	CR974570	CR974570 Sus scrof
961		23	0.6	155332	14	BX927284	BX927284 Danio rer
962		23	0.6	155362	14	AC040900	AC040900 Homo sapi
963	c	23	0.6	155367	14	AC148434	AC148434 Sorex ara
964	c	23	0.6	155512	14	AC154778	AC154778 Mus muscu
965	c	23	0.6	155663	14	AC148909	AC148909 Otolemur
966	c	23	0.6	155710	14	AC152857	AC152857 Atelerix
967		23	0.6	155710	4	AC092875	AC092875 Sus scrof

Qy 121 GATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGTCGGATGGAGGGATGGGACC 180
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Db 121 GATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGTCGTCGGATGGAGGGATGGGACC 180

Qy 181 ATGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAATTTAAAGATCAT 240
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Db 181 ATGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAATTTAAAGATCAT 240

Qy 241 GCCAGGCCGCTGAAAGGCACAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTAC 300
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Db 241 GCCAGGCCGCTGAAAGGCACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTAC 300

Qy 301 CAAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGC 360
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Db 301 CAAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGC 360

Qy 361 AGCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATG 420
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Db 361 AGCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATG 420

Qy 421 TGCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAG 480
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Db 421 TGCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAG 480

Qy 481 AGGTTTGTGGCAGGGGCTCTGGGTCCAGACTAATAAGACACTCTCTGTCCCCATCTGTG 540
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Db 481 AGGTTTGTGGCAGGGGCTCTGGGTCCAGACTAATAAGACACTCTCTGTCCCCATCTGTG 540

Qy 541 GAAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGTGAAGCATACCAAGAGCAG 600
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Db 541 GAAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGTGAAGCATACCAAGAGCAG 600

Qy 601 GCCAAAGGACTTCTGGATGCAGCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCC 660
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Db 601 GCCAAAGGACTTCTGGATGCAGCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCC 660

Qy 661 GCCAATGCCAAGGCACCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCC 720
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Db 661 GCCAATGCCAAGGCACCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCC 720

Qy 721 CGGCTATCTTTATTTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTTCCGGACAG 780
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Db 721 CGGCTATCTTTATTTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTTCCGGACAG 780

Qy 781 ACAGGAGGAGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAT 840
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Db 781 ACAGGAGGAGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAT 840

Qy 841 TGTGCTTTGGGTGCAGTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACA 900
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Db 841 TGTGCTTTGGGTGCAGTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACA 900

Qy 901 GCCTATGTCCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAA 960
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Db 901 GCCTATGTCCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAA 960

Qy 961 ACGCCTTCTATGATGCCAAGCACCAAGGATTTTGCTATCAGGGAAGTGTCTGCAATATA 1020
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Db 961 ACGCCTTCTATGATGCCAAGCACCAAGGATTTTGCTATGATGGCTGTCTGCAATATA 1020

Qy 1021 GTTGGAGATGCTGTGGGTCAACACCAGATCATATCAGGGAATTGCTGAAGCTGTGAA 1080
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Db 1021 GTTGGAGATGCTGTGGGTCAACACCAGATCATATCAGGGAATTGCTGAAGCTGTGAA 1080

Qy 1081 AATTGTAAGCCTAGAGTTCCACCTGCTTTGAAGGACATATGTTACTGTCTGGT 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 AATTGTAAGCCTAGAGTTCCACCTGCCTTTGAAGGACATATGTTACTGTCTGGT 1140

Qy 1141 CTAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGGCCTGTAAT 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 CTAGAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGGCCTGTAAT 1200

Qy 1201 GTTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCGAGAAACATGAAGAAGCCTTG 1260

AR482278

c 968   0.6 155992 14 AC083854 AC083854 Homo sapi
c 969   0.6 155992 14 AC034184 AC034184 Homo sapi
  970   0.6 156328 14 AC148280 AC148280 Sorex ara
  971   0.6 156331 15 AC144700 AC144700 Oryza sat
  972   0.6 156678 14 AC145026 AC145026 Sus scrof
c 973   0.6 156700 14 AC027051 AC027051 Homo sapi
  974   0.6 156818 14 AC104463 AC104463 Homo sapi
  975   0.6 156945 9   AC105944 AC105944 Mus muscu
c 976   0.6 157248 9   AC002312 AC002312 Human Chr
  977   0.6 157654 14 AC091791 AC091791 Sus scrof
c 978   0.6 157870 4   AB192509 AB192509 Sus scrof
  979   0.6 157965 14 AC011220 AC011220 Homo sapi
  980   0.6 158423 14 AC114299 AC114299 Homo sapi
  981   0.6 158527 14 AC027640 AC027640 Homo sapi
  982   0.6 158608 8   AC051635 AC051635 Homo sapi
  983   0.6 159150 14 AC022863 AC022863 Homo sapi
c 984   0.6 159350 14 AC136882 AC136882 Sus scrof
c 985   0.6 160429 5   BX004784 BX004784 Zebrafish
  986   0.6 160460 14 AC144692 AC144692 Sus scrof
c 987   0.6 160574 9   AC140192 AC140192 Mus muscu
  988   0.6 160831 9   AL732450 AL732450 Mouse DNA
c 989   0.6 160951 14 AC112181 AC112181 Homo sapi
  990   0.6 161180 14 AC146771 AC146771 Canis fam
  991   0.6 161309 4   AC100839 AC100839 Homo sapi
c 992   0.6 161823 4   AC097231 AC097231 Sus scrof
c 993   0.6 162029 14 AC145046 AC145046 Sus scrof
  994   0.6 162029 14 AC145046 AC145046 Sus scrof
c 995   0.6 162065 14 AC117061 AC117061 Rattus no
c 996   0.6 162111 14 AC138170 AC138170 Sus scrof
c 997   0.6 162111 14 AC138170 AC138170 Sus scrof
c 998   0.6 162405 8   AC002352 AC002352 Homo sapi
  999   0.6 162681 8   AC087835 AC087835 Pan trogl
c1000   0.6 162770 9   AC121904 AC121904 Mus muscu

ALIGNMENTS

RESULT 1
AR482278
LOCUS   AR482278   3919 bp   DNA   linear   PAT 14-MAY-2004
DEFINITION   Sequence 1 from patent US 6703197.
ACCESSION   AR482278
VERSION   AR482278.1   GI:47244567
KEYWORDS
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 3919)
  AUTHORS   Gravel,R.A., Rozen,R., LeClerc,D., Goyette,P. and Campeau,E.
  TITLE   Human methionine synthase; cloning, and methods for evaluating risk
             of neural tube defects, cardiovascular disease, and cancer
  JOURNAL   Patent: US 6703197-A 1 09-MAR-2004;
             Martinex R&D, Inc.; Montreal;
             CAX;
FEATURES   Location/Qualifiers
     source   1..3919
                     /organism="unknown"
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ORIGIN

Query Match   100.0%; Score 3919; DB 6; Length 3919;
Best Local Similarity 100.0%;
Matches 3919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCGCCCCTCTGCGCAAGGAGGAGACTCGAC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCGCCCCTCTGCGCAAGGAGGAGACTCGAC 60

Qy   61 AACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCGAAGAAAACCCTGCGG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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(DNA sequence alignment — two columns of Qy/Db aligned nucleotide sequences with position numbering)

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CDS             64..3861
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                AEAVKNCKPRVVPPATAFEGHMLLSGLBPFRIGPYTNFVNIGERCNVAGSRKFAKLIMA
                GNYBEALCVAKVQVEMGAQVLDVNMDDGMLDGPSAMTRFCNLIASBPDIAKVPLCIDS
                SNPAVIBAGLKCCOGKCIVNSISLKEGEDDFLEKARKIKKYGAAMVVNAFPDBEQOATE
                TDTKIRVCTRAYHILVKKLGPNPNDIIFDPNILITGTGMEBHNLYAINFIHATKVIKE
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                KELIQLCEDLIWNKDPEATEKLLRYAQTQGTGKKVIQTDEWRNGPVEERLEYALVKG
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                KKAVGHLIPFMEKBREETRVLNGTVEBEDPYQGTIVLATVKGVHDIGKNIVGVVLGC
                NNFRVIDLGVMTPCDKILKAALDHKADIIGLSGLITPSLDEMIFVAKEMERLAIRIPL
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                IDWKPFFDVWQLRGKYPNRGFPKIFNDKTVGGRARKVVDDAHNMLNTLISQKKLRARG
                VVGFWPAQSIQDDIHLYABAAVPQAAEPIATFYGLRQQARKDSASTEPYYCLSDFIAP
                LHSGIRDYLGLFAVACFGVBELSKAYAEDDDYSSIMVKALGDRLAEBAFABELHERVR
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variation      2819
                /note="D919G polymorphism site; creates conversion of
                aspartic acid to glycine"
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variation      2821
                /note="mutation H920D in cblG patient; creates conversion
                of histidine to aspartic acid"
                /replace="g"
ORIGIN
Query Match             97.6%;  Score 3823;  DB 8;  Length 3917;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 3873;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy      2 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCCTGCCGCAAGGAGGAGGAGACTCGACA   61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCCTGCCGCAAGGAGGAGGAGACTCGACA   61

Qy     62 ACATGTCACCCGCTCCAAGACCTGTCGCAACCCGAAGGTCGAAGAAAACCCTGCGGG  121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 ACATGTCACCCGCTCCAAGACCTGTCGCAACCCGAAGGTCGAAGAAAACCCTGCGGG  121

Qy    122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGGGATGGGGACCA  181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGGGATGGGGACCA  181

Qy    182 TGATCCAGCGGAGAAGCTAAACGAAGCTAAACACTTCCGAGGTCAGGAATTTAAAGATCATG  241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 TGATCCAGCGGAGAAGCTAAACGAAGCTAAACACTTCCGAGGTCAGGAATTTAAAGATCATG  241

Qy    242 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC  301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC  301

Qy    302 AAATCCATAAGGAATACTTGCTGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA  361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 AAATCCATAAGGAATACTTGCTGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA  361
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Qy   3421 GACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCAGAGGCCTTTGCAGAA   3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 GACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCAGAGGCCTTTGCAGAA   3480

Qy   3481 GAGTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGAC   3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAGTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGAC   3540

Qy   3541 GTCGCGAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGGCCTCCTGCTACCCCAGC   3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 GTCGCGAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGGCCTCCTGCTACCCCAGC   3600

Qy   3601 CAGCCCGACCACACCCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACA   3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CAGCCCGACCACACCCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACA   3660

Qy   3661 GGCATTAGGTTAACAGAATCATTAGCAATGCAACTGCACCTGCTTCAGCAGTCTCAGGCCTCTAC   3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GGCATTAGGTTAACAGAATCATTAGCAATGCAACTGCACCTGCTTCAGCAGTCTCAGGCCTCTAC   3720

Qy   3721 TTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAG   3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAG   3780

Qy   3781 GATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATT   3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATT   3840

Qy   3841 TTGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCC   3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TTGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCC   3900

Qy   3901 TCAAGAAATACAACCTAG   3919
          ||||||||||||||||||
Db   3901 TCAAGAAATACAACCTAG   3919
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RESULT 2
HSU71285
LOCUS       HSU71285           3917 bp    mRNA    linear   PRI 03-APR-1997
DEFINITION  Human 5-methyltetrahydrofolate-homocysteine methyltransferase mRNA,
            complete cds.
ACCESSION   U71285
VERSION     U71285.1  GI:1923220
KEYWORDS    vitamin B12; cobalamin binding site; methionine synthase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3917)
  AUTHORS   Leclerc,D., Campeau,E., Goyette,P., Adjalla,C.E., Christensen,B.,
            Ross,M., Eydoux,P., Rosenblatt,D.S., Rozen,R. and Gravel,R.A.
  TITLE     Human methionine synthase: cDNA cloning and identification of
            mutations in patients of the cblG complementation group of
            folate/cobalamin disorders
  JOURNAL   Hum. Mol. Genet. 5 (12), 1867-1874 (1996)
   PUBMED   8968737
REFERENCE   2  (bases 1 to 3917)
  AUTHORS   Leclerc,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-SEP-1996) Human Genetics, McGill University, Montreal
            Children's Hospital - Research Institute, Place Toulon, Room 222,
            4060 Ste-Catherine West, Montreal H3Z 2Z3, Canada
COMMENT     On Apr 3, 1997 this sequence version replaced gi:1731672.
FEATURES             Location/Qualifiers
     source          1..3917
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1q43"
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The page contains a DNA sequence alignment between two sequences labeled "Qy" (query) and "Db" (database), shown in two panels. Each alignment block lists the query sequence, a match line of vertical bars ("|"), and the database sequence, with flanking position numbers.

Right panel (positions 1442–2581):

Label	Start	Sequence	End
Qy	1442	TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAGGAGGAGGACG	1501
Db	1442	TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAGGAGGAGGACG	1501
Qy	1502	ACTTCTTGGAAGGCCAGGAAGTTAAAAGTATGGAGCTGCTATGGTTGGTGTCATGGCTT	1561
Db	1502	ACTTCTTGGAAGGCCAGGAAGTTAAAAGTATGGAGCTGCTATGGTTGGTGTCATGGCTT	1561
Qy	1562	TTGATGAAGAGGACAGGCAACAGACAGAAACAGACACAAAATCAGAGTGTGCACCCGGCCT	1621
Db	1562	TTGATGAAGAGGACAGGCAACAGACAGAAACAGACACAAAATCAGAGTGTGCACCCGGCCT	1621
Qy	1622	ACCATCTGCTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA	1681
Db	1622	ACCATCTGCTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA	1681
Qy	1682	TCCTAACCATTGGGACTGGAAATGAGGAACAACTTGTATGCCATTATTTATCCATG	1741
Db	1682	TCCTAACCATTGGGACTGGAAATGAGGAACAACTTGTATGCCATTATTTATCCATG	1741
Qy	1742	CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTTCAACT	1801
Db	1742	CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTTCAACT	1801
Qy	1802	TGTCCTTCTCCTTCCGAGGAAATGGAAGCCATTCAGAGAAGCAATGCAATGCGGTTTTCTTT	1861
Db	1802	TGTCCTTCTCCTTCCGAGGAAATGGAAGCCATTCAGAGAAGCAATGCAATGCGGTTTTCTTT	1861
Qy	1862	ACCATGCAATCAAGTCTGGCATGGAAGTAGTGAATGCTGAAGACTCCCTGTGT	1921
Db	1862	ACCATGCAATCAAGTCTGGCATGGAAGTAGTGAATGCTGAAGACTCCCTGTGT	1921
Qy	1922	ATGATGATATCCATAAGGAACTTCTGCAGTCTGTGAAGATCTCATCTGGAATAAAGACC	1981
Db	1922	ATGATGATATCCATAAGGAACTTCTGCAGTCTGTGAAGATCTCATCTGGAATAAAGACC	1981
Qy	1982	CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAG	2041
Db	1982	CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAG	2041
Qy	2042	TCATTCAGACTGATGAGTGGAGAAATGGCCCTTGAGTGTGTCGAGAGATGCCCTTG	2101
Db	2042	TCATTCAGACTGATGAGTGGAGAAATGGCCCTTGAGTGTGTCGAGAGATGCCCTTG	2101
Qy	2102	TGAAGGGCATTGAAAAACATATATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAA	2161
Db	2102	TGAAGGGCATTGAAAAACATATATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAA	2161
Qy	2162	AATATCCCGACCCTCTCAATATAATTGAAGGACCCCTGATGAATGAAAATTGTTG	2221
Db	2162	AATATCCCGACCCTCTCAATATAATTGAAGGACCCCTGATGAATGAAAATTGTTG	2221
Qy	2222	GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA	2281
Db	2222	GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA	2281
Qy	2282	TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAGAGAAACCAGAG	2341
Db	2282	TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAGAGAAACCAGAG	2341
Qy	2342	TGCTTAACGGCACAGTAGAAGAGGACACCCTTACCAGGGCACCATCGTGTGCCACTG	2401
Db	2342	TGCTTAACGGCACAGTAGAAGAGGACACCCTTACCAGGGCACCATCGTGTGCCACTG	2401
Qy	2402	TTAAAGGGCGACGTGCACAGTAGGCAAGAACATAGTTGGACAAGAACATAGTGGAGTAGTC	2461
Db	2402	TTAAAGGGCGACGTGCACAGTAGGCAAGAACATAGTTGGACAAGAACATAGTGGAGTAGTC	2461
Qy	2462	ATTTCCGAGTTATTGATTTGAGTTTAGGAGTTTAGGAGTGATAAGATACTGAAAGTGCTC	2521
Db	2462	ATTTCCGAGTTATTGATTTGAGTTTAGGAGTGATAAGATACTGAAAGTGCTC	2521
Qy	2522	TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCCTCTTCCCTGATGAAA	2581

Left panel (positions 362–1441):

Label	Start	Sequence	End
Qy	362	GCACTAGTATTGCCCAAGCTGACTATGGCTTGAACACTTGGCTACCGGATGAACATGT	421
Db	362	GCACTAGTATTGCCCAAGCTGACTATGGCTTGAACACTTGGCTACCGGATGAACACATGT	421
Qy	422	GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGA	481
Db	422	GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGA	481
Qy	482	GGTTTGTGCGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTTCTGTCCCATCTGG	541
Db	482	GGTTTGTGCGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTTCTGTCCCATCTGTG	541
Qy	542	AAAGGCCGGATTATAGGAACATCACATTGATGAGCTTGTTGAAGCATACCAAGAGCAGG	601
Db	542	AAAGGCCGGATTATAGGAACATCACATTGATGAGCTTGTTGAAGCATACCAAGAGCAGG	601
Qy	602	CCAAAGGACTTCTCGGATGGCGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG	661
Db	602	CCAAAGGACTTCTCGGATGGCGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG	661
Qy	662	CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGACGGAGAAATATGCTCCCC	721
Db	662	CCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGACGGAGAAATATGCTCCCC	721
Qy	722	GGCCTATCTTTATTTCAGGGACGATCGTTGTTGATAAAGTCGGGCGGACTCTTTCCGACAGA	781
Db	722	GGCCTATCTTTATTTCAGGGACGATCGTTGTTGATAAAGTCGGGCGGACTCTTTCCGACAGA	781
Qy	782	CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT	841
Db	782	CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT	841
Qy	842	GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAAAAATGTACAACAG	901
Db	842	GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAAAAATGTACAACAG	901
Qy	902	CCTATGTCCTCGTTATCCCAATGCAGTCTCTTCCCAACACCTTTGGTGACTATGATGAAA	961
Db	902	CCTATGTCCTCTGTTATCCCAATGCAGTCTCTTCCCAACACCTTTGGTGACTATGATGAAA	961
Qy	962	CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG	1021
Db	962	CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG	1021
Qy	1022	TTGGAGGATGCTGTGTGGGTCAACACCAGGATCATATCAGGGAAAGTGCTGAAGCTGTGAAAA	1081
Db	1022	TTGGAGGATGCTGTGTGGGTCAACACCAGGATCATATCAGGGAAAGTGCTGAAGCTGTGAAAA	1081
Qy	1082	ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTAAACTCATCATGGCCAGGAAACTATGTCTGGTC	1141
Db	1082	ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTAAACTCATCATGGCCAGGAAACTATGTCTGGTC	1141
Qy	1142	TAGAGCCCTTCAGGATTGGACCGTACACCACCAACCTTTGTTAACATTGGAGAGCGCTGTAATG	1201
Db	1142	TAGAGCCCTTCAGGATTGGACCGTACACCACCAACCTTTGTTAACATTGGAGAGCGCTGTAATG	1201
Qy	1202	TTGGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAAGAGCCTTGGTC	1261
Db	1202	TTGGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATGAAGAGCCTTGT	1261
Qy	1262	GTGTTGCCAAAGTGCCAGGTGGAAATGGGAGCCCCAGGTGTTGGATGTCAACATGGATGATG	1321
Db	1262	GTGTTGCCAAAGTGCCAGGTGGAAATGGGAGCCCCAGGTGTTGGATGTCAACATGGATGATG	1321
Qy	1322	GCATGCTGTAGGTTGCCAAGTGCAATGACCAGATTTTGCAACTTAATTGTTCCGAGCCAG	1381
Db	1322	GCATGCTAGTAGGTTGCCAAGTGCAATGACCAGATTTTGCAACTTAATTGTTCCGAGCCAG	1381
Qy	1382	ACATCCGCAAAGGTACCTTTTGTCATGCGAGTTTGCTGTGATTGAAGCTGGGT	1441
Db	1382	ACATCCGCAAAGGTACCTTTTGTCATGCGAGTTTGCTGTGATTGAAGCTGGGT	1441

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Db                 ||||||||||||||||||||||||||||||||||||||||||||
Qy   2522  TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA  2581

Qy   2582  TGATTTTGTTGTGCCAAGGAAATGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGG  2641
Db   2582  TGATTTTGTTGTGCCAAGGAAATGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGG  2641

Qy   2642  GAGCAACACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  2701
Db   2642  GAGCAACACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  2701

Qy   2702  TAATCCATGTCCTGACGCGTCCAAGAGTTGTGGTGTGTTCCCAGCTGTTAGATGAAA  2761
Db   2702  TAATCCATGTCCTGACGCGTCCAAGAGTTGTGGTGTGTTCCCAGCTGTTAGATGAAA  2761

Qy   2762  ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGATATTAGACAGGACC  2821
Db   2762  ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGATATTAGACAGGACC  2821

Qy   2822  ATTATGAGTCTCTCAAGGAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT  2881
Db   2822  ATTATGAGTCTCTCAAGGAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT  2881

Qy   2882  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG  2941
Db   2882  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG  2941

Qy   2942  TCTTTGAAGACTATGACCTGTCAGAGAGCTGGTGGACTACATTGACTGGAGCCTTTCTTTG  3001
Db   2942  TCTTTGAAGACTATGACCTGTCAGAGAGCTGGTGGACTACATTGACTGGAGCCTTTCTTTG  3001

Qy   3002  ATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAACGACA  3061
Db   3002  ATGTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAACGACA  3061

Qy   3062  AAACAGTAGGTGGAGAGGCCAGGAAGGTCACGGAAGGTCACGATGATGCCCACAAATGCTGAACACAC  3121
Db   3062  AAACAGTAGGTGGAGAGGCCAGGAAGGTCACGATGATGCCCACAAATGCTGAACACAC  3121

Qy   3122  TGATTAGTCAAAAGAAACTCCGGGCCCGGGGCGTGTGGTTCGTGCTGGCCAGCACAGAGTA  3181
Db   3122  TGATTAGTCAAAAGAAACTCCGGGCCCGGGGCGTGTGGTTCGTGCTGGCCAGCACAGAGTA  3181

Qy   3182  TCCAAGACGACATTCACCTGTACGGCAGAGGCTGCTGTGCCCAGCGCTGAGAGCCCATAG  3241
Db   3182  TCCAAGACGACATTCACCTGTACGGCAGAGGCTGCTGTGCCCAGCGCTGAGAGCCCATAG  3241

Qy   3242  CCACTTTCTATGGGTTAAGGCAACAGGCTCGAGAAGGACTCTGCCACCGGCACACGAGCCGAGGAC  3301
Db   3242  CCACTTTCTATGGGTTAAGGCAACAGGCTCGAGAAGGACTCTGCCACCGGCACACGAGCCGAGGAC  3301

Qy   3302  ACTGCCTCTCCAGACTTCATCGTCTTTGCATTCTGGCCATCCGTCCGTGACTACCTGGGGCCTGT  3361
Db   3302  ACTGCCTCTCCAGACTTCATCGTCTTTGCATTCTGGCCATCCGTCCGTGACTACCTGGGGCCTGT  3361

Qy   3362  TTGCCGTTGCCTGCTGTTTGGGGTAGAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG  3421
Db   3362  TTGCCGTTGCCTGCTGTTTGGGGTAGAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG  3421

Qy   3422  ACTACAGCAGCATCATGGTTCGCGCCGAAGAGTTCGCGCCGGGGACTCGGGGGACCGGTGGGGGACGACG  3481
Db   3422  ACTACAGCAGCATCATGGTTCGCGCCGAAGAGTTCGCGCCGGGGACTCGGGGGACCGGTGGGGGACGACG  3481

Qy   3482  AGCTCCATGAAAGAGTTCGCGCAGAGACTGTGGGCCTACTGTGCCAGTGAGCAGCTGGACG  3541
Db   3482  AGCTCCATGAAAGAGTTCGCGCAGAGACTGTGGGCCTACTGTGCCAGTGAGCAGCTGGACG  3541

Qy   3542  TCGCAGGACCTGCGAAGGTTGCCGGTACAAGGGCATCCGGCTCCTGCGGCTCACCCCAGCC  3601
Db   3542  TCGCAGGACCTGCGAAGGTTGCCGGTACAAGGGCATCCGGCTCCTGCGGCTCACCCCAGCC  3601

Qy   3602  AGCCCGACCACACCGAGAAGCTCACCATGTGGAGACTCGGAGCATCGAGCAGTCTCACAG  3661
Db                 ||||||||||||||||||||||||||||||||||||||||||||
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Db   3602  AGCCCGACCACACCGAGAAGCTCACCATGTGGAGACTCGGAGCATCGAGCAGTCTCACAG  3661

Qy   3662  GCATTAGGTTAACAGAATCATTAGCAGTCAATGGCACCTGCTTCAGCAGTCTCAGGCCTTCACT  3721
Db   3662  GCATTAGGTTAACAGAATCATTAGCAGTCAATGGCACCTGCTTCAGCAGTCTCAGGCCTTCACT  3721

Qy   3722  TCTCCAATTGAAGTCCAAATATTTGCTGTGGGAAGATTTCCAAGGATCAGGTTGAGG  3781
Db   3722  TCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG  3781

Qy   3782  ATTATGCATTGAGGAAGAACATATCTGTGCGCTGAGGTTGAGAAATGGCTTGGACCCATTT  3841
Db   3782  ATTATGCATTGAGGAAGAACATATCTGTGCGCTGAGGTTGAGAAATGGCTTGGACCCATTT  3841

Qy   3842  TGGGATATGATACAGACTAACTTTTTTTTTTTTTT  3875
Db   3842  TGGGATATGATACAGACTAACTTTTTTTTTTTTTT  3875
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RESULT 3
LOCUS   AR482320
DEFINITION   AR482320 Sequence 75 from patent US 6703197.   3856 bp   DNA   linear   PAT 14-MAY-2004
ACCESSION   AR482320
VERSION   AR482320.1 GI:4724609
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
              Unclassified.
REFERENCE   1 (bases 1 to 3856)
  AUTHORS   Gravel,R.A., Rozen,R., LeClerc,D., Goyette,P. and Campeau,B.
  TITLE   Human methionine synthase: cloning, and methods for evaluating risk
              of neural tube defects, cardiovascular disease, and cancer
  JOURNAL   Patent: US 6703197-A 75 09-MAR-2004;
              Martinex R&D, Inc.; Montreal;
              CAX;
FEATURES   Location/Qualifiers
     source   1..3856
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match   91.9%; Score 3601; DB 6; Length 3856;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3851; Conservative 0; Mismatches 0; Indels 5; Gaps 0;

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Qy     64  ATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGGAAGGTCGAAGAAAACCCTGCGCGGAT  123
Db      1  ATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGGAAGGTCGAAGAAAACCCTGCGGGAT   60

Qy    124  GAGATCAATGCCATTCTGCAGAAGAAGAGGATTATGGTGCTGGAGGTGGGACCATG  183
Db     61  GAGATCAATGCCATTCTGCAGAAGAAGAGGATTATGGTGCTGGAGGTGGGACCATG  120

Qy    184  ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAGATCAGGAATTAAAGATCATGCC  243
Db    121  ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAGATCAGGAATTAAAGATCATGCC  180

Qy    244  AGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACCAA  303
Db    181  AGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACCAA  240

Qy    304  ATCCATAAGGAATACTTGCTGGCCAGAGATCATTGAAACAAATACTTTAGCAGC  363
Db    241  ATCCATAAGGAATACTTGCTGGCCAGAGATCATTGAAACAAATACTTTAGCAGC  300

Qy    364  ACTAGTATTGCCCAAGCTGACTATGGCCTTGGCCTCACCTTGAACACTGCCTACCGCAGCC  423
Db    301  ACTAGTATTGCCCAAGCTGACTATGGCCTTGGCCTCACCTTGAACACTGCCTACCGCAGCC  360

Qy    424  TCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGAGG  483
Db    361  TCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGAGG  420
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Db  3661  TCCAATTTGAAGTCCAAATATTTGTGTGGGGAAGATTCCAAGGATCAGTTGAGGAT  3720
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Qy  3784  TATGCATTGAGGAAGAACATATCTGGCTGGAGGTTGAGAAATGGCTTGGACCCATTTTG  3843
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  TATGCATTGAGGAAGAACATATCTGGCTGGAGGTTGAGAAATGGCTTGGACCCATTTTG  3780
Qy  3844  GGATATGATACAGACTAACTTTTTTTTTTTTTGCCTTTTATCTTGATGATCCTCA  3903
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Db  3781  GGATATGATACAGACTAACTTTTTTTTTTTTTTTTTGCCTTTTATCTTGATGATCCTCA  3840
Qy  3904  AGGAAATACAACCTAG  3919
          ||||||||||||||||
Db  3841  AGGAAATACAACCTAG  3856
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RESULT 4
LOCUS   AR144957   7122 bp   DNA   linear   PAT 08-AUG-2001
DEFINITION   Sequence 2 from patent US 6210950.
ACCESSION   AR144957
VERSION   AR144957.1 GI:15106824
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 7122)
  AUTHORS   Johnson,W.G. and Stenroos,E.Scott.
  TITLE   Methods for diagnosing, preventing, and treating developmental
             disorders due to a combination of genetic and environmental factors
  JOURNAL   Patent: US 6210950-A 2 03-APR-2001;
FEATURES   Location/Qualifiers
     source 1..7122
             /organism="unknown"
             /mol_type="unassigned DNA"
ORIGIN

Query Match   89.7%; Score 3517; DB 6; Length 7122;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 3867; Conservative 0; Mismatches 0; Indels 7; Gaps 0;

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Qy    2  GTCACCTGTGAGGAGCACGTCTTCTCGCCGCGGCCCTCGGGCAAGGAGGAGACTCGACA   61
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Db  225  GTCACCTGTGAGGAGCACGTCTTCTCTCGCCGCGGCCCCTCGGGCAAGGAGGAGACTCGACA  284
Qy   62  ACATGTCACCCGCGTCCAAGACCTGTCGCAACCCGGAAGGTCTGAAGAAAACCCTGCGGGG  121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  285  ACATGTCACCCGCGTCCAAGACCTGTCGCAACCCGGAAGGTCTGAAGAAAACCCTGCGGG  344
Qy  122  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGGATGGGGACCA  181
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  345  ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGGATGGGGACCA  404
Qy  182  TGATCCAGCGGGAGAAGCGAGAAACGAACAACACTTCCGAGGTCAGGAATTTAAAGATCATG  241
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Db  405  TGATCCAGCGGGAGAAGCGAGAAACGAACAACACTTCCGAGGTCAGGAATTTAAAGATCATG  464
Qy  242  CCAGGCCGCTGAAAGGCAACAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC  301
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  465  CCAGGCCGCTGAAAGGCAACAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC  524
Qy  302  AAATCCATAAGGATATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA  361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  525  AAATCCATAAGGATATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA  584
Qy  362  GCACTAGTATTGCCCAAGTCGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT  421
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  585  GCACTAGTATTGCCCAAGTCGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT  644
Qy  422  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCAGAGGAGGTAACTCTTCCAGACAGAATTAAGA  481
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Db  645  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCAGAGGAGGTAACTCTTCCAGACAGAATTAAGA  704
Qy  482  GGTTTGTGCGACGGGGGCTTCGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG  541
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Db  2581  GCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTN  2640
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Qy  2704  ATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTAGATGAAAAT  2763
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Db  2641  NNCCATGTCCTGGACGCGTCCAAGAGTGTGGTGGTGTCCCAGCTGTTAGATGATGAAAAT  2700
Qy  2764  CTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAAGATATTAGACACAGACCAT  2823
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Db  2701  CTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAAGATATTAGACAGNCNAT  2760
Qy  2824  TATGAGTCTCTCAAGAGAGAGATACTTACCCCTTAAGTCAAGCCAGAAAAAGTGTTTC  2883
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Db  2761  TATGAGTCTCTCAAGAGAGAGATACTTACCCCTTAAGTCAAGCCAGAAAAAGTGTTTC  2820
Qy  2884  CAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTC  2943
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Db  2821  CAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTC  2880
Qy  2944  TTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTGAT  3003
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Db  2881  TTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTGAT  2940
Qy  3004  GTCTGGCAGCTCCGGGGCAAGTACCCGGGCGAATCGAGCGTTCCCCAAGATATTAACGACAAA  3063
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Db  2941  GTCTGGCAGCTCCGGGGCAAGTACCCGGGCGAATCGAGCGTTCCCCAAGATATTAACGACAAA  3000
Qy  3064  ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCAACAATATGCTGAACACACTG  3123
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Db  3001  ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCAACAATATGCTGAACACACTG  3060
Qy  3124  ATTAGTCAAAAGAAAACTCCGGGCCCGGGGGTGGTTGGGTTCTGGCCAGCACAGAGTATC  3183
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Db  3061  ATTAGTCAAAAGAAAACTCCGGGCCCGGGGGTGGTTGGGTTCTGGCCAGCACAGAGTATC  3120
Qy  3184  CAAGACGACATTCACCTGTACGCAGAGCTGCTGTGCCCAGGCTGCAGAGCCCATAGCC  3243
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  CAAGACGACATTCACCTGTACGCAGAGCTGCTGTGCCCAGGCTGCAGAGCCCATAGCC  3180
Qy  3244  ACTTTCTATGGGTTAAGGCAACAGACTCGCCGAGGACTCTGAGAGGACTGAGAGCTACTAC  3303
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Db  3181  ACTTTCTATGGGTTAAGGCAACAGACTCGCCGAGGACTCTGAGAGGACTGAGCAGCTGAGACTACTAC  3240
Qy  3304  TGCCCTCAGACTTCATCGCTCATCGGCATCCGTGACTACCTGGGCCTGTTT  3363
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Db  3241  TGCCCTCAGACTTCATCGCTCATCGGCATCCGTGACTACCTGGGCCTGTTT  3300
Qy  3364  GCCGGTTGCCTGCTTTGGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGAC  3423
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Db  3301  GCCGGTTGCCTGCTTTGGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGAC  3360
Qy  3424  TACAGCAGCATCATGGTCAAGGCGTCGGCGGCGGACCGGCTTTGCAGAGAGAG  3483
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Db  3361  TACAGCAGCATCATGGTCAAGGCGTCGGCGGCGGACCGGCTTTGCAGAGAGAG  3420
Qy  3484  CTCCATGAAAGAGTTAAGGCAACAGAGTTCGCCGGAGACTGTGGGCGCTCGCCGAGCAGCGTC  3543
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Db  3421  CTCCATGAAAGAGTTAAGGCAACAGAGTTCGCCGGAGACTGTGGGCGCTCGCCGAGCAGCGTC  3480
Qy  3544  GCAGACCTGCGAAGGTTGCGGTTACAAGGGCATCCGCCCGGCTCTGGCTACCCCAGCCAG  3603
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Db  3481  GCAGACCTGCGAAGGTTGCGGTTACAAGGGCATCCGCCCGGCTCTGGCTACCCCAGCCAG  3540
Qy  3604  CCCGACCACCAGGAAGCTCACCATGGGAGACTCGGAGACATGGGAGACATGGAGAGGCTCTACAGGGC  3663
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Db  3541  CCCGACCACCAGGAAGCTCACCATGTGGAGACTCGGAGACATGGGAGACATGGAGAGGCTCTACAGGGC  3600
Qy  3664  ATTAGGTTAACAGAATCATTAGCAATGGACAATGGCACCAGTGCTCCAGCAGTCTCCAGGCCTCTACTTC  3723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  ATTAGGTTAACAGAATCATTAGCAATGGACAATGGCACCAGTGCTCCAGCAGTCTCCAGGCCTCTACTTC  3660
Qy  3724  TCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTCCAAGGATCAGTTGAGGAT  3783
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Db  1785 TTGATGAAGAGGACAGGCAACAGAAACAGACACAAAATCAGAGTGTGCACCCGGGCCT 1844
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Qy  1622 ACCATCTGCTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1681
Db  1845 ACCATCTGCTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1904

Qy  1682 TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTTATCCATG 1741
Db  1905 TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTTATCATG 1964

Qy  1742 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 1801
Db  1965 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 2024

Qy  1802 TGTCCTTCTCCTTCCGGAGGAATGGAAGCCATTGGAGAAGCAATGCATGGGGTTTCCTTT 1861
Db  2025 TGTCCTTCTCCTTCCGGAGGAATGGAAGCCATTGGAGAAGCAATGCATGGGGTTTCCTTT 2084

Qy  1862 ACCATGCAATCAAGTCTGCATGGACATGAGATAGTGAATGCTGAAAACCTCCCTGTGT 1921
Db  2085 ACCATGCAATCAAGTCTGGCATGGACATGGGGATATGGGGATAGTGAAAACCTCCCTGTGT 2144

Qy  1922 ATGATGATATCCATAAGGAACTTCTGCAGCTTCGCAGTCTCGTGAAGATCTCATCTGCAGACC 1981
Db  2145 ATGATGATATCCATAAGGAACTTCTGCAGCTTCGCAGTCTCGTGAAGATCTCATCTGGAATAAGACC 2204

Qy  1982 CTGAGGCCACTGAGAGAGTCTCTACGTTATGCCGACTCAAGGCACAGGAGGAAGAAAG 2041
Db  2205 CTGAGGCCACTGAGAGAGTCTCTACGTTATGCCCAGACTCAAGGCACAGGAGGGAGAAAG 2264

Qy  2042 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGTGAAGAACGCCTTGAGTGATGCCCTTG 2101
Db  2265 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGTGAAGAACGCCTTGAGTGATGCCCTTG 2324

Qy  2102 TGAAGGGCATTGAAAAACATATTATTGAGGATAATGAAGCCAGTTGAATGAAAATTGTTG 2161
Db  2325 TGAAGGGCATTGAAAAACATATTATTGAGGATAATGAAGCCAGTTGAATGAAAATTGTTG 2384

Qy  2162 AATATCCCGACCTCTCAATATAATTGAAGACACCCTGATGAATAAAGTCAGCCCCGGGTTA 2221
Db  2385 AATATCCCGACCTCTCAATATAATTGAAGACACCCTGATGAATAAAGTCAGCCCCGGGTTA 2444

Qy  2222 GTGATCTTTTGGAGCTGGAAAATGTTCTACCTCAGGTTATAAAGTCAGCCCCGGGTTA 2281
Db  2445 GTGATCTTTTGGAGCTGGAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCCGGGTTA 2504

Qy  2282 TGAAGAAGGCTGTTGGCCCACCTTATCCCTTTCATGGAAAAAGAAGAAAACCAGAG 2341
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Qy  2342 TGCTTAACGGCACAGTAGAGAAGAGGACCCTTACCAGGGCACCATCGTGCTGGCCACTG 2401
Db  2565 TGCTTAACGGCACAGTAGAGAAGAGGACCCTTACCAGGGCACCATCGTGCTGGCCACTG 2624

Qy  2402 TTAAAGGGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA 2461
Db  2625 TTAAAGGGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA 2684

Qy  2462 ATTTCCGAGTTATTGATTTAGGAGTCATGAGTCATGTGGGT 2521
Db  2685 ATTTCCGAGTTATTGATTTAGGAGTCATGAGTCATGTGGGT 2744

Qy  2522 TTGACCACAAAGCAGATATATTGGCTGCTGTCAGGACTCATCGTCCTGGATGAAA 2581
Db  2745 TTGACCACAAAGCAGATATATTGGCTGCTGTCAGGACTCATCGTCCTGGATGAAA 2804

Qy  2582 TGATTTTTGTTGCCAAGGAAATGGAGAATTAGCTATAAGGATTCCATTGTTGATTGGAG 2641
Db  2805 TGATTTTTGTTGCCAAGGAAATGGAGAATTAGCTATAAGGATTCCATTGTTGATTGGAG 2864

Qy  2642 GAGCAACCACTTCAAAAACCCACAGCAGTAAAATAGTCCGAGATACAGTGCACCTG 2701
Db  2865 GAGCAACCACTTCAAAAACCCACAGCAGTAAAATAGTCCGAGATACAGTGCACCTG 2924
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Db   705 GGTTTGTGGCAGGGGCTCTGGGTTCCGACTAATAAGACACTCTCTGTCCCCATCTGTGG 764
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Qy   542 AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 601
Db   765 AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 824

Qy   602 CCAAAGGAGACTTCTGGATGCGGGGGTTGATATCTTACTACTTTGTGATACTG 661
Db   825 CCAAAGGAGACTTCTGGATGCGGGGGTTGATATCTCATTGAAAACTATTTTGATACTG 884

Qy   662 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCC 721
Db   885 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC 944

Qy   722 GGCCTATCTCTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGACAGA 781
Db   945 GGCCTATCTCTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGACAGA 1004

Qy   782 CAGGAGGAGGGATTTGTCATCAGCCGTGCTCATGGGAGAACCACTCGCATTGGATTAAAAT 841
Db  1005 CAGGAGGAGGGATTTGTCATCAGCCGTGCTCATGGGAGAACCACTCGCATTGGATTAAAAT 1064

Qy   842 GTGCTTTGGGGTGCAGTGAGATGAGACCTTTATTGAAAATGTACAACAG 901
Db  1065 GTGCTTTGGGGTGCAGTGAGATGAGACCTTTATTGAAAATGTACAACAG 1124

Qy   902 CCTATGTCCTCTGTTATCCCAATGCGAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA 961
Db  1125 CCTATGTCCTCTGTTATCCCAATGCGAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA 1184

Qy   962 CGCCTTCTATGATGATGCCAAGCACCACTTAAGGATTTGCTATGGATGGCTTGGTCAATATAG 1021
Db  1185 CGCCTTCTATGATGATGCCAAGCACCACTTAAGGATTTGCTATGGATGGCTTGGTCAATATAG 1244

Qy  1022 TTGGAGGATGCTGTGTGGTCAACACCAGATCATATCAGGGAAATTGCTGAAAA 1081
Db  1245 TTGGAGGATGCTGTGTGGTCAACACCAGATCATATCAGGGAAATTGCTGAAAA 1304

Qy  1082 ATTGTAAGCCTAGAAGTTCCACCTGCCACTGCTTTTTGAAGGACATATGTTACTGTCTGGTC 1141
Db  1305 ATTGTAAGCCTAGAAGTTCCACCTGCCACTGCTTTTTGAAGGACATATGTTACTGTCTGGTC 1364

Qy  1142 TAGAGCCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGACGCGCTGTAATG 1201
Db  1365 TAGAGCCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGACGCGCTGTAATG 1424

Qy  1202 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATCATGGCAGAGAAACATGAAGAAGCCTTGT 1261
Db  1425 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATCATGGCAGAGAAACATGAAGAAGCCTTGT 1484

Qy  1262 GTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGATGTCAACATGGATGATG 1321
Db  1485 GTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATG 1544

Qy  1322 GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAGTTGCTTCCGAGCCAG 1381
Db  1545 GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAGTTGCTTCCGAGCCAG 1604

Qy  1382 ACATCGCAAAGTACCTTTGTCGACTCCTCCAATTTGCTGTGATTGAAAGCTGGGT 1441
Db  1605 ACATCGCAAAGGTACCTTTGTCATCGCAATCCTCCTCCAATTTTGCTGTGATTGAAAGCTGGGT 1664

Qy  1442 TAAAGTGCTTGCCAAGGGAAGTGCAATAGCATTAGTCTGAAGGAAGGAGGAGGACG 1501
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Qy  1502 ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1561
Db  1725 ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1784

Qy  1562 TTGATGAAGAGGACAGGCAACAGAAACAGACACAAAATCAGAGTGTGCACCCGGGCCT 1621
Db      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3782  ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT  3841
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Db  4005  ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT  4064

Qy  3842  TGGGATATGATACAGACTAACTTTTTTTTTTTTT            3875
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Db  4065  TGGGATATGATACAGACTAACTTTTTTTTTTTTTTTT         4098
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RESULT 5
AR367907

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LOCUS       AR367907                7122 bp    DNA        linear   PAT 12-SEP-2003
DEFINITION  Sequence 4 from patent US 6376210.
ACCESSION   AR367907
VERSION     AR367907.1  GI:34601378
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unclassified.
REFERENCE   1  (bases 1 to 7122)
  AUTHORS   Yuan,C.-S.
  TITLE     Methods and compositions for assaying analytes
  JOURNAL   Patent: US 6376210-A 4 23-APR-2002;
            General Atomics; San Diego, CA
FEATURES             Location/Qualifiers
     source          1..7122
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match     89.7%;  Score 3517;  DB 6;  Length 7122;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 3867;  Conservative   0;  Mismatches   0;  Indels   7;  Gaps   0;
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Qy     2  GTCACCTGTGGAGAGCAGTCGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACA   61
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Db   225  GTCACCTGTGGAGAGCAGTCGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACA  284

Qy    62  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCGTCTGCGAGAAAACCCTGCGGG       121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285  ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCGTCTGCGAGAAAACCCTGCGGG       344

Qy   122  ATGAGATCAATGCCATTCTGCGAAGAGGATTATGGTGCTGATGAGGGGATGGGGACCA     181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345  ATGAGATCAATGCCATTCTGCGAAGAGGATTATGGTGCTGATGAGGGGATGGGGACCA     404

Qy   182  TGATCCAGCGGGAGAAGCTAAACGAACGAAGAACACTTCCGAGGTCAGGATTTAAAGATCATG  241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405  TGATCCAGCGGGAGAAGCTAAACGAACGAAGAACACTTCCGAGGTCAGGATTTAAAGATCATG  464

Qy   242  CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC    301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465  CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC    524

Qy   302  AAATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCAATTACTTTTAGCA          361
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Qy   362  GCACTAGTATTGCCCCAGTCGACTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT  421
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Db   585  GCACTAGTATTGCCCCAGTCGACTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT  644

Qy   422  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAAGA   481
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Db   645  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAAGA   704

Qy   482  GGTTGTGCGCAGGGGCTCTGGGTCCGACTAATAAGACTCTCTGTGTCCCATCTGTGG      541
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Db   705  GGTTTGTGCGCAGGGGCTCTGGGTCCGACTAATAAGACTCTCTGTGTCCCATCTGTGG     764

Qy   542  AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATCACCAAGAGCAGG    601
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   765  AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG    824
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Qy  2702  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTCGTGTGTTCCCAGCTGTTAGATGAAA  2761
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Db  2925  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTCGTGTGTTCCCAGCTGTTAGATGAAA  2984

Qy  2762  ATCTAAAGGATGAATACTTTGAGGAAGAATCATGGAAATATGAGAGATATTAGACAGGACC  2821
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Db  2985  ATCTAAAGGATGAATACTTTGAGGAAGAATCATGGAAATATGAGAGATATTAGACAGGACC  3044

Qy  2822  ATTATGAGTCTCTCAAGGAGGAGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT  2881
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Db  3045  ATTATGAGTCTCTCAAGGAGGAGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT  3104

Qy  2882  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTATTGGGACCCAGG   2941
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Db  3105  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTATTGGGACCCAGG   3164

Qy  2942  TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG   3001
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Db  3165  TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG   3224

Qy  3002  ATGTCTGGCAGCTCCGGGGCAAGTACCCGGAATCGAGCGCTTCCCAAGATATTTAACGACA  3061
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Db  3225  ATGTCTGGCAGCTCCGGGGCAAGTACCCGGAATCGAGCGCTTCCCAAGATATTTAACGACA  3284

Qy  3062  AAACAGTAGGTGGAGAGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACAC   3121
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Db  3285  AAACAGTAGGTGGAGAGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACAC   3344

Qy  3122  TGATTAGTAGTCAAAAGAAACTCCCGGGCCGGGGTGTGGTTGGGTTCTGGCCACAGAGTA   3181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3345  TGATTAGTAGTCAAAAGAAACTCCCGGGCCGGGGTGTGGTTGGGTTCTGGCCACAGAGTA   3404

Qy  3182  TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAG   3241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3405  TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAG   3464

Qy  3242  CCACTTTCTATGGGTTAAGGCAACACGGCTGAGAAGACTCTGCCAGCACGGAGCCCATACT  3301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3465  CCACTTTCTATGGGTTAAGGCAACACGGCTGAGAAGACTCTGCCAGCACGGAGCCCATACT  3524

Qy  3302  ACTGGCCTCGAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT   3361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3525  ACTGGCCTCGAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT   3584

Qy  3362  TTGCCGGTTGCCTGCTTTGGGGTAGAAGACTGAGCAAGGCCTATGAGGATGATGGTGACG   3421
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Db  3585  TTGCCGGTTGCCTGCTTTGGGGTAGAAGACTGAGCAAGGCCTATGAGGATGATGGTGACG   3644

Qy  3422  ACTACAGCAGACATCATGGTCAAGGCGCTGGGGACCGGCTGGGAGGGCCTTGCGAGAAG    3481
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Db  3645  ACTACAGCAGACATCATGGTCAAGGCGCTGGGGACCGGCTGGGAGGGCCTTGCGAGAAG    3704

Qy  3482  AGCTCCATGAAAGAGTTCGCCGAGAACTTGCTGGCTGGCAGCAGCTGGACG          3541
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Db  3705  AGCTCCATGAAAGAGTTCGCCGAGAACTTGCTGGCTGGCAGCAGCTGGACG          3764

Qy  3542  TCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCCGGCTTCCTGCTACCCCAGCC  3601
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Db  3765  TCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCCGGCTTCCTGCTACCCCAGCC  3824

Qy  3602  AGCCCGACCACCACCGAGAGCTTCACCATGTGGAGACTCGAGACATCGAGCAGTCTACAG  3661
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Db  3825  AGCCCGACCACCACCGAGAGCTTCACCATGTGGAGACTCGAGACATCGAGCAGTCTACAG  3884

Qy  3662  GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGTCTCAGCCCTCTACT     3721
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Db  3885  GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGTCTCAGCCCTCTACT     3944

Qy  3722  TCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG  3781
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Db  3945  TCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG  4004
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Qy  1682 TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCGCATTAATTTATCCATG 1741
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Db  1905 TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATG  1964

Qy  1742 CAACAAAAGTCATTAAAGAAACATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTCCAACT 1801
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Qy  1802 TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTGAGAAGCAATGCATGGGGTTTCCTTT 1861
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Db  2025 TGTCCTTCTCCTTCCGAGGAATGGAAGCCATTGAGAAGCAATGCATGGGGTTTCCTTT 2084

Qy  1862 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGAAACCTCCCTGTGT 1921
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Db  2085 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGAAACCTCCCTGTGT 2144

Qy  1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCGTGAAGATCTCATCTGGAATAAAGACC 1981
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Db  2145 ATGATGATATCCATAAGGAACTTCTGCAGCTCGTGAAGATCTCATCTGGAATAAAGACC 2204

Qy  1982 CTGAGGCCACTGAGAAGCTCTTACGTATGCCAGACTCAAGGCACAGGAGGGAAGAAAG 2041
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2205 CTGAGGCCACTGAGAAGCTCTTACGTATGCCAGACTCAAGGCACAGGAGGGAAGAAAG 2264

Qy  2042 TCATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGACGCCTGAGTATGCCCTTG 2101
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Qy  2102 TGAAGGGCATTGAAAAACATATTATTGAGGATAACTGGAGAGAGAGCCAGTTAAACCAAAAAA 2161
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2325 TGAAGGGCATTGAAAAACATATTATTGAGGATAACTGGAGAGAGAGCCAGTTAAACCAAAAAA 2384

Qy  2162 AATATCCCGACCTCTCAATATAATGAAGACCCCTGATGAATGAAATTGTTG 2221
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Db  2385 AATATCCCGACCTCTCAATATAATGAAGACCCCTGATGAATGAAATTGTTG 2444

Qy  2222 GTGATCTTTTTGGAGCTGAAAAATGTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
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Db  2445 GTGATCTTTTTGGAGCTGAAAAATGTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2504

Qy  2282 TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAGAGAAAACCAGAG 2341
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Qy  2522 TTGACCACAAAGCAGATATATTGGCCTGTGAAGGAAGGAAGGAGGACG 2581
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Qy  2702 TAATCCATGTCCGACGCGTCCAAGAGTGTGGTGTGTTCCCAGCTGTTAGATGAAA 2761
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Qy   602 CCAAAGGACTTCTGGATGCGGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG  661
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Db   825 CCAAAGGACTTCTGGATGCGGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG  884

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Db   885 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC  944

Qy   722 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGACAGA  781
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Db   945 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGACAGA 1004

Qy   782 CAGGAGAGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAAT  841
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Qy   842 GTGCTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGACAAACAG  901
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RESULT 6
LOCUS        AX050442                7122 bp    DNA        linear    PAT 12-JAN-2001
DEFINITION   Sequence 2 from Patent WO0071754.
ACCESSION    AX050442
VERSION      AX050442.1  GI:12226649
KEYWORDS     .
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1
  AUTHORS    Johnson,W.G. and Stenroos,E.S.
  TITLE      Methods for diagnosing, preventing, and treating developmental
             disorders due to a combination of genetic and environmental factors
  JOURNAL    Patent: WO 0071754-A 2 30-NOV-2000;
             University of Medicine and Dentistry of New Jersey (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

ORIGIN

Query Match         89.7%;  Score 3517;  DB 6;  Length 7122;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 3867;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy     2 GTCACCTGTGGAGGACACGTCTTCTTCTCTGCGCAAGGAGGAGACTCGACA 61
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Db   225 GTCACCTGTGGAGGACACGTCTTCTTCTCTGCGCAAGGAGGAGACTCGACA 284

Qy    62 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAA CCCTGCGGG 121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAA CCCTGCGGG 344

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Db   405 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 464

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Qy   362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 421
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Db   705 GGTTTGTTGGCAGGGGCTTCTGGGTCCCATCTGTGG 764

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Db 825 CCAAAGGACTTCTGATGGATGCGGGGGTTGATATCTTACTACTTTTGAAACTATTTTGATTACTG 884
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Qy 662 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC 721
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Db 1905 (see above)

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RESULT 7
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DEFINITION  Sequence 4 from Patent WO0102600.
ACCESSION   AX069340
VERSION     AX069340.1  GI:12579203
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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REFERENCE   1
  AUTHORS   Yuan,C.S.
  TITLE     Detection of analytes using attenuated enzymes
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ORIGIN
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Qy        182  TGGGATATGATACAGACTAACTTTTTTTTTTTT                           241
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Qy  1322  GCATGTGTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCAG  1381
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Qy  1742  CAACAAAGTCATTAAAGAACATTACCTGCAGCCAGAATAAGTGAGGTCTTTCCAACT  1801
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Db  1965  CAACAAAGTCATTAAAGAACATTACCTGCAGCCAGAATAAGTGAGGTCTTTCCAACT  2024

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Qy  1862  ACCATGCAATCAAGTCTGGCATGGACATGAGATAGTGAATGCTGGAAACCTCCCTGTGT  1921
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Db  2085  ACCATGCAATCAAGTCTGGCATGGACATGAGATAGTGAATGCTGGAAACCTCCCTGTGT  2144

Qy  1922  ATGATGATATCCATAGGAGAACTTCTGCAGCTCGTGTTGAAGATCTCATCTGGAATAAGACC  1981
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Db  2145  ATGATGATATCCATAGGAGAACTTCTGCAGCTCGTGTTGAAGATCTCATCTGGAATAAGACC  2204

Qy  1982  CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAG  2041
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Qy  2042  TCATTCAGACTGATGAGTGGAAATGGCCCCTGTCGAAGAACGCCCTGAGTATGCCCCTG  2101
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Db  2445  GTGATCTTTTGGAGCTGGAAAAATGTTCTCACCTTATAAAGTAGAGAGAAACCAGAG  2504

Qy  2282  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAGAAGGCCTTGT  2341
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Qy  2402  TTAAAGGCCGACCTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA  2461
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Qy  362   GCACTAGTATTGCCCAAGCTGACTATGGCCTGAACACTTGGCCTACCGGATGAACATGT  421
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Qy  782   CAGGAGAGGATTGTCATCAGCGTGTCTCCATGCATGGGAGAACCACTCTGCATTGGATT  841
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Qy  842   GTGCTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGAAAATGTACAACAG  901
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Qy  902   CCTATGTCCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA  961
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Qy  962   CGCCTTCTCTGATGATGGCCAAGCACCACCTAAAGGATTTGCTATGGCTTGGTGCTATATGG  1021
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Qy  1022  TTGGAGGATGCTGTGGGTGCAGCTGAGAGTTTTGCAGGATCAAGGAAACTTGCTGAAGCCTTGT  1081
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Qy  1202  TTGCAGGATCAAGGAAGTTTGCTAAACTCATGCTGCAGAAACTATGAAGAAGCCTTGT  1261
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Db  1425  TTGCAGGATCAAGGAAGTTTGCTAAACTCATGCTGCAGAAACTATGAAGAAGCCTTGT  1484

Qy  1262  GTGTTGCCAAAGTGCAGGTGCGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATG  1321
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Db  1485  GTGTTGCCAAAGTGCAGGTGCGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATG  1544
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Qy  2462 ATTTCCGAGTTATTGATTTAGGAGTCATGATCCATGTGATAAGATACTGAAAGCTGCTC 2521
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Qy  2522 TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA 2581
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Qy  2642 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 2701
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RESULT 8
HSU75743
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DEFINITION  Human methionine synthase mRNA, complete cds.
ACCESSION   U75743
VERSION     U75743.1  GI:1763339
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 7122)
  AUTHORS   Li,Y.N., Gulati,S., Baker,P.J., Brody,L.C., Banerjee,R. and
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  TITLE     Cloning, mapping, and RNA analysis of the human methionine synthase
            gene
  JOURNAL   Hum. Mol. Genet. (1996) In press
REFERENCE   2  (bases 1 to 7122)
  AUTHORS   Li,Y.N., Gulati,S., Baker,P.J., Brody,L.C., Banerjee,R. and
            Kruger,W.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-1996) Population Science, Fox Chase Cancer
            Center, 7701 Burholme Ave., Philadelphia, PA 19111, USA
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                     RPDYRNITFDELVEAYQEQAKGLLDGGVDLLLIETIFDTANAKAALFALQNLFEEKYA
                     PRPIFLSGTIVDKSGRTLSGQTGEGFVISVSHGEPLYIGLNCALGAAEMRPFIEIIGK
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ORIGIN

Query Match    89.7%;    Score 3517;    DB 8;    Length 7122;
Best Local Similarity  99.8%;    Pred. No. 0;
Matches 3867;    Conservative  0;    Mismatches  7;    Indels  0;    Gaps  0;

Qy      2 GTCACCTGTGGAGAGCACGTCTTCTCTGCGCGCCCTCTGCGCAAGGAGGAGACTCGACA 61
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Qy     62 ACATGTCACCCGCCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAACCCTGCGGG 121
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Qy    362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 421
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Qy    422 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCAGGAGGTAACTCTCCAGACAGGAATTAAGA 481
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Qy 3422 ACTACAGCAGCATCATGTGCCGAGAACTGTCGGCCTACTGTGGCAGTCGAGCTCGACG 3481
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Qy 2402 TTAAAGGCGACGTGCACGACATAGGCAAGAACACATAGTTGGATGAGTCCTTGGCTGCAATA 2461
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Qy 2462 ATTTCCGAGTTATTGATTTAGGAGTCATGATCCATGTGATAAGATAACTGAAAGCTGCTC 2521
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ORGANISM Unknown.
          Unclassified.
REFERENCE 1 (bases 1 to 7224)
AUTHORS   Yuan,C.-S.
TITLE   Methods and compositions for assaying analytes
JOURNAL   Patent: US 6376210-A 6 23-APR-2002;
          General Atomics; San Diego, CA
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   88.4%; Score 3466; DB 6; Length 7224;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 3866; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy     62 ACATGTCACCCGCCTCCAAGACCTGTCGCAAGTCTGAAGAAACCCTGCGGG 121
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Qy    122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGAGGTGGATGGGGACCA 181
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Db   1233 CCTATGTCCTCTGTTATCCCAATGCAGTCTTCCCAACACCTTGGTGACTATGATGAAA 1292

Qy    962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAG 1021
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Qy   1622 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA 1681
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Qy   1742 CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGTGCTTTTCCAACT 1801
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Qy 3482 AGCTCCATGACCTGCGAAGGTTGCGGTACAAGGGCATCGGAGACTGTGGACGTGGACG 3541
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TITLE   Detection of analytes using attenuated enzymes
JOURNAL   Patent: WO 0102600-A 6 11-JAN-2001;
            GENERAL ATOMICS (US)
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ORIGIN

            Query Match   88.4%;   Score 3466;   DB 6;   Length 7224;
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Db   513 TGATCCAGCGGCGGAGAAGCTAAACGAAGAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 572

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Db 1113 CAGGAGAGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT 1172

Qy   842 GTGCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG 901
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Qy  2222 GTGATCTTTTTGGAGCTGGAAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
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Qy  2282 TGAAGAGGCTGTTGCCCACCTTATCCCTTTCATGGAAAAAGAGAAGAAACCAGAG 2341
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Db  2613 TGAAGAGGCTGTTGCCCACCTTATCCCTTTCATGGAAAAAGAGAAGAAACCAGAG 2672

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		of Cys to Tyr at amino acid 255"
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RESULT 11
HSU73338
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DEFINITION Human methionine synthase mRNA, complete cds.
ACCESSION   U73338
VERSION   U73338.1 GI:1763268
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 7224)
  AUTHORS   Chen,L.H., Liu,M.-L., Hwang,H.-Y., Chen,L.-S., Korenberg,J. and
            Shane,B.
  TITLE   Human methionine synthase: cDNA cloning, gene localization and
            expression
  JOURNAL   J. Biol. Chem. (1996) In press
REFERENCE   2 (bases 1 to 7224)
  AUTHORS   Chen,L.H., Liu,M.-L., Hwang,H.-Y., Chen,L.-S., Korenberg,J. and
            Shane,B.
  TITLE   Direct Submission
  JOURNAL   Submitted (03-OCT-1996) Nutritional Sciences, University of
            California, 117 Morgan Hall, Berkeley, CA 94720-3104, USA
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ORIGIN

Query Match   88.4%; Score 3466; DB 8; Length 7224;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 3866; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

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Db   333 GTCACCTGTGGAGAGCACGTCTTCTCTGCCCGCGCCCTGCCCAAGGAGGAGACTCGACA 392

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Db   453 ATGAGATCAATGCCATTCTGCAGAGAGGATTATGTGCTGGATGGAGGGATGGGACCA 512

Qy   182 TGATCAGCGGGAGAAGCTAAACGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 241
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Qy   362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 421
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Qy   602 CCAAAGGACTTCTGGATGGCGGGGTGATATCTTGATATCTTCACTCAATGAAAACTATTTTGATACTG 661
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Qy   662 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC 721
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REFERENCE    1
AUTHORS      Kroeger,B., Zelder,O., Klopproge,C., Schroeder,H. and Haefner,S.
TITLE        Methods for producing sulphurous fine chemicals
JOURNAL      Patent: WO 03087386-A 43 23-OCT-2003;
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             GNYBEALCVAKVQVEMGAQVLDVNMDDGMLDGPSAMTRFCNLIASEPDIAKVPLCIDS
             SNFAVIEAGLKCCQGKCIVNSISLKEGEDDFLEKARKIKKYGAAMVVMAPDEEGQATE
             TDTKIRVCTRAYHLLVKKLGFNPNDIIFDPNILTIGTGMEEHNLYAINFIHATKVIKE
             TLPGARISGGLSNLSFSFRGMEAIREAMHGVFLYHAIKSGMDMGIVNAGNLPVDDIH
             KELLQLCEDLIWNKDPEATEKLLRYAQTGTGKKVIQTDEWRNGPVEBRLEYALVKG
             IEKHIIEDTEEARLNQKKYPRPLNIIEGPLMNGMKIVGDLFGAGKMFLPQVIKSARVM
             KKAVGHLIPFMEKEREETRVLNGTVEEEDPYQGTIVLATVKGDVHDIGKNIVGVVLGC
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             VVGFWPAQSIQDDIHLYABAAVPQAAEPIATFYGLRQQAEKDSASTEPYYCLSDFIAP
             LHSGIRDYLGLFAVACFGVEELSKAYEDDGDDYSSIMVKALGDRLAEAFAEELEHRVR
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             DTD"
ORIGIN
Query Match         86.5%;  Score 3390;  DB 6;  Length 3798;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 3790;  Conservative   0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        64 ATGTCACCCGGCTCCAAGACCTGTCGCAACCGAAGGTCTGAAGAAAACCCTGCGGGAT 123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGTCACCCGGCTCCAAGACCTGTCGCAACCGAAGGTCTGAAGAAAACCCTGCGGGAT  60

Qy       124 GAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGATGGGACCATG 183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GAGATCAATGCCATTCTGCAGAAGACGATTATGGTGCTGGATGGAGGGATGGGACCATG 120

Qy       184 ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAGTCAGGAATTTAAAGATCATCATGCC 243
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Qy       244 AGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCATTGGAAACAAATACTTTTAGCAGC 303
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Db       181 AGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACTCATTGGAAACAAATACTTTTAGCAGC 240

Qy       304 ATCCATAAGGAATACTTGCTGGCTGGGCGCAGATATCATTGGAAACAAATACTTTTAGCAGC 363
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Db       241 ATCCATAAGGAATACTTGCTGGCTGGGCGCAGATATCATTGAAACAAATACTTTTAGCAGC 300

Qy       364 ACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGCCGATGGATGGAACAGTGC 423
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Db       301 ACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGCCGATGGATGGAACAGTGC 360

Qy       424 TCTGCAGGAGTGGCCAGAAAGCTGCCAGAAGCTGCCGGAGTAACTCTTCCAGACAGGAGGAATTAAGAGG 483
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TCTGCAGGAGTGGCCAGAAAGCTGCCGGAGTAACTCTTCCAGACAGGAGGAATTAAGAGG 420

Qy       484 TTTGTGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGGAA 543
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Qy      3002 ATGTCTGGCAGCTCCCGGGGCAAGTACCCGAAATCGAGGCTTCCCCAAGATATTTAACGACA 3061
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Db      3333 ATGTCTGGCAGCTCCCGGGGCAAGTACCCGAAATCGAGGCTTCCCCAAGATATTTAACGACA 3392

Qy      3062 AAACAGTAGGTGGAGAGGCCAGAGGTCTACGATGATGCCACAATGCTGAACACAC 3121
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3393 AAACAGTAGGTGGAGAGGCCAGAGGTCTACGATGATGCCACAATGCTGAACACAC 3452

Qy      3122 TGATTAGTCAAAAGAAACTCCGGGGCCCGGGGTGTCGTTGGTTCGGCCAGCACAGAGTA 3181
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Db      3453 TGATTAGTCAAAAGAAACTCCGGGGCCCGGGGTGTCGTTGGTTCGGCCAGCACAGAGTA 3512

Qy      3182 TCCAAGACGACATTCACCTGTACGCAGGAGGCTGCTGTGCCCAGGCTGCAGAGCCCATAG 3241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      3242 CCACTTTCATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCGAGCCATACT 3301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3573 CCACCTTCATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCGAGCCATACT 3632

Qy      3302 ACTGGCCTCCAGACTTCATCGCTCCCTTGCATTCTGCGATCCGTGACTACCTGGGCCTGT 3361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3633 ACTGGCCTCCAGACTTCATCGCTCCCTTGCATTCTGCGATCCGTGACTACCTGGGCCTGT 3692

Qy      3362 TGGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG 3421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3693 TTGCCCGTTGCCTGCTTTGGGGTAGAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG 3752

Qy      3422 ACTACAGCAGCACATGGTCAAGGGCCTGGGGGACCGGCCTGGGGGACCGCCTTTGCAGAAG 3481
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Db      3753 ACTACAGCAGCACATGGTCAAGGGCCTGGGGGACCGGCCTGGGGGACCGCCTTTGCAGAAG 3812

Qy      3482 AGTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGACG 3541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3813 AGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGACG 3872

Qy      3542 TCGCAGACCTTGCGAAGGTTGCGTGCGCAGGCGTGCGGGTACAAGGGCATCCCGCCGCTCCTGGCTCCTGGCTACCCCAGCC 3601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3873 TCGCAGACCTTGCGAAGGTTGCGTGCGCAGGCGTGCGGGTACAAGGGCATCCCGCCGCTCCTGGCTCCTGGCTACCCCAGCC 3932

Qy      3602 AGCCCGACCACCACCGAGAAGCTCACCATGTGGAGACTCGACAGCATCGAGACTCTACAG 3661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3933 AGCCCGACCACCACCGAGAAGCTCACCATGTGGAGACTTGCAGACATCGAGACTCTACAG 3992

Qy      3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCCCTTCACT 3721
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3993 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCCCTTCACT 4052

Qy      3722 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGAAGAGATTTCCAAGGATCAGGTTGAGG 3781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4053 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGAAGAGATTTCCAAGGATCAGGTTGAGG 4112

Qy      3782 ATTATGCATTGAGGAGGAAGAACATATCTGTGTGGCTGGCTTGAGGAAATGGCTTGGACCATTT 3841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4113 ATTATGCATTGAGGAGGAAGAACATATCTGTGTGGCTGGCTTGAGGAAATGGCTTGGACCATTT 4172

Qy      3842 TGGGATATGATACAGACTAACTTTTTTTTTTTTTTTT 3875
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Db      4173 TGGGATATGATACAGACTAACTTTTTTTTTTTTTTTT 4206
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RESULT 12
AX930571
LOCUS       AX930571          3798 bp    DNA     linear     PAT 22-DEC-2003
DEFINITION  Sequence 43 from Patent WO03087386.
ACCESSION   AX930571
VERSION     AX930571.1  GI:40312319
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
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Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      421 TTTGTGGCAGGGGCTCGGGTTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGGAA 480

Qy    544 AGGCCGGATTATAGGAACATCACATTGATGAGCTTGTTGTGAAGCATACCAAGAGCAGGCC 603
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Db    481 AGGCCGGATTATAGGAACATCACATTGATGAGCTTGTTGTGAAGCATACCAAGAGCAGGCC 540

Qy    604 AAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAAACTATTTTGATACTGCC 663
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Qy    664 AATGCCAAGGCAGCCAGCCCTGTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCCGG 723
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Db    601 AATGCCAAGGCAGCCAGCCCTGTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCCGG 660

Qy    724 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGCCGGACTCTTTCCGGACAGACA 783
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Db    661 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGCCGGACTCTTTCCGGACAGACA 720

Qy    784 GGAGAGGGATTTGTCATCAGCCGTGTCTCATGGAGAACCACTCTGCATTGATTAAATTGT 843
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Db    721 GGAGAGGGATTTGTCATCAGCCGTGTCTCATGGAGAACCACTCTGCATTGATTAAATTGT 780

Qy    844 GCTTTGGGTGCAGCTGAGATGAGACCCTTTATTGAAATAATTGGAAAAATGTACAACAGCC 903
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Db    781 GCTTTGGGTGCAGCTGAGATGAGACCCTTTATTGAAATAATTGGAAAAATGTACAACAGCC 840

Qy    904 TATGTCCTGTGTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAACG 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TATGTCCTGTGTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAACG 900

Qy    964 CCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAGTT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCTTCTATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAGTT 960

Qy   1024 GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1020

Qy   1084 TGTAAGCCTAGAGTTCCACCTGCTCGCTTTTGAAGGACACATATGTTACTGTCTCGGTCTA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGTAAGCCTAGAGTTCCACCTGCTCGCTTTTGAAGGACACATATGTTACTGTCTCGGTCTA 1080

Qy   1144 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGGCGCTGTAATGTT 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGGCGCTGTAATGTT 1140

Qy   1204 GCAGGATCAAGGAAGTTGCTAAACTCATCATGGCCAGGAACTATGAAGAAGCCTTGTGT 1263
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Db   1141 GCAGGATCAAGGAAGTTGCTAAACTCATCATGGCCAGGAACTATGAAGAAGCCTTGTGT 1200

Qy   1264 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTGTGGAAATGGGAGGC 1323
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Db   1201 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTGTGGAAATGGGAGGC 1260

Qy   1324 ATGCTAGATGGTTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGAC 1383
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Db   1261 ATGCTAGATGGTTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGAC 1320

Qy   1384 ATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGTGGGTTA 1443
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Db   1321 ATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGTGGGTTA 1380

Qy   1444 AAGTGCTGCCAAGGGAAGGCCAGGAAGTTTGCTAAAAGTATGAGAGGAGGAGGAGGACGAC 1503
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Db   1381 AAGTGCTGCCAAGGGAAGGCCAGGAAGTTTGCTAAAAGTATGAGAGGAGGAGGAGGACGAC 1440

Qy   1504 TTCTTGGAAGGCCAGGAAGTTTCTTGTCATTGGTCTATGGCTATGGGTCATGGCTTTT 1563
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Db   1441 TTCTTGGAAGGCCAGGAAGTTTCTTGTCATTGGTCTATGGCTATGGGTCATGGCTTTT 1500

Qy   1564 GATGAAGAAGGACAGGCAACAGAAACAGACACAAAAATCAGATGTGCACCCGGGCCTAC 1623
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Db   1501 GATGAAGAAGGACAGGCAACAGAAACAGACACAAAAATCAGATGTGCACCCGGGCCTAC 1560


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Qy   1624 CATCTGCTTGTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAATATC 1683
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Qy   1684 CTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTTATCCATGCA 1743
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Db   1621 CTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTTATCCATGCA 1680

Qy   1744 ACAAAGTCATTAAAGAAAACATTACCTGGAGCCAGAATAGTGGAGGTCTTTCCAACTTG 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACAAAGTCATTAAAGAAAACATTACCTGGAGCCAGAATAGTGGAGGTCTTTCCAACTTG 1740

Qy   1804 TCCTTCTTCCTTCCGACGAATGGAAGCCATTCGAGAGAGCAATGCATGAGAGCAATGTGA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 TCCTTCTTCCTTCCGACGAATGGAAGCCATTCGAGAGAGCAATGCATGAGAGCAATGTGA 1800

Qy   1864 CATGCAATCAAGTCTCGGCATGACATGGGACATGGGACTGGAAACCTCCCTGTGTAT 1923
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Db   1801 CATGCAATCAAGTCTCGGCATGACATGGGACATGGGACTGGAAACCTCCCTGTGTAT 1860

Qy   1924 GATGATATCCATAAGAACTCTCGAGATCTCATCTGGAATAAAGACCCCT 1983
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Db   1861 GATGATATCCATAAGAACTCTCGAGATCTCATCTGGAATAAAGACCCCT 1920

Qy   1984 GAGGCCACTGAGGAAGTCTTACGTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAGTC 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GAGGCCACTGAGGAAGTCTTACGTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAGTC 1980

Qy   2044 ATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACACGCTTGAGTATGCCCTGTG 2103
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Db   1981 ATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACACGCTTGAGTATGCCCTGTG 2040

Qy   2104 AAGGGCATTGAAAAACATATTATTGAGGATAATATTGAGGAAGCCAGGTTAAACCAAAAAA 2163
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Db   2041 AAGGGCATTGAAAAACATATTATTGAGGATAATATTGAGGAAGCCAGGTTAAACCAAAAAA 2100

Qy   2164 TATCCCCGACCTTCTCAATATCAGGGAAGTTGCTGAATGGAATGAATGAAAATTGTTGGT 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TATCCCCGACCTTCTCAATATCAGGGAAGTTGCTGAATGGAATGAATGAAAATTGTTGGT 2160

Qy   2224 GATCTTTTGGAGCTGAAAAATGTTTCTACCTCAGTTATAAAGTCAGCCCGGGTTATG 2283
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Db   2161 GATCTTTTGGAGCTGAAAAATGTTTCTACCTCAGTTATAAAGTCAGCCCGGGTTATG 2220

Qy   2284 AAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAGAAGAAGAGAGAGAGAAACCAGAGTG 2343
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Db   2221 AAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAGAAGAAGAGAGAGAGAAACCAGAGTG 2280

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Qy 3784 TATGCATTGAGGAAGAACATATCTGTGGCTGGACCT...GAGAAATGGCTTGAGAGGTTGAGAAATGGCTTGGACCCATTTTG 3843
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Db 3721 TATGCATTGAGGAAGAACATATCTGTGGCTGGACCT...GAGAAATGGCTTGGACCCATTTTG 3780

Qy 3844 GGATATGATACAGACTAA 3861
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Db 3781 GGATATGATACAGACTAA 3798

RESULT 13
AR300095
LOCUS   AR300095   7224 bp   DNA   linear   PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6537759.
ACCESSION   AR300095
VERSION   AR300095.1 GI:31687382
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 7224)
  AUTHORS   Stanton,V.P. Jr.
  TITLE   Folylpolyglutamate synthetase gene sequence variances having
            utility in determining the treatment of disease
  JOURNAL   Patent: US 6537759-A 1 25-MAR-2003;
            Variagenics, Inc.; Cambridge, MA
FEATURES   Location/Qualifiers
     source   1..7224
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match   79.3%; Score 3109; DB 6; Length 7224;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3859; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy   2 GTCACCTGTGAGAGACGTCTTCTGCGCCCTCTGCCAAGGAGGAGACTCGACA 61
         |||||||||||||||||||||||||||||||||||||||||||||
Db   333 GTCACCTGTGAGAGACACGTCTTCTGCGCCCTCTGCCAAGGAGGAGACTCGACA 392

Qy   62 ACATGTCACCCGCTCCAAGACCTTGCTCGCAACCGTCGAACCCGAAGGTCGAAGAAACCCTGCGGG 121
         ||||||||||||||||||||||||||||||||||||||||||||
Db   393 ACATGTCACCCGCTCCAAGACCTTGCTCGCAACCGTCGAACCCGAAGGTCGAAGAAACCCTGCGGG 452

Qy   122 ATGAGGATCAATGCCATTCTGCGAGAAGAGATTATGGTGCTGCTGATGGGGATGGGGACCA 181
         ||||||||||||||||||||||||||||||||||||||||||||
Db   453 ATGAGGATCAATGCCATTCTGCGAGAAGAGATTATGGTGCTGCTGATGGGGATGGGGACCA 512

Qy   182 TGATCCAGCGGGGAGAAGCTAAACGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 241
         ||||||||||||||||||||||||||||||||||||||||||||
Db   513 TGATCCAGCGGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 572

Qy   242 CCAGGCCGCTGAAAGGCAACAATGACAATTTTAAGTATAACTCAGCCTGATGTCATTACC 301
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Db   573 CCAGGCCGCTGAAAGGCAACAATGACAATTTTAAGTATAACTCAGCCTGATGTCATTACC 632

Qy   302 AAATCCATAAGGAATACTTCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA 361
         ||||||||||||||||||||||||||||||||||||||||||||
Db   633 AAATCCATAAGGAATACTTCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA 692

Qy   362 GCACTAGTATTGCCCAAGCTGACTATGCCTTGCCGAGGAGGTAACTCACTTGGCCTTACC 421
         ||||||||||||||||||||||||||||||||||||||||||||
Db   693 GCACTAGTATTGCCCAAGCTGACTATGCCTTGCCGAGGAGGTAACTCACTTGGCCTTACC 752

Qy   422 GCTCTGCAGAGTGGCCAGAAAAGCTGCCGAGAAAAGCTGCCGAGAAAAGCTGCCGAGAATTAAGA 481
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Db   753 GCTCTGCAGAGTGGCCAGAAAAGCTGCCGAGAAAAGCTGCCGAGAATTAAGA 812

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Qy   542 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACAACAAGAGCAGG 601
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Qy 2704 ATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTGAGATGAAAAT 2763
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Qy 2764 CTAAAGGATGAATACTTTGAGGAAATCATGGAAGATATTAGAACAGGACCAT 2823
         ||||||||||||||||||||||||||||||||||||||||||||
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Qy 2824 TATGAGTCTCTCAAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGTTTC 2883
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Qy 3124 ATTAGTCAAAAGAAACTCCGGGCCCGGGGTGGTTCTGGCCAGCACAGAGTATC 3183
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Db 3061 ATTAGTCAAAAGAAACTCCGGGCCCGGGGTGGTTCTGGCCAGCACAGAGTATC 3120

Qy 3184 CAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGTCCGTGTCCCATAGCC 3243
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Qy 3244 ACTTTCTATGGGTTAAGGCAACAGACAGCTCGCCAGGAGCTGAGAAGGACTACTAC 3303
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Qy 3304 TGCCTCTCAGACTTCATCGGCATCCGTGACTACCTGGGCCTGTTT 3363
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Qy 3424 TACAGCAGCATCATGGTCAAGGCGGTTGCCTGTGGGGGGACCGGCCTTGCGAGAAGAG 3483
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Qy       2102 TGAAGGGCATTGAAAAACATATTATTGAGGATAATACTGAGGAGCCAGTTAAACCAAAAAA 2161
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Qy       2162 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAAAATTGTTG 2221
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Db       2493 AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAAAATTGTTG 2552

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Db     4173 TGGGATATGATACAGACTAACTTTTTTTTTTTTTT 4206


RESULT 14
AR438495
LOCUS       AR438495              7224 bp    DNA      linear   PAT 20-FEB-2004
DEFINITION  Sequence 1 from patent US 6664062.
ACCESSION   AR438495
VERSION     AR438495.1  GI:42263366
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7224)
  AUTHORS   Stanton,V.P. Jr.
  TITLE     Thymidylate synthase gene sequence variances having utility in
            determining the treatment of disease
  JOURNAL   Patent: US 6664062-A 1 16-DEC-2003;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match             79.3%;  Score 3109;  DB 6;  Length 7224;
Best Local Similarity   99.6%;            Pred. No. 0;
Matches 3859; Conservative     0; Mismatches    15; Indels    0; Gaps     0;
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Qy         2 GTCACCTGTGGAGGAGCACGTCTTCTCTGCGCCGCCCTCTGCGCAGGAGGAGACTCGACA 61
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Db       333 GTCACCTGTGGAGGAGCACGTCTTCTCTGCGCCGCCCTCTGCGCAGGAGGAGACTCGACA 392

Qy        62 ACATGTCACCCGCGTCCAAGACCTGTCGCAACCCGAAGTCTGAAGAAAACCCTGCGGG 121
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Db       393 ACATGTCACCCGCGTCCAAGACCTGTCGCAACCCGAAGTCTGAAGAAAACCCTGCGGG 452

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Db       453 ATGAGATCAATGCCATTCTGCAGAGAGGATTATGTGCTGGATGGAGGGATGGGGACCA 512

Qy       182 TGATCCAGCCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAGTTAAAGATCATG 241
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Db      3753 ACTACAGCAGCATCATGGTCAAGGTGGTCAAGGCGCGGGCTGGGGAGAGGCCTTTGCAGAAG 3812

Qy      3482 AGCTCCATGAAAAGAGAGTTCGCGCGAGACTGTGGGCGCCGAGAACTGTGGCGCAGCTGGACG 3541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3813 AGCTCCATGAAAAGAGAGTTCGCGCGAGACTGTGGGCGCCGAGAACTGTGGCGCAGCTGGACG 3872

Qy      3542 TCGGCAGACCTGCGAAGGTTGCCGGTACAAGGGCATCCGGCCTCCGCTTCGCGTCCCGGCC 3601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3873 TCGGCAGACCTGCGAAGGTTGCCGGTACAAGGGCATCCGGCCTCCGCTTCGCGTCCCGGCC 3932

Qy      3602 AGCCCGACCACACCGAGAAGTCACCATGTGCAGACTCGACAGACATCGAGCAGTCTACAG 3661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3933 AGCCCGACCACACCGAGAAGTCACCATGTGCAGACTCGACAGACATCGAGCAGTCTACAG 3992

Qy      3662 GCATTAGGTTAACAGAATCATTAGCAATGGCAACGTCGCACCTGCTTCAGGGCCTTCTACT 3721
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3993 GCATTAGGTTAACAGAATCATTAGCAATGGCAACGTCGCACCTGCTTCAGGGCCTTCTACT 4052

Qy      3722 TCTCCAATTTGAAGTCCAAATATTTTGCTCGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 3781
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4053 TCTCCAATTTGAAGTCCAAATATTTTGCTCGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 4112

Qy      3782 ATTATGCATTGAGGAGACATATCGTGCTGCGCGAGAAATGGCTTGGACCCATTT 3841
             ||||||||||||||||||||||||||||||||||||| |||||||||||||||
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Qy      3842 TGGGATATGATACAGACTAACTTTTTTTTTTTTTTTT 3875
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Qy   662 CCAATGCCAAGGCAGCCTTGTTTGCACTCACTCTTTTTGAGGAGAAATATGCTCCCC 721
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Db   993 CCAATGCCAAGGCAGCCTTGTTTGCACTCACTCTTTTTGAGGAGAAATATGCTCCCC 1052

Qy   722 GGCCTATCTTTATTTCAGGGACGATCGTTGACTCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA 781
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  1053 GGCCTATCTTTATTTCAGGGACGATCGTTGACTCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA 1112

Qy   782 CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT 841
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  1113 CAGGAGAGGGATTTGTCATCAGCGNTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT 1172

Qy   842 GTGCTTGGGTGCAGCTGAGTGAGCACCTTTATTGAAATAATTGGAAAATGTACAACAG 901
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1173 GTGCTTGGGTGCAGCTGAGTGAGCACCTTTATTGAAATAATTGGAAAATGTACAACAG 1232

Qy   902 CCTATGTCCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA 961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1233 CCTATGTCCCTCTGTTATCCNAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA 1292

Qy   962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGCTTGGTCAATATAG 1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1293 CGCCTTCTATGATGGGCCAAGCACCTAAAGGATTTTGCTATGGATGCTTGGTCAATATAG 1352

Qy  1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCCAGGGAGAATTGCTAGCTGTGAAAA 1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1353 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCCAGGGAGAATTGCTAGCTGTGAAAA 1412

Qy  1082 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCCACTGCTTTTGAGGACATATGTTACTGTCTGGTC 1141
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1413 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCCACTGCTTTTGAGGACATATGTTACTGTCTGGTC 1472

Qy  1142 TAGAGCCCTTCAGGATTGACCGTACACCCAACTTGTTAACATTGGAGAGCGCTGTAATG 1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1473 TAGAGCCCTTCAGGATTGACCGTACACCCAACTTGTTAACATTGGAGAGCGCTGTAATG 1532

Qy  1202 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGCGCAGAAACTATGAAGAAGCCTTGT 1261
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Db  1533 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGCGCAGAAACTATGAAGAAGCCTTGT 1592

Qy  1262 GTGTTGCCAAAGTCAGGTGGAAATGGGAGCCCAGTTGTTGGATGTCAACATGATGATG 1321
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Db  1593 GTGTTGCCAAAGTCAGGTGGAAATGGGAGCCCAGTTGTTGGATGTCAACATGATGATG 1652

Qy  1322 GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCTTCCGAGCCAG 1381
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Db  1653 GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCTTCCGAGCCAG 1712

Qy  1382 ACATGCAAAGTACCTTGTGTCATGCAGCTCCTCCAATTTTGCTGTGATTGAAGCTGGGT 1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1713 ACATGCAAAGTACCTTGTGTCATGCAGCTCCTCCAATTTTGCTGTGATTGAAGCTGGGT 1772

Qy  1442 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAAGGACG 1501
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Db  1773 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAAGGACG 1832

Qy  1502 ACTTCTTGGAGAAGAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGTGGTCATGCGTT 1561
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Db  1833 ACTTCTTGGAGAAGAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGTGGTCATGCGTT 1892

Qy  1562 TTGATGAAGAAGGACAGGCAACAGCAACAGAAAAATCAGAGAGTGTGCACCCGGCCT 1621
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Db  1893 TTGATGAAGAAGGACAGGCAACAGCAACAGAAAAATCAGAGAGTGTGCACCCGGCCT 1952

Qy  1622 ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAATA 1681
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1953 ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAATA 2012

Qy  1682 TCCTAACCATTGGAACTGGAATGGGACTTTAATCCAAATGACAACTTGTATGCCATTAATTTTATCCATG 1741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2013 TCCTAACCATTGGAACTGGAATGGGACTTTAATCCAAATGACAACTTGTATGCCATTAATTTTATCCATG 2072
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Qy  1742 CAACAAAGTCATTAAAGAACATTACCTGGAGCCAGAATAAGTGGAGTCTTTCCAACT 1801
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Db  2073 CAACAAAGTCATTAAAGAACATTACCTGGAGCCAGAATAAGTGGAGTCTTTCCAACT 2132

Qy  1802 TGTCCTTCTCCTTCCCGGAGAATGGAAGCCATTCGAAGCCAATGCATGGGGTTTCCTTT 1861
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Db  2133 TGTCCTTCTCCTTCCCGGAGAATGGAAGCCATTCGAAGCCAATGCATGGGGTTTCCTTT 2192

Qy  1862 ACCATGCAATCAAGTCTGGCATGGACATGGACATGTCTGAAACCTCCCTGTGT 1921
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2193 ACCATGCAATCAAGTCTGGCATGGACATGGACATGTCTGAAACCTCCCTGTGT 2252

Qy  1922 ATGATGATATCCATAAGGAACTTCTGCAGCTTCTGTGAAGATCTCATCTGAATAAAGACC 1981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2253 ATGATGATATCCATAAGGAACTTCTGCAGCTTCTGTGAAGATCTCATCTGAATAAAGACC 2312

Qy  1982 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACCAGGGAGGAAGAAAG 2041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2313 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACCAGGGAGGAAGAAAG 2372

Qy  2042 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTGAGTGCCCTTG 2101
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Db  2373 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTGAGTGCCCTTG 2432

Qy  2102 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGCCAGTTAAACCAAAAA 2161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2433 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAGCCAGTTAAACCAAAAA 2492

Qy  2162 AATATCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAATGAAAAATTGTTG 2221
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Db  2493 AATATCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAATGAAAAATTGTTG 2552

Qy  2222 GTGATCTTTTTTGGAGCTGGCACCTTTGTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
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Db  2553 GTGATCTTTTTTGGAGCTGGCACCTTTGTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2612

Qy  2282 TGAAGAAGGCTGTTGGCCACCTTTCATGGAAAAGATCATAGTTGGAGTAGTTCCTTGG 2341
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2613 TGAAGAAGGCTGTTGGCCACCTTTCATGGAAAAGATCATAGTTGGAGTAGTTCCTTGG 2672

Qy  2342 TGCTTAACGGCACAGTAGAGAAGAGGACCCTTACCAGGGCACCATCGTGTCTGGCCACTG 2401
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2673 TGCTTAACGGCACAGTAGAGAAGAGGACCCTTACCAGGGCACCATCGTGTCTGGCCACTG 2732

Qy  2402 TTAAAGGCGACGTGCACGATAATTTAGGAGTCATGATTAAGGATTCATCCTTGATGAAA 2461
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Db  2733 TTAAAGGCGACGTGCACGATAATTTAGGAGTCATGATTAAGGATTCATCCTTGATGAAA 2792

Qy  2462 ATTTCCGAGTTATTGATTTAGGAGTCATGATTAAGTGATAAGACTCTGAAAGCTGTC 2521
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2793 ATTTCCGAGTTATTGATTTAGGAGTCATGATTAAGTGATAAGACTCTGAAAGCTGTC 2852

Qy  2522 TTGACCACAAAGCAGATAATAATTGGCCTGTCGAGGACTCATCATCCTCCTGATGAAA 2581
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2853 TTGACCACAAAGCAGATAATAATTGGCCTGTCGAGGACTCATCATCCTCCTGATGAAA 2912

Qy  2582 TGATTTTTGTTGCCAAGGAAATGGAAATGGGAGATTAGCTATAAGAATTGTTGATTGGAG 2641
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Db  2913 TGATTTTTGTTGCCAAGGAAATGGAAATGGGAGATTAGCTATAAGAATTGTTGATTGGAG 2972

Qy  2642 GAGCAACACTTCAAAAACCCACACAGTAAATAGCTCCGAGATACAGTGCACCTG 2701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2973 GAGCAACACTTCAAAAACCCACACAGTAAATAGCTCCGAGATACAGTGCACCTG 3032

Qy  2702 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTTCCCAGCTGTTAGATGAAA 2761
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Db  3033 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTTCCCAGCTGTTAGATGAAA 3092

Qy  2762 ATCTAAAGGATGAATGAATACTTTGAGGAAAATCATGAAGAAATATGAAGAAGATTAGACAGGACC 2821
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3093 ATCTAAAGGATGAATGAATACTTTGAGGAAAATCATGAAGAAATATGAAGAAGATTAGACAGGNCC 3152

Qy  2822 ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGTT 2881
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LOCUS           AR562003                    7224 bp    DNA              linear   PAT 08-OCT-2004
DEFINITION      AR562003 Sequence 1 from patent US 6759200.
ACCESSION       AR562003
VERSION         AR562003.1  GI:53975655
KEYWORDS        .
SOURCE          Unknown.
  ORGANISM      Unknown.
                Unclassified.
REFERENCE       1  (bases 1 to 7224)
  AUTHORS       Stanton,V.P.Jr.
  TITLE         Thymidine phosphorylase gene sequence variances having utility in
                determining the treatment of disease
  JOURNAL       Patent: US 6759200-A 1 06-JUL-2004;
                Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
  source          1..7224
                  /organism="unknown"
                  /mol_type="genomic DNA"
ORIGIN

Query Match             79.3%;  Score 3109;  DB 6;  Length 7224;
Best Local Similarity   99.6%;  Pred. No. 0;
Matches 3859;           Conservative   0;  Mismatches  15;  Indels    0;  Gaps    0;
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Qy          2 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACA 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACA 392

Qy         62 ACATGTCACCCGCGTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 ACATGTCACCCGCGTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG 452

Qy        122 ATGAGATCAATGCCATTCTGCAGAGAGGATTATGTGCTGGATGGAGGATGGGGGACCA 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATGAGATCAATGCCATTCTGCAGAGAGGATTATGTGCTGGATGGAGGATGGGGGACCA 512

Qy        182 TGATCCAGCGGGAGAGAGCTAAACGAGAAGAACACTTCCGAGGTCAGGAGTTAAAGATCATG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 TGATCCAGCGGGAGAGAGCTAAACGAGAAGAACACTTCCGAGGTCAGGAGTTAAAGATCATG 572

Qy        242 CCAGGGCGCTGAAAGGCAACAATGACACATTTTAAGTATAACTCAGCCTGATGTCATTTACC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 CCAGGGCGCTGAAAGGCAACAATGACACATTTTAAGTATAACTCAGCCTGATGTCATTTACC 632

Qy        302 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCGACACTTGGCCTACCGGATGAACATGT 361
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCGACACTTGGCCTACCGGATGAACATGT 692

Qy        362 GCACTAGTATTGCCCAAGCTGACTATGCCCGAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGAATTAAGA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 GCACTAGTATTGCCCAAGCTGACTATGCCCGAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGAATTAAGA 752

Qy        422 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA 812

Qy        482 GGTTTGTGGCAGGGGCTTCTGGGTCCGGCTTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGG 541
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Db        813 GGTTTGTGGCAGGGGCTTCTGGGTCCGGCTTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGG 872

Qy        542 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGGAAGCATACCAAGAGCAGG 601
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Db        873 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGGAAGCATACCAAGAGCAGG 932

Qy        602 CCAAAGGACTTCTGATCTGAGTGGCGGGGTTGATATCTTTACTCATTGAAACTATTTTGATACTG 661
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Db        933 CCAAAGGACTTCTGATGGCGGGGTTGATATCTTTACTCATTGAAACTATTTTGATACTG 992

Qy        662 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC 1052
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Db       3153 ATTATGAGTCTCTCAAGAGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAANTNGTT 3212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||

Qy       2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG 2941
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3213 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG 3272

Qy       2942 TCTTTGAAGACTATGACCTGCGAGAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG 3001
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Db       3273 TCTTTGAAGACTATGACCTGCGAGAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG 3332

Qy       3002 ATGTCTGGCCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACA 3061
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3333 ATGTCTGGCCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTTCCCAAGATATTTAACGACA 3392

Qy       3062 AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAAATATGCTGAACACAC 3121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3393 AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAAATATGCTGAACACAC 3452

Qy       3122 TGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTCGTTGGGTTCTCGGCCAGCACAGAGTA 3181
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Db       3453 TGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTCGTTGGGTTCTCGGCCAGCACAGAGTA 3512

Qy       3182 TCCAAGACGACATTCACCTGTACGCAGCAGAGGCTGCTGTCCCCAGGCTGCAGAGCCCATAG 3241
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Db       3513 TCCAAGACGACATTCACCTGTACGCAGCAGAGGCTGCTGTCCCCAGGCTGCAGAGCCCATAG 3572

Qy       3242 CCACTTTCTATGGGTTAAGGCAACAGGCTCTGCCAGCACGGACTCTGAGAGCACGGAGCACTACT 3301
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Db       3573 CCACCTTCTATGGGTTAAGGCAACAGGCTCTGCCAGCACGGACTCTGAGAGCACGGAGCACTACT 3632

Qy       3302 ACTGCCTCTCAGACTTCATCGCTTCATTGCCTCCCTTGCATCCGTTGACTACCTGGCCTGT 3361
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Db       3633 ACTGCCTCTCAGACTTCATCGCTTCATTGCCTCCCTTGCATCCGTTGACTACCTGGCCTGT 3692

Qy       3362 TTGCCGTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCTATGAGGATGATGGTGACG 3421
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Db       3693 TTGCCGTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCTATGAGGATGATGGTGACG 3752

Qy       3422 ACTACAGCAGCATCATGGTCAAGGCGTCAAGGGCGCTGGCAGAGGCCTTTGCAGAAG 3481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3753 ACTACAGCAGCATCATGGTCAAGGCGTCAAGGGCGCTGGCAGAGGCCTTTGCAGAAG 3812

Qy       3482 AGCTTCCATGAAAGAGTTCGCGCCAAGGTTGGCGTACAAGGGCATCCGCCCGGCTCCTGCAGCCAGCC 3541
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Db       3813 AGCTTCCATGAAAGAGTTCGCGCCAAGGTTGGCGTACAAGGGCATCCGCCCGGCTCCTGCAGCCAGCC 3872

Qy       3542 TCGCAGACCTGCGAAGGTTGGCGTACAAGGGCATCCGCCCGGCTCCTGCAGCCAGCC 3601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3873 TCGCAGACCTGCGCAGGCTGCGGTACAAGGGCATCCGCCCGGCTCCTGCAGCCAGCC 3932

Qy       3602 AGCCCGACCACCACCAGAAGCTCACCATGTGGAGACTGCGCAGACATCGAGCAGTCTACAG 3661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3933 AGCCCGACCACCACCAGAAGCTCACCATGTGGAGACTGCGCAGACATCGAGCAGTCTACAG 3992

Qy       3662 GCATTAGGTTAACAGAATCATTAGCAATGCAATGCACTTGCTTCAGCGTCTCAGGCCTCTACT 3721
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Db       3993 GCATTAGGTTAACAGAATCATTAGCAATGCAATGCACTTGCTTCAGCGTCTCAGGCCTCTACT 4052

Qy       3722 TCTCCAATTTGAAGTCAAATATTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 3781
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Db       4053 TCTCCAATTTGAAGTCAAATATTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 4112

Qy       3782 ATTATGCATTGAGGAAGAACATATCTGTGGCTTGTGGCTGAGTTGAAAATGGCTTGGACCCATTT 3841
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Db       4113 ATTATGCATTGAGGAAGAACATATCTGTGGCTTGTGGCTGAGTTGAAAATGGCTTGGACCCATTT 4172

Qy       3842 TGGGATATGATGATCACAGACTAACTTTTTTTTTTTTT 3875
              |||||||||||||||||||||||||||||||

Db       4173 TGGGATATGATGATCACAGACTAACTTTTTTTTTTTTTT 4206
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RESULT 15

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Qy    722  GGCCTATCTTATTTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTCCGGACAGA   781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1053  GGCCTATCTTATTTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTCCGGACAGA  1112

Qy    782  CAGGAGAGGGATTTGTCATCAGCGTGTCTCAGTGAGAACCACTCTGCATTGGATTAAATT   841
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Db   1113  CAGGAGAGGGATTTGTCATCAGCGNTGTCTCAGTGAGAACCACTCTGCATTGGATTAAATT  1172

Qy    842  GTGCTTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAG   901
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Db   1173  GTGCTTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAG  1232

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Qy   2462  ATTTCCGAGTTATTGATTTAGGAGTCATGAGTCCATGTGATAAGATACTGAAAGCTGCTC  2521
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SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 5240)
  AUTHORS   Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  CONSRTM   The German Human cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            This clone (DKFZp686A22123) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
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RESULT 16
HSM807075

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LOCUS       HSM807075               5240 bp    mRNA    linear   PRI 17-APR-2005
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686A22123 (from clone DKFZp686A22123).
ACCESSION   BX641132
VERSION     BX641132.1  GI:34365460
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Db    766 CCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAAATTGTTGGTGATC  825

Qy   2228 TTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTATGAAGA 2287
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 TTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTATGAAGA  885

Qy   2288 AGGCGCACAGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCC 2347
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 AGGCGCACAGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCC  945

Qy   2348 ACGGCACAGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCC 2407
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 ACGGCACAGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATAATTTCC 1005

Qy   2408 GCGACGTGCAGGTTGCGTACAGGGTACAGGGCATCCGCCCGGCTGCTCCTGGCTGCAATAATTTCC 2467
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 GCGACGTGCAGGTTGCGTACAGGGTACAGGGCATCCGCCCGGCTGCTCCTGGCTGCAATAATTTCC 1065

Qy   2468 GAGTTATTGATTTGATTTAGGAGTCATGAGTCATGTCAATAGTGATAAGATACTGAAAGCTGCTCTTGACC 2527
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 GAGTTATTGATTTGATTTAGGAGTCATGAGTCATGTCAATAGTGATAAGATACTGAAAGCTGCTCTTGACC 1125

Qy   2528 ACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGAATGAAATGAATT 2587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 ACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGAATGAAATGAATT 1185

Qy   2588 TTGTTGCCAAGGAAATGGAGAAGAATGGAGAGAGATTAGCTATAAGGAATTCCATTGTTGATTGGAGGAGCAA 2647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2588 TTGTTGCCAAGGAAATGGAGAAGAATGGAGAGAGATTAGCTATAAGGAATTCCATTGTTGATTGGAGGAGCAA 2707
```

Db   2266 GGTTAACGAGAATCATTAGCAATGGCAATGCACCTGCTTCAGCAGTCTCAGGCCTCTACTTCTCCA 2325
Qy   3728 ATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTCCAAGGATCAGGTTGAGGATTATG 3787
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 ATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTCCAAGGATCAGGTTGAGGATTATG 2385
Qy   3788 CATTGAGGAAGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATTTTGGGAT 3847
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 CATTGAGGAAGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATTTTGGGAT 2445
Qy   3848 ATGATACAGACTAACTTTTTTTTTTTTT 3875
          ||||||||||||||||||||||||||||
Db   2446 ATGATACAGACTAACTTTTTTTTTTTTT 2473

RESULT 17
CQ721809
LOCUS   CQ721809   1835 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION Sequence 7743 from Patent WO02068579.
ACCESSION   CQ721809
VERSION   CQ721809.1 GI:42282666
KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE   Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 7743 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
     source   1..1835
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   18.2%; Score 714; DB 6; Length 1835;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 764; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1252 GAAGCCTTGTGTGTTGCCAAAGTGCGAGGTGCAAAATGGGAGCCCAGTGTGTTGGATGTCAAC 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1071 GAAGCCTTGTGTGTTGCCAAAGTGCGAGGTGCAAAATGGGAGCCCAGTGTGTTGGATGTCAAC 1130
Qy   1312 ATGGATGATGGCCATGCTAGATGGTCCAAGTGCAATGCAATGGAGATTTTGCAACTTAAATTGCT 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1131 ATGGATGATGGCCATGCTAGATGGTCCAAGTGCAATGCAATGGAGATTTTGCAACTTAAATTGCT 1190
Qy   1372 TCCGAGCCAGACATCGCAAAGTACCTTTGTCATCGACTCCTCCAATTTTGCTGTGATT 1431
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1191 TCCGAGCCAGACATCGCAAAGTACCTTTGTCATCGACTCCTCCAATTTTGCTGTGATT 1250
Qy   1432 GAAGCTGGGTTAAAGTGCTCGCCAAGGGAAGTGCATTGCAATAGCATTAGTCTGAAGGAA 1491
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1251 GAAGCTGGGTTAAAGTGCTCGCCAAGGGAAGTGCATTGCAATAGCATTAGTCTGAAGGAA 1310
Qy   1492 GGGAGGACGACTTCTTGGAGAAGAGGCCAGGAAGATTAAAAGTAATGGAGTGCTATGGTG 1551
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1311 GGGAGGACGACTTCTTGGAGAAGAGGCCAGGAAGATTAAAAGTAATGGAGTGCTATGGTG 1370
Qy   1552 GTCATGGCTTTTGATGAAGAAGAGGACAGGCAACAGAAACAGACAGAAATCAGAGTGTGC 1611
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1371 GTCATGGCTTTTGATGAAGAAGAGGACAGGCAACAGAAACAGACAGAAATCAGAGTGTGC 1430
Qy   1612 ACCCGGCGCTACCATCTGCTTGTGAAAAAACTGGCTTTAATCCAAATGACATTATTTTT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1431 ACCCGGCGCTACCATCTGCTTGTGAAAAAACTGGCTTTAATCCAAATGACATTATTTTT 1490

Db   1672 GACCCTAATATCCTAACCATTGGACTGGAATGGAGGAACACAACCTGTATGCCATTAAT 1731
Qy   1491 GACCCTAATATCCTAACCATTGGACTGGAATGGAGGAACACAACCTGTATGCCATTAAT 1550
Qy   1732 TTTATCCATGCAACAAAAGTCATTAAAGAAACATTACCTGAGCCCAGAATAAGTAGTGGAGGT 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1551 TTTATCCATGCAACAAAAGTCATTAAAGAAACATTACCTGAGCCCAGAATAAGTAGTGGAGGT 1610
Qy   1792 CTTTCCAACTTGTCCTTCCTTCCTTCCGGAGGAATGGAAGCCATTCGAGAGAGCAATGCAATGGG 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1611 CTTTCCAACTTGTCCTTCCTTCCTTCCGGAGGAATGGAAGCCATTCGAGAGAGCAATGCAATGGG 1670
Qy   1852 GTTTTCCTTTACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGGAAAC 1911
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1671 GTTTTCCTTTACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGGAAAC 1730
Qy   1912 CTCCCTGTGTGATGATGATATCCATAAGGAACTTCTGCAGCTCGTGAAGATCTCATCTGG 1971
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1731 CTCCCTGTGTGATGATGATATCCATAAGGAACTTCTGCAGCTCGTGAAGATCTCATCTGG 1790
Qy   1972 AATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAG 2016
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1791 AATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAG 1835

RESULT 18
CQ850206
LOCUS   CQ850206   4172 bp   DNA   linear   PAT 23-AUG-2004
DEFINITION Sequence 675 from Patent EP1447413.
ACCESSION   CQ850206
VERSION   CQ850206.1 GI:51508418
KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,
            Otsuki,T., Wakamatsu,A., Ishii,S., Nagai,K. and Irie,R.
  TITLE   Full-length human cDNA
  JOURNAL   Patent: EP 1447413-A 675 18-AUG-2004;
            Research Association for Biotechnology (JP)
FEATURES   Location/Qualifiers
     source   1..4172
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   7.9%; Score 308; DB 6; Length 4172;
Best Local Similarity   99.5%; Pred. No. 5.3e-168;
Matches 408; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   3467 AGGCCTTTGCAGAAGAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCA 3526
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1015 AGGCCTTTGCAGAAGAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCA 1074
Qy   3527 GTGAGCAGCTGGACGTCGCGACCTGCGAAGGTTGCGCGGTACAAGGGCATCCGCCCCGCTC 3586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1075 GTGAGCAGCTGGACGTCGCGACCTGCGAAGGTTGCGCGGTACAAGGGCATCCGCCCCGCTC 1134
Qy   3587 CTGGCTACCCCAGCCAGCCCGACCACACCGAGAAGCTCACCATGTGGAGACTGCAGACA 3646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1135 CTGGCTACCCCAGCCAGCCCGACCACACCGAGAAGCTCACCATGTGGAGACTGCAGACA 1194
Qy   3647 TCGAGCAGTCACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAG 3706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1195 TCGAGCAGTCACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAG 1254
Qy   3707 TCTCAGGCCTCTACTTCTCCAATTTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCA 3766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1255 TCTCAGGCCTCTACTTCTCCAATTTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCA 1314

RESULT 19

```
AK127317
LOCUS       AK127317                4172 bp    mRNA    linear   PRI 19-FEB-2004
DEFINITION  Homo sapiens cDNA FLJ45386 fis, clone BRHIP3023922, highly similar
            to 5-methyltetrahydrofolate--homocysteine methyltransferase (EC
            2.1.1.13).
ACCESSION   AK127317
VERSION     AK127317.1  GI:34534177
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kanehori,K., Ishibashi,T., Chiba,Y., Fujimori,K., Hiraoka,S.,
            Tanai,H., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Watanabe,M.,
            Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
            Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
            Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Takahashi-Fujii,A., Oshima,A., Sugiyama,A.,
            Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K.,
            and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 4172)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: Reverse Proteomics Research Institute, HRI and
            RAB.
FEATURES             Location/Qualifiers
     source          1..4172
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="BRHIP3023922"
                     /tissue_type="hippocampus"
                     /clone_lib="BRHIP3"
                     /note="cloning vector: pME18SFL3"
ORIGIN

Query Match             7.9%;  Score 308;  DB 8;  Length 4172;
Best Local Similarity  99.5%;  Pred. No. 5.3e-168;
Matches  408;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   3467 AGGCCCTTGCAGAAGAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCA 3526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1015 AGGCCCTTGCAGAAGAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCA 1074

Qy   3527 GTGAGCAGCTGGACGTCGCGAGACCTGCCGAGGTTGCGGTACAAGGGCATCCGCCCGGCTC 3586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1075 GTGAGCAGCTGGACGTCGCGAGACCTGCCGAGGTTGCGGTACAAGGGCATCCGCCCGGCTC 1134

Qy   3587 CTGGCTACCCCAGCCCAGCCCGACCACACCGAGAAGCTCACCATGTGGAGACTCGCAGACA 3646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1135 CTGGCTACCCCAGCCCAGCCCGACCACACCGAGAAGCTCACCATGTGGAGACTCGCAGACA 1194

Qy   3647 TCGAGCAGTCTACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAG 3706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1195 TCGAGCAGTCTACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAG 1254

Qy   3707 TCTCAGGCCCTCACTTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGGAAGATTCCA 3766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1255 TCTCAGGCCCTCACTTCTCCAATTGAAGTCCAAATATTTGCTGTGGGGGAAGATTTCCA 1314

Qy   3767 AGGATCAGGTTGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAAT 3826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1315 AGGATCAGGTTGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAAT 1374

Qy   3827 GGCTTGGACCCATTTGGGATATGATACAGACTAACTTTTTTTTTTTTTT 3876
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1375 GGCTTGGACCCATTTGGGATATGATACAGACTAACTTTTTTTTTTTTTT 1424
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RESULT 20

```
AY429553
LOCUS       AY429553                 435 bp    mRNA    linear   PRI 27-APR-2004
DEFINITION  Homo sapiens MTRv_1 mRNA sequence, alternatively spliced.
ACCESSION   AY429553
VERSION     AY429553.1  GI:46488815
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 435)
  AUTHORS   Johnson,J.M., Castle,J., Garrett-Engele,P.W., Kan,Z., Loerch,P.M.,
            Armour,C.D., Santos,R., Schadt,E.E., Stoughton,R. and
            Shoemaker,D.D.
  TITLE     Genome-wide survey of human alternative pre-mRNA splicing with exon
            junction microarrays
  JOURNAL   Science 302 (5653), 2141-2144 (2003)
   PUBMED   14684825
REFERENCE   2  (bases 1 to 435)
  AUTHORS   Johnson,J.M., Castle,J., Garrett-Engele,P.W., Loerch,P.M., Kan,Z.,
            Armour,C.D., Santos,R., Schadt,E.E., Stoughton,R. and
            Shoemaker,D.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-2003) Genomic Discovery, Rosetta/MRL, 12040 115th
            Ave NE, Kirkland, WA 98034, USA
FEATURES             Location/Qualifiers
     source          1..435
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     misc_feature    <1..>435
                     /note="MTRv_1; alternatively spliced compared to
                     NM_000254"
ORIGIN

Query Match             7.6%;  Score 297;  DB 8;  Length 435;
Best Local Similarity  100.0%;  Pred. No. 1.6e-161;
Matches  297;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    530 CCCCATCTGTGAAGAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCAT 589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCCCATCTGTGAAGAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCAT 60

Qy    590 ACCAAGAGCAGGCCAAAGGACTTCTCGGATGGCGGGGTTGATATCTTACTCATTGAAACTA 649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACCAAGAGCAGGCCAAAGGACTTCTCGGATGGCGGGGTTGATATCTTACTCATTGAAACTA 120

Qy    650 TTTTTGATACTGCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGA 709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTTTTGATACTGCCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGA 180
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RESULT 21
BD060282
LOCUS       BD060282              305 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Secreted expressed sequence tags (sESTs).
ACCESSION   BD060282
VERSION     BD060282.1  GI:22605888
KEYWORDS    JP 2001518793-A/642.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 305)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secreted expressed sequence tags (sESTs)
  JOURNAL   Patent: JP 2001518793-A 642 16-OCT-2001;
            GENETICS INSTITUTE INC
COMMENT     PN   JP 2001518793-A/642
            PD   16-OCT-2001
            PF   10-APR-1998 JP 198543070
            PR   10-APR-1997 US 08/837312
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
            DAVID MERBERG,
            PI   MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
            C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC   Strandedness:
            Double;
            CC   Topology: Linear;
FEATURES             Location/Qualifiers
     source          1..305
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"
ORIGIN

Query Match             5.7%;  Score 222;  DB 6;  Length 305;
  Best Local Similarity   99.6%;
  Matches  272;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy       2751 GTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAAATGAAGATAT 2810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 GTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAAATGAAGATAT 81

Qy       2811 TAGACAGGACCATTATGAGTCTTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAG 2870
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 TAGACAGGGGCCATTATGAGTCTTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAG 141

Qy       2871 AAAAAGTGGTTTCCAAATGGATTGGCTGTCTGAACCTTCACCCAGTGAAGCCCACGTTTAT 2930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 AAAAAGTGGTTTCCAAATGGATTGGCTGTCTGAACCTTCACCCAGTGAAGCCCACGTTTAT 201

Qy       2931 TGGGACCCAGGTCTTTGAAGACTATGACCTGCGAGAGCTGGTGGACTACATTGACTGGAA 2990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TGGGACCCAGGTCTTTGAAGACTATGACCTGCGAGAGCTGGTGGACTACATTGACTGGAA 261

Qy       2991 GCCTTTCTTTGATGTCTGGCCAGCTCCGGGGCAA 3023
              ||||||||||||||||||||||||||||||||||
Db        262 GCCTTTCTTTGATGTCTGGCCAGCTCCGGGGCAA 294

RESULT 22
AL359185
LOCUS       AL359185             108841 bp    DNA     linear   PRI 18-MAY-2005
DEFINITION  Human DNA sequence from clone RP11-382M16 on chromosome 1 Contains
            the 3' end of the ACTN2 gene for actinin, alpha 2, the 5' end of
            the MTR gene for 5-methyltetrahydrofolate-homocysteine
            methyltransferase, a laminin receptor 1 (ribosomal protein.SA,
            67kDa) (LAMR1) pseydogene and a CpG island, complete sequence.
ACCESSION   AL359185
VERSION     AL359185.25  GI:1885190
KEYWORDS    HTG; ACTN3; CpG island; LAMR1; MTR.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 108841)
  AUTHORS   Skuce,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Feb 21, 2002 this sequence version replaced gi:18655978.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
            Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1
            RP11-382M16 is from the library RPCI-11.2 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            ---------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            ----------------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e. phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compression and repeats; all regions were covered by at least
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                     AL359921.13:204778..204856,AL359921.13:208333..208414,
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Qy   770 TTTCCGACAGACAGGAGAGGAGGATTGTCATCAGCGTGTCTCATGGAGAACCACTCT 826
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                    AL359921.13:204778.   .204856,AL359921.13:208333.  .208414,
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                    AL359921.13:204778.   .204856,AL359921.13:208333.  .208414,
                    AL359921.13:211533.   .211618,977.   .1062,2464.  .2556,
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RESULT 23
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DEFINITION  Homo sapiens chromosome 1 clone RP11-519B18, 21 unordered pieces.
ACCESSION   AL357554
VERSION     AL357554.5  GI:9930950
KEYWORDS    HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burton,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Aug 27, 2000 this sequence version replaced gi:9863824.
            ------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ---------- Project Information
            Center project name: bA519B18
            ---------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 170239 bases at least Q40
            Consensus quality: 174637 bases at least Q30
            Consensus quality: 177473 bases at least Q20
            Insert size: 181166; sum-of-contigs
            Insert size: 190445; agarose-fp
            Quality coverage: 3.39x in Q20 bases; sum-of-contigs Quality
            coverage: 3.38x in Q20 bases; agarose-fp
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          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 21 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *         1        6704: contig of 6704 bp in length
          *      6705        6804: gap of 100 bp
          *      6805       12664: contig of 5860 bp in length
          *     12665       12764: gap of 100 bp
          *     12765       19106: contig of 6342 bp in length
          *     19107       19206: gap of 100 bp
          *     19207       33463: contig of 14257 bp in length
          *     33464       33563: gap of 100 bp
          *     33564       41253: contig of 7690 bp in length
          *     41254       41353: gap of 100 bp
          *     41354       43907: contig of 2554 bp in length
          *     43908       44007: gap of 100 bp
          *     44008       58491: contig of 14484 bp in length
          *     58492       58591: gap of 100 bp
          *     58592       68531: contig of 9940 bp in length
          *     68532       68631: gap of 100 bp
          *     68632       74641: contig of 6010 bp in length
          *     74642       74741: gap of 100 bp
          *     74742       88760: contig of 14019 bp in length
          *     88761       88860: gap of 100 bp
          *     88861       94546: contig of 5686 bp in length
          *     94547       94646: gap of 100 bp
          *     94647       96751: contig of 2105 bp in length
          *     96752       96851: gap of 100 bp
          *     96852      107533: contig of 10682 bp in length
          *    107534      107633: gap of 100 bp
          *    107634      115732: contig of 8099 bp in length
          *    115733      115832: gap of 100 bp
          *    115833      132328: contig of 16496 bp in length
          *    132329      132428: gap of 100 bp
          *    132429      139993: contig of 7505 bp in length
          *    139934      140033: gap of 100 bp
          *    140034      148812: contig of 8779 bp in length
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          *    148913      164368: contig of 15456 bp in length
          *    164369      164468: gap of 100 bp
          *    164469      167514: contig of 3046 bp in length
          *    167515      167614: gap of 100 bp
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ORIGIN

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Qy     157 GTGCTGGATGAGGGATGGGGACCATGATCCAGCGGGAGAAGCTAAACGAAGAACACTTC 216
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Qy     217 CGAGGTCAGGAATTTAAAGATCATGCCAGGCCGCTGAAAGGCCAACAATGACATTTTAAGT 276
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Qy     277 ATAACTCAGCCTGATGTCATTTACCAAATCCATAAGG 313
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RESULT 24
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DEFINITION  Homo sapiens chromosome 1 clone RP11-11N21 map 1, WORKING DRAFT
            SEQUENCE, 37 unordered pieces.
ACCESSION   AC079975
VERSION     AC079975.2  GI:11276222
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 164529)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 1, clone RP11-11N21
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 164529)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
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COMMENT     On Nov 22, 2000 this sequence version replaced gi:10198369.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ------------------- Genome Center
              Center: Whitehead Institute/ MIT Center for Genome Research
              Center code: WIBR
              Web site: http://www-seq.wi.mit.edu
              Contact: sequence_submissions@genome.wi.mit.edu
            ------------------- Project Information
              Center project name: L11095
              Center clone name: 11_N_21
            ------------------- Summary Statistics
              Sequencing vector: Plasmid; n/a; 100% of reads
              Chemistry: Dye-terminator Big Dye; 100% of reads
              Assembly program: Phrap; version 0.960731
              Consensus quality: 147566 bases at least Q40
              Consensus quality: 155962 bases at least Q30
              Consensus quality: 159155 bases at least Q20
              Insert size: 170000; agarose-fp
              Insert size: 160929; sum-of-contigs
              Quality coverage: 3.7 in Q20 bases; agarose-fp
              Quality coverage: 3.9 in Q20 bases; sum-of-contigs
            --------------------------------------------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 37 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            --------------------------------------------------
            *        1:       638: contig of 638 bp in length
            *      639:       738: gap of 100 bp
            *      739:      1280: contig of 542 bp in length
            *     1281:      1380: gap of 100 bp
            *     1381:      2021: contig of 641 bp in length
            *     2022:      2121: gap of 100 bp
            *     2122:      2830: contig of 709 bp in length
            *     2831:      2930: gap of 100 bp
            *     2931:      3970: contig of 1040 bp in length
            *     3971:      4070: gap of 100 bp
            *     4071:      4923: contig of 853 bp in length
            *     4924:      5023: gap of 100 bp
            *     5024:      6063: contig of 1040 bp in length
            *     6064:      6163: gap of 100 bp
            *     6164:      7446: contig of 1283 bp in length
            *     7447:      7546: gap of 100 bp
            *     7547:      9381: contig of 1835 bp in length
            *     9382:      9481: gap of 100 bp
            *     9482:     11219: contig of 1738 bp in length
            *    11220:     11319: gap of 100 bp
            *    11320:     12350: contig of 1031 bp in length
            *    12351:     12450: gap of 100 bp
            *    12451:     13291: contig of 841 bp in length
            *    13292:     13391: gap of 100 bp
            *    13392:     14939: contig of 1548 bp in length
            *    14940:     15039: gap of 100 bp
            *    15040:     17136: contig of 2097 bp in length
            *    17137:     17236: gap of 100 bp
            *    17237:     19620: contig of 2384 bp in length
            *    19621:     19720: gap of 100 bp
            *    19721:     22736: contig of 3016 bp in length
            *    22737:     22836: gap of 100 bp
            *    22837:     45780: contig of 22944 bp in length
            *    45781:     45880: gap of 100 bp
            *    45881:     48594: contig of 2714 bp in length
            *    48595:     48694: gap of 100 bp
            *    48695:     51084: contig of 2390 bp in length
            *    51085:     51184: gap of 100 bp
            *    51185:     53490: contig of 2306 bp in length
            *    53491:     53590: gap of 100 bp
            *    53591:     55545: contig of 1955 bp in length
```

```
*     55546    55645: gap of 100 bp
*     55646    57961: contig of 2316 bp in length
*     57962    58061: gap of 100 bp
*     58062    59375: contig of 1314 bp in length
*     59476    59475: gap of 100 bp
*     59476    63078: contig of 3603 bp in length
*     63079    63179: gap of 100 bp
*     63179    65356: contig of 2178 bp in length
*     65357    65456: gap of 100 bp
*     65457    68583: contig of 3127 bp in length
*     68584    68683: gap of 100 bp
*     68684    73074: contig of 4391 bp in length
*     73075    73174: gap of 100 bp
*     73175    76675: contig of 3501 bp in length
*     76676    76775: gap of 100 bp
*     76776    81036: contig of 4261 bp in length
*     81037    81136: gap of 100 bp
*     81137    86818: contig of 5682 bp in length
*     86819    86918: gap of 100 bp
*     86919    94761: contig of 7843 bp in length
*     94762    94861: gap of 100 bp
*     94862   102806: contig of 7945 bp in length
*    102807   102906: gap of 100 bp
*    102907   117954: contig of 15048 bp in length
*    117955   118054: gap of 100 bp
*    118055   130927: contig of 12873 bp in length
*    130928   131027: gap of 100 bp
*    131028   145686: contig of 14659 bp in length
*    145687   145786: gap of 100 bp
*    145787   162777: contig of 16991 bp in length
*    162778   162877: gap of 100 bp
*    162878   164529: contig of 1652 bp in length.

FEATURES         Location/Qualifiers
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                 /mol_type="genomic DNA"
                 /db_xref="taxon:9606"
                 /chromosome="1"
                 /map="1"
                 /clone="RP11-11N21"
                 /clone_lib="RPCI-11 Human Male BAC"
     misc_feature 1..638
                 /note="assembly_fragment
                 clone_end:SP6
                 vector_side:left"
     gap         639..738
                 /estimated_length=100
     misc_feature 739..1280
                 /note="assembly_fragment"
     gap         1281..1380
                 /estimated_length=100
     misc_feature 1381..2021
                 /note="assembly_fragment"
     gap         2022..2121
                 /estimated_length=100
     misc_feature 2122..2830
                 /note="assembly_fragment"
     gap         2831..2930
                 /estimated_length=100
     misc_feature 2931..3970
                 /note="assembly_fragment"
     gap         3971..4070
                 /estimated_length=100
     misc_feature 4071..4923
                 /note="assembly_fragment"
     gap         4924..5023
                 /estimated_length=100
     misc_feature 5024..6063
                 /note="assembly_fragment"
     gap         6064..6163
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     misc_feature 6164..7446
                 /note="assembly_fragment"
     gap         7447..7546
                 /estimated_length=100
     misc_feature 7547..9381
                 /note="assembly_fragment"
     gap         9382..9481
                 /estimated_length=100
     misc_feature 9482..11219
                 /note="assembly_fragment"
     gap         11220..11319
                 /estimated_length=100
     misc_feature 11320..12350
                 /note="assembly_fragment"
     gap         12351..12450
                 /estimated_length=100
     misc_feature 12451..13291


Query Match     5.2%;  Score 204;  DB 14;  Length 164529;
Best Local Similarity  100.0%;  Pred. No. 7.6e-107;
Matches 204;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   3266 AGGCTGAGAAGGACTTCGCCAGCACGGAGCCATACTACTGCCTCTCCAGACTTCATCGCTC 3325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  41412 AGGCTGAGAAGGACTTCGCCAGCACGGAGCCATACTACTGCCTCTCCAGACTTCATCGCTC 41353

Qy   3326 CCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTTGCCGTTGCCGTTTGGGGTAG 3385
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  41352 CCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTTGCCGTTGCCGTTTGGGGTAG 41293

Qy   3386 AAGAGCTGAGCAAGGCCTATGAGGATGAGGATGATGTGACGACTACAGCAGCATCATGGTCAAGG 3445
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  41292 AAGAGCTGAGCAAGGCCTATGAGGATGAGGATGATGTGACGACTACAGCAGCATCATGGTCAAGG 41233

Qy   3446 CGCTGGGGGACCGGCTGGCCAGAGG 3469
          |||||||||||||||||||||||||
Db  41232 CGCTGGGGGACCGGCTGGCCAGAGG 41209


RESULT 25
AC074231
LOCUS       AC074231          164933 bp    DNA     linear   HTG 21-JUL-2000
DEFINITION  Homo sapiens chromosome 1 clone RP11-192B19, WORKING DRAFT
            SEQUENCE, 9 ordered pieces.
ACCESSION   AC074231
VERSION     AC074231.1  GI:9309505
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 164933)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Human Chromosome 1
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 164933)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     -----Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -----
            Sequence Quality Assessment:
            This entry has been annotated with sequence quality
            estimates computed by the Phrap assembly program.
            All manually edited bases have been reduced to quality zero.
            Quality levels above 40 are expected to have less than
            1 error in 10,000 bp.
            Base-by-base quality values are not generally visible from the
            GenBank flat file format but are available as part
            of this entry's ASN.1 file.
```

```
RESULT 26
AL359259
LOCUS       AL359259              172753 bp    DNA     linear   PRI 18-MAY-2005
DEFINITION  Human DNA sequence from clone RP11-182B22 on chromosome 1 Contains
            the 3' end of the MTR gene for
            5-methyltetrahydrofolate-homocysteine methyltransferase, a novel
            gene (LOC149948), a ribosomal protein L35 (RPL35) pseudogene, and a
            novel gene similar to metallothionein 1H (MT1H), complete sequence.
ACCESSION   AL359259
VERSION     AL359259.18  GI:1957239?
KEYWORDS    HTG; LOC149948; MT1H; MTR; RPL35.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 172753)
AUTHORS     Mashreghi-Mohammadi,M.
TITLE       Direct Submission
JOURNAL     Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Mar 21, 2002 this sequence version replaced gi:17426972.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1
            RP11-182B22 is from the library RPCI-11.1 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            -------------------------------------
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            -------------------------------------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one subclone; and the assembly was confirmed by restriction digest,
            except on the rare occasion of the clone being a YAC.
FEATURES             Location/Qualifiers
     source          1..172753
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP11-182B22"
                     /clone_lib="RPCI-11.1"
     misc_feature    1
                     /note="Clone_left_end: RP11-182B22"
     gene            join(AL359185.25:60652..61079,AL359185.25:68770..68984,
                     AL359185.25:71486..71575,AL359185.25:74046..74115,
                     AL359185.25:75845..75937,AL359185.25:78080..78186,
                     AL359185.25:80946..81005,AL359185.25:81791..81885,
                     AL359185.25:89461..89561,AL359185.25:90680..90741,
                     AL359185.25:92171..92238,AL359185.25:94531..94610,
                     AL359185.25:97308..97420,AL359185.25:100889..101029,
                     AL359185.25:103756..103941,8845..9024,11022..11138,
                     11449..11589,18334..18423,19626..19778,20737..20844,
                     21955..22055,32274..32341,33227..33347,39256..39337,
                     43622..43720,44793..44868,47682..47837,49634..49730,
                     52858..53058,53859..54051,55507..55619,56059..62482)
                     /gene="MTR"
                     /locus_tag="RP11-182B22.1-001"
```
```
            * -----------------------------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 9 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *      1      21033: contig of 21033 bp in length
            *  21034      21133: gap of unknown length
            *  21134      32645: contig of 11512 bp in length
            *  32646      32745: gap of unknown length
            *  32746      45829: contig of 13084 bp in length
            *  45830      45929: gap of unknown length
            *  45930     128181: contig of 82252 bp in length
            * 128182     128281: gap of unknown length
            * 128282     130330: contig of 2049 bp in length
            * 130331     130430: gap of unknown length
            * 130431     141292: contig of 10862 bp in length
            * 141293     141392: gap of unknown length
            * 141393     151367: contig of 9975 bp in length
            * 151368     151467: gap of unknown length
            * 151468     161306: contig of 9839 bp in length
            * 161307     161406: gap of unknown length
            * 161407     164933: contig of 3527 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
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     gap             161307..161406
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ORIGIN

Query Match       5.2%;  Score 204;  DB 14;  Length 164933;
Best Local Similarity   100.0%;
Matches  204;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;  Pred. No. 7.6e-107;

Qy   3266 AGGCTGAGAAGGACTCTGCCAGCACGGACCGCACGGAGCCCATACTACTGCCTCTCAGACTTCATCGCTC 3325
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1448 AGGCTGAGAAGGACTCTGCCAGCACGGACCGCACGGAGCCCATACTACTGCCTCTCAGACTTCATCGCTC 1507

Qy   3326 CCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTGCCGTTGCCGTTGCCGTTTGGGGTAG 3385
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1508 CCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTGCCGTTGCCGTTGCCGTTTGGGGTAG 1567

Qy   3386 AAGAGCTGAGCAAGGCCTATGAGGATGATGATGGTGACGACTACAGCAGCAGCATCATGGTCAAGG 3445
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1568 AAGAGCTGAGCAAGGCCTATGAGGATGATGATGGTGACGACTACAGCAGCAGCATCATGGTCAAGG 1627

Qy   3446 CGCTGGGGGACCCGGCTGGCAGAGG 3469
               |||||||||||||||||||||||||
Db   1628 CGCTGGGGGACCCGGCTGGCAGAGG 1651
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mRNA

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         join(AL359185.25:60652.     .61079,AL359185.25:68770.   .68984,
         AL359185.25:71486.    .71575,AL359185.25:74046.   .74115,
         AL359185.25:75845.    .75937,AL359185.25:78080.   .78186,
         AL359185.25:80946.    .81005,AL359185.25:81791.   .81885,
         AL359185.25:89461.    .89561,AL359185.25:90680.   .90741,
         AL359185.25:92171.    .92238,AL359185.25:94531.   .94610,
         AL359185.25:97308.    .97420,AL359185.25:100889.   .101029,
         AL359185.25:103756.   .103941,8845.    .9024,11022.   .11138,
         11449.   .11589,18334.   .18423,19626.   .19778,20737.   .20844,
         21955.   .22055,32274.   .32341,33227.   .33347,39256.   .39337,
         43622.   .43720,44793.   .44868,47682.   .47837,49634.   .49830,
         52858.   .53058,53859.   .54051,55507)
         /locus_tag="RP11-182B22.1-001"
         /product="5-methyltetrahydrofolate-homocysteine
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         /note="match: ESTs: Em:AA233650.1 Em:AA356439.1
         Em:AA676323.1 Em:AA782469.1 Em:AA843354.1 Em:AAB57538.1
         Em:AA975197.1 Em:AI130762.1 Em:AI141234.1 Em:AI202545.1
         Em:AI337887.1 Em:AI425009.1 Em:AI692587.1 Em:AI697569.1
         Em:AI742646.1 Em:AI829040.1 Em:AI872333.1 Em:AL598311.1
         Em:AU077264.1 Em:AU100277.1 Em:AW277117.1 Em:AW299977.1
         Em:AW589940.1 Em:AW958815.1 Em:BE463498.1 Em:BE673742.1
         Em:BE879762.1 Em:BF034321.1 Em:BF215782.1 Em:BF381641.1
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         Em:BX498595.1 Em:BX499278.1 Em:BX510153.1 Em:CD516382.1
         Em:CB857945.1 Em:CB858029.1 Em:CD515399.1 Em:U71285.1
         Em:CF887086.1 Em:CF890798.1
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gene

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         join(AL359185.25:<100958.   .101029,
         AL359185.25:103756.   .103860,8845.    .9024,11022.   .11138,
         11449.   .11589,18334.   .18423,19626.   .19778,20737.   .20844,
         21955.   .22055,32274.   .32341,33227.   .33347,39256.   .39337,
         43622.   .43720,44793.   .44868,47682.   .47837,49634.   .49830,
         52858.   .53058,53859.   .54051,55507.   .55619,56059.   .58919)
         /gene="MTR"
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mRNA

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         11449.   .11589,18334.   .18423,19626.   .19778,20737.   .20844,
         21955.   .22055,32274.   .32341,33227.   .33347,39256.   .39337,
         43622.   .43720,44793.   .44868,47682.   .47837,49634.   .49830,
         52858.   .53058,53859.   .54051,55507.   .55619,56059.   .58919)
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         /gene="MTR"
         /product="5-methyltetrahydrofolate-homocysteine
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         /note="match: cDNAs: Em:BX641132.1"
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CDS

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         AL359185.25:75845.   .75937,AL359185.25:78080.   .78186,
         AL359185.25:80946.   .81005,AL359185.25:81791.   .81885,
         AL359185.25:89461.   .89561,AL359185.25:90680.   .90741,
         AL359185.25:92171.   .92238,AL359185.25:94531.   .94610,
         AL359185.25:97308.   .97420,AL359185.25:100889.   .101029,
         AL359185.25:103756.   .103941,8845.    .9024,11022.   .11138,
         11449.   .11589,18334.   .18423,19626.   .19778,20737.   .20844,
         21955.   .22055,32274.   .32341,33227.   .33347,39256.   .39337,
         43622.   .43720,44793.   .44868,47682.   .47837,49634.   .49830,
         52858.   .53058,53859.   .54051,55507.   .55619,56059.   .56145)
         /gene="MTR"
         /standard_name="OTTHUMP00000037964"
         /note="match: proteins: Sw:Q99707 Tr:Q8JIY6 Tr:Q9ZZQ4"
         /codon_start=1
         /product="5-methyltetrahydrofolate-homocysteine
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methyltransferase

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         /protein_id="CAH70983.1"
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         /db_xref="InterPro:IPR000489"
         /db_xref="InterPro:IPR003726"
         /db_xref="InterPro:IPR003759"
         /db_xref="InterPro:IPR004223"
         /db_xref="InterPro:IPR006158"
         /db_xref="InterPro:IPR010988"
         /db_xref="InterPro:IPR011005"
         /db_xref="InterPro:IPR011007"
         /translation="MSPALQDLSQPEGLKKTLRDEINAILQKRIMVLDGGMGTMIQRE
         KLNEEHFRGQEFKDHARPLKGNNDILSITQPDVIYQIHKEYLLAGADIETNTFSSTS
         IAQADYGLEHLAYRMNMCSAGVARKAAEEVTLQTGIKRFVAGALGPTNKTLSVSPSVE
         RPDYRNITFDELVEAYQEQAKGLLDGGVDLLLIETIFPDTANAKAALFALQNLFEEKYA
         PRPIFISGTIVDKSGRTLSGQTGEGFVISVSHGEPLCIGLNCALGAAEMRPFIEIIGK
         CTRAYVLCYPNAGLPNTFGDYDETPSMMAKHLKDFAMDGLVNIVGGCCGSTPDHIREI
         AEAVNCKPRVPPATAFEGHMLLSGLEPFRIGPYTNFVNIGERCNVAGSRKFAKLIMA
         GNYEEALCVAKVQVEMGACQVLDVNMDDGMLDGPSAMTRFCNLIASEPDIAKVPLCIDS
         SNFAVIEAGLKCCQGKCIVNSISLKEGEDFLEKARKIKKYGAAMVMAFDEEGQATE
         TDTKIRVCTRAYHLLVKKLGFNPNDIIFDPNILTIGTGMEHNLYAINFIHATKVIKE
         TLPGARISGGLSNLSFSFRGMEAIREAMHGVFLYHAIKSGMDMGIVNAGNLPVYDDIH
         KELLQLCEDLIWNKDPEATEKLLRYAQTQGTGKKVIQTDEWRNGPVEERLEYALVKG
         IEKHIIEDTEEARLNQKKYPRPLNIIEGPLMNGMKIVGDLFGAGKMFLPQVIKSARVM
         KKAVGHLIPFMEKEREETRVLNGTVEEEDPYQGTIVLATVKGDVHDIGKNIVGVVLGC
         NNFRVIDLGVMTPCDKILKAALDHKADIIGLSGLITPSLDEMIFVAKEMERLAIRIPL
         LIGGATTSKTHTAVKIAPRYSAPVIHVLDASKSVVCSQLLDENLKDEYFEIMEEYE
         DIRQDHYESLKERRYLPLSQARKSGFQMDWLSEPHPVKPTFIGTQVFEDYDLQKLVDY
         IDWKPFFDVWQLRGKYPNRGFPKIFNDKTVGGEARKVYDDAHNMLNTLISQKKLRARG
         VVGFWPAQSIQDDIHLYAEAAVPQAAEPIATFYGLRQQAEKDSASTEPYYCLSDFIAP
         LHSGIRDYLGLFAVACFGVEELSKAYEDDGDDYSSIMVKALGDRLAEAAFAEELHERVR
         RELWAYCGSEQLDVADLRRLRYKGIRPAPGYPSQPDHTEKLTMWRLADIEQSTGIRLT
         ESLAMAPASAVSGLYFSNLKSKYFAVGKISKDQVEDYALRKNISVAEVEKWLGPIIGY
         DTD"
```

CDS

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         join(AL359185.25:<100958.   .101029,
         AL359185.25:103756.   .103860,8845.    .9024,11022.   .11138,
         11449.   .11589,18334.   .18423,19626.   .19778,20737.   .20844,
         21955.   .22055,32274.   .32341,33227.   .33347,39256.   .39337,
         43622.   .43720,44793.   .44868,47682.   .47837,49634.   .49830,
         52858.   .53058,53859.   .54051,55507)
         /locus_tag="RP11-182B22.1-002"
         /standard_name="OTTHUMP00000037965"
         /codon_start=1
         /product="5-methyltetrahydrofolate-homocysteine
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methyltransferase

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         /protein_id="CAH70984.1"
         /db_xref="GI:55664392"
         /db_xref="GOA:Q5VXE0"
         /db_xref="InterPro:IPR000489"
         /db_xref="InterPro:IPR003759"
         /db_xref="InterPro:IPR004223"
         /db_xref="InterPro:IPR006158"
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Query Match          5.2%;   Score 204;   DB 8;   Length 172753;
Best Local Similarity   100.0%;   Pred. No. 7.6e-107;
Matches 204;   Mismatches    0;   Conservative    0;   Indels    0;   Gaps    0;

Qy   3266 AGGCTGAGAAGGACTCTGCCAGCACCGGAGCCATACTACTGCCTCTCCAGACTTCATCGCTC 3325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  52856 AGGCTGAGAAGGACTCTGCCAGCACCGGAGCCATACTACTGCCTCTCCAGACTTCATCGCTC 52915

Qy   3326 CCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTTGCCGTTGCCGTTGCCGTTGGGGTAG 3385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  52916 CCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTTGCCGTTGCCGTTGCCGTTGGGGTAG 52975

Qy   3386 AAGAGCTGAGCAAGGCCTATGCAGCAGCATGGTGACGACTACAGCAGCATCAGTGGTCAAGG 3445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  52976 AAGAGCTGAGCAAGGCCTATGCAGCAGCATGGTGACGACTACAGCAGCATCAGTGGTCAAGG 53035
```

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Qy     3446  CGCTGGGGGACCGGCTGGCAGAGG 3469
             ||||||||||||||||||||||||
Db    53036  CGCTGGGGGACCGGCTGGCAGAGG 53059
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RESULT 27
AC080149/c
LOCUS        AC080149            176671 bp    DNA     linear   HTG 24-AUG-2002
DEFINITION   Homo sapiens chromosome 14 clone RP11-10110 map 14, WORKING DRAFT
             SEQUENCE, 21 unordered pieces.
ACCESSION    AC080149
VERSION      AC080149.2  GI:11276221
KEYWORDS     HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1  (bases 1 to 176671)
  AUTHORS    Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE      Homo sapiens chromosome 14, clone RP11-10110
  JOURNAL    Unpublished
REFERENCE    2  (bases 1 to 176671)
  AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
             Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
             Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
             Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
             DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
             FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
             Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
             Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
             Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G.,
             Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
             McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
             Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
             O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K.,
             Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
             Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
             Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
             Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
             Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
             Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
             Zimmer,A. and Zody,M.
  TITLE      Direct Submission
  JOURNAL    Submitted (26-SEP-2000) Whitehead Institute/MIT Center for Genome
             Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE    3  (bases 1 to 176671)
  AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
             Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
             Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
             Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
             DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
             FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
             Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
             Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
             Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G.,
             Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
             McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
             Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
             O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K.,
             Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
             Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
             Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
             Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
             Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
             Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
             Zimmer,A. and Zody,M.
  TITLE      Direct Submission
  JOURNAL    Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
             Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT      On Nov 22, 2000 this sequence version replaced gi:10305243.
             All repeats were identified using RepeatMasker:
             Smit, A.F.A. & Green, P. (1996-1997)
             http://ftp.genome.washington.edu/RM/RepeatMasker.html
             -------- Genome Center
             Center: Whitehead Institute/ MIT Center for Genome Research
             Center code: WIBR
             Web site: http://www-seq.wi.mit.edu
             Contact: sequence_submissions@genome.wi.mit.edu
             -------- Project Information
             Center project name: L11093
             Center clone name: 10.I.10
             -------- Summary Statistics
             Sequencing vector: Plasmid; n/a; 100% of reads
             Chemistry: Dye-terminator Big Dye; 100% of reads
             Assembly program: Phrap; version 0.960731
             Consensus quality: 169296 bases at least Q40
             Consensus quality: 172583 bases at least Q30
             Consensus quality: 173740 bases at least Q20
             Insert size: 186000; agarose-fp
             Insert size: 174671; sum-of-contigs
             Quality coverage: 5.3 in Q20 bases; agarose-fp
             Quality coverage: 5.7 in Q20 bases; sum-of-contigs
             --------
             * NOTE: This is a 'working draft' sequence. It currently
             * consists of 21 contigs. The true order of the pieces
             * is not known and their order in this sequence record is
             * arbitrary. Gaps between the contigs are represented as
             * runs of N, but the exact sizes of the gaps are unknown.
             * This record will be updated with the finished sequence
             * as soon as it is available and the accession number will
             * be preserved.
             *         1:    171: contig of 171 bp in length
             *       172:    271: gap of 100 bp
             *       272:    866: contig of 595 bp in length
             *       867:    966: gap of 100 bp
             *       967:   1667: contig of 701 bp in length
             *      1668:   1767: gap of 100 bp
             *      1768:   2728: contig of 961 bp in length
             *      2729:   2828: gap of 100 bp
             *      2829:   3495: contig of 667 bp in length
             *      3496:   3595: gap of 100 bp
             *      3596:   4294: contig of 699 bp in length
             *      4295:   4394: gap of 100 bp
             *      4395:   5091: contig of 697 bp in length
             *      5092:   5191: gap of 100 bp
             *      5192:   5814: contig of 623 bp in length
             *      5815:   5914: gap of 100 bp
             *      5915:   6560: contig of 646 bp in length
             *      6561:   6660: gap of 100 bp
             *      6661:   7288: contig of 628 bp in length
             *      7289:   7388: gap of 100 bp
             *      7389:   8033: contig of 645 bp in length
             *      8034:   8133: gap of 100 bp
             *      8134:  11152: contig of 3019 bp in length
             *     11153:  11252: gap of 100 bp
             *     11253:  16926: contig of 5674 bp in length
             *     16927:  17026: gap of 100 bp
             *     17027:  48247: contig of 31221 bp in length
             *     48248:  48347: gap of 100 bp
             *     48348:  56048: contig of 7701 bp in length
             *     56049:  56148: gap of 100 bp
             *     56149:  68742: contig of 12594 bp in length
             *     68743:  68842: gap of 100 bp
             *     68843:  86438: contig of 17596 bp in length
             *     86439:  86538: gap of 100 bp
             *     86539: 107927: contig of 21389 bp in length
             *    107928: 108027: gap of 100 bp
             *    108028: 135702: contig of 27675 bp in length
             *    135703: 135802: gap of 100 bp
             *    135803: 170129: contig of 34327 bp in length
             *    170130: 170229: gap of 100 bp
             *    170230: 176671: contig of 6442 bp in length.
FEATURES             Location/Qualifiers
     source          1..176671
                     /organism="Homo sapiens"
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Qy    3386  AAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGACTACAGCAGCATCATGGTCAAGG  3445
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Db   35316  AAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGACTACAGCAGCATCATGGTCAAGG  35257

Qy    3446  CGCTGGGGAGGACCGGCTGGCAGAGG  3469
            ||||||||||||||||||||||||||
Db   35256  CGCTGGGGAGGACCGGCTGGCAGAGG  35233
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RESULT 28
AL357554/c
LOCUS       AL357554              18166 bp    DNA     linear   HTG 11-SEP-2001
DEFINITION  Homo sapiens chromosome 1 clone RP11-519B18, 21 unordered pieces.
ACCESSION   AL357554
VERSION     AL357554.5  GI:9930950
KEYWORDS    HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burton,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Aug 27, 2000 this sequence version replaced gi:9863824.
            -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bA519B18
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 170239 bases at least Q40
            Consensus quality: 174637 bases at least Q30
            Consensus quality: 177473 bases at least Q20
            Insert size: 181166; sum-of-contigs
            Insert size: 190445; agarose-fp
            Quality coverage: 3.39x in Q20 bases; sum-of-contigs Quality
            coverage: 3.38x in Q20 bases; agarose-fp
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 21 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1      6704: contig of 6704 bp in length
            *     6705      6804: gap of 100 bp
            *     6805     12664: contig of 5860 bp in length
            *    12665     12764: gap of 100 bp
            *    12765     19106: contig of 6342 bp in length
            *    19107     19206: gap of 100 bp
            *    19207     33463: contig of 14257 bp in length
            *    33464     33563: gap of 100 bp
            *    33564     41253: contig of 7690 bp in length
            *    41254     41353: gap of 100 bp
            *    41354     43907: contig of 2554 bp in length
            *    43908     44007: gap of 100 bp
            *    44008     58491: contig of 14484 bp in length
            *    58492     58591: gap of 100 bp
            *    58592     68531: contig of 9940 bp in length
            *    68532     68631: gap of 100 bp
            *    68632     74641: contig of 6010 bp in length
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             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /chromosome="14"
             /map="14"
             /clone="RP11-10I10"
             /clone_lib="RPCI-11 Human Male BAC"
misc_feature 1..171
             /note="assembly_fragment
             clone_end:SP6
             vector_side:left"
gap          172..271
             /estimated_length=100
misc_feature 272..866
             /note="assembly_fragment"
gap          867..966
             /estimated_length=100
misc_feature 967..1667
             /note="assembly_fragment"
gap          1668..1767
             /estimated_length=100
misc_feature 1768..2728
             /note="assembly_fragment"
gap          2729..2828
             /estimated_length=100
misc_feature 2829..3495
             /note="assembly_fragment"
gap          3496..3595
             /estimated_length=100
misc_feature 3596..4294
             /note="assembly_fragment"
gap          4295..4394
             /estimated_length=100
misc_feature 4395..5091
             /note="assembly_fragment"
gap          5092..5191
             /estimated_length=100
misc_feature 5192..5814
             /note="assembly_fragment"
gap          5815..5914
             /estimated_length=100
misc_feature 5915..6560
             /note="assembly_fragment"
gap          6561..6660
             /estimated_length=100
misc_feature 6661..7288
             /note="assembly_fragment"
gap          7289..7388
             /estimated_length=100
misc_feature 7389..8033
             /note="assembly_fragment"
gap          8034..8133
             /estimated_length=100
misc_feature 8134..11152
             /note="assembly_fragment"
gap          11153..11252
             /estimated_length=100
misc_feature 11253..16926
             /note="assembly_fragment"
gap          16927..17026
             /estimated_length=100
misc_feature 17027..48247
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Query Match     5.2%;   Score 204;  DB 14;  Length 176671;
Best Local Similarity  100.0%;  Pred. No. 7.6e-107;
Matches 204;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    3266  AGGCTGAGAAGGACTTCGCCAGCACGGAGCCATACTACTGCCTTCAGACTTCATCGCGTC  3325
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   35436  AGGCTGAGAAGGACTTCGCCAGCACGGAGCCATACTACTGCCTTCAGACTTCATCGCGTC  35377

Qy    3326  CCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTGCCGTTGCCTGCTTTGGGGTAG  3385
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   35376  CCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTGCCGTTGCCTGCTTTGGGGTAG  35317
```

```
                74642         74741: gap of 100 bp
        *       74742         88760: contig of 14019 bp in length
        *       88761         88860: gap of 100 bp
        *       88861         94546: contig of 5686 bp in length
        *       94547         94646: gap of 100 bp
        *       94647         96751: contig of 2105 bp in length
        *       96752         96851: gap of 100 bp
        *       96852        107533: contig of 10682 bp in length
        *      107534        107633: gap of 100 bp
        *      107634        115732: contig of 8099 bp in length
        *      115733        115832: gap of 100 bp
        *      115833        132328: contig of 16496 bp in length
        *      132329        132428: gap of 100 bp
        *      132429        139933: contig of 7505 bp in length
        *      139934        140033: gap of 100 bp
        *      140034        148812: contig of 8779 bp in length
        *      148813        148912: gap of 100 bp
        *      148913        164368: contig of 15456 bp in length
        *      164369        164468: gap of 100 bp
        *      164469        167514: contig of 3046 bp in length
        *      167515        167614: gap of 100 bp
        *      167615        179223: contig of 11609 bp in length
        *      179224        179323: gap of 100 bp
        *      179324        183166: contig of 3843 bp in length.
FEATURES             Location/Qualifiers
     source          1..183166
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP11-519B18"
                     /clone_lib="RPCI-11.2"
     misc_feature    1..6704
                     /note="assembly_fragment:01430
                     clone_end:SP6
                     vector_side:left"
     misc_feature    6805..12664
                     /note="assembly_fragment:02073
                     fragment_chain:1"
     misc_feature    12765..19106
                     /note="assembly_fragment:01812
                     fragment_chain:1"
     misc_feature    19207..33453
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                     fragment_chain:1"
     misc_feature    33564..41253
                     /note="assembly_fragment:00536
                     fragment_chain:2"
     misc_feature    41354..43907
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                     fragment_chain:2"
     misc_feature    44008..58491
                     /note="assembly_fragment:00818
                     fragment_chain:3"
     misc_feature    58592..68531
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                     fragment_chain:3"
     misc_feature    68632..74641
                     /note="assembly_fragment:00900
                     fragment_chain:4"
     misc_feature    74742..88760
                     /note="assembly_fragment:00002
                     fragment_chain:4"
     misc_feature    88861..94546
                     /note="assembly_fragment:01286
                     fragment_chain:5"
     misc_feature    94647..96751
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     misc_feature    96852..107533
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                     fragment_chain:6"
     misc_feature    115833..132328
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     misc_feature    132429..139933
                     /note="assembly_fragment:01112"
     misc_feature    140034..148812
                     /note="assembly_fragment:01320"
     misc_feature    148913..164368
                     /note="assembly_fragment:01509"
     misc_feature    164469..167514
                     /note="assembly_fragment:01886"
     misc_feature    167615..179223
                     /note="assembly_fragment:01970"
     misc_feature    179324..183166
                     /note="assembly_fragment:02051"
ORIGIN

Query Match          4.8%;   Score 189;   DB 14;   Length 183166;
Best Local Similarity 100.0%;  Pred. No. 5e-98;
Matches 189;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     1391 AGGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTAAAGTGCT 1450
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   146952 AGGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTAAAGTGCT 146893

Qy     1451 GCCAAGGGAAGTGCATTGTCAATAGCATTAGTTGAGGAGGAGGAGGACGACTTCTTGG 1510
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   146892 GCCAAGGGAAGTGCATTGTCAATAGCATTAGTTGAGGAGGAGGAGGACGACTTCTTGG 146833

Qy     1511 AGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTTTTGATGAAG 1570
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   146832 AGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTTTTGATGAAG 146773

Qy     1571 AAGGACAGG 1579
            |||||||||
Db   146772 AAGGACAGG 146764


RESULT 29
AC080149
LOCUS       AC080149              176671 bp    DNA     linear   HTG 24-AUG-2002
DEFINITION  Homo sapiens chromosome 14 clone RP11-10I10 map 14, WORKING DRAFT
            SEQUENCE, 21 unordered pieces.
ACCESSION   AC080149
VERSION     AC080149.2  GI:11276221
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 176671)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 14, clone RP11-10I10
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 176671)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
            FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
            Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
            Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G.,
            Macdonald,P., Marquis,R., McCarthy,M., McEwan,P., McKernan,K.,
            McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
            O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K.,
            Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
            Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
            Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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                Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
                Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
                Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
                Zimmer.A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-SEP-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3 (bases 1 to 176671)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
            FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
            Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
            Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G.,
            Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
            McPheeters,R., Meldrin,J., Meneus,L., Mihova,T., Mlenga,V.,
            Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
            O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K.,
            Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
            Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
            Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
            Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
            Zimmer.A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Nov 22, 2000 this sequence version replaced gi:10305243.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------------- Genome Center
              Center: Whitehead Institute/ MIT Center for Genome Research
              Center code: WIBR
              Web site: http://www-seq.wi.mit.edu
              Contact: sequence submissions@genome.wi.mit.edu
            -------------------- Project Information
              Center project name: L11093
              Center clone name: 10_I_10
            -------------------- Summary Statistics
              Sequencing vector: Plasmid; n/a; 100% of reads
              Chemistry: Dye-terminator Big Dye; 100% of reads
              Assembly program: Phrap; version 0.960731
              Consensus quality: 169296 bases at least Q40
              Consensus quality: 172583 bases at least Q30
              Consensus quality: 173740 bases at least Q20
              Insert size: 186000; agarose-fp
              Insert size: 174671; sum-of-contigs
              Quality coverage: 5.3 in Q20 bases; agarose-fp
              Quality coverage: 5.7 in Q20 bases; sum-of-contigs

            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 21 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *       1    171: contig of 171 bp in length
            *     172    271: gap of 100 bp
            *     272    866: contig of 595 bp in length
            *     867    966: gap of 100 bp
            *     967   1667: contig of 701 bp in length
            *    1668   1767: gap of 100 bp
            *    1768   2728: contig of 961 bp in length
            *    2729   2828: gap of 100 bp
            *    2829   3495: contig of 667 bp in length
            *    3496   3595: gap of 100 bp
            *    3596   4294: contig of 699 bp in length
            *    4295   4394: gap of 100 bp
            *    4395   5091: contig of 697 bp in length
            *    5092   5191: gap of 100 bp
            *    5192   5814: contig of 623 bp in length
            *    5815   5914: gap of 100 bp
            *    5915   6560: contig of 646 bp in length
            *    6561   6660: gap of 100 bp
            *    6661   7288: contig of 628 bp in length
            *    7289   7388: gap of 100 bp
            *    7389   8033: contig of 645 bp in length
            *    8034   8133: gap of 100 bp
            *    8134  11152: contig of 3019 bp in length
            *   11153  11252: gap of 100 bp
            *   11253  16926: contig of 5674 bp in length
            *   16927  17026: gap of 100 bp
            *   17027  48247: contig of 31221 bp in length
            *   48248  48347: gap of 100 bp
            *   48348  56048: contig of 7701 bp in length
            *   56049  56148: gap of 100 bp
            *   56149  68742: contig of 12594 bp in length
            *   68743  68842: gap of 100 bp
            *   68843  86438: contig of 17596 bp in length
            *   86439  86538: gap of 100 bp
            *   86539 107927: contig of 21389 bp in length
            *  107928 108027: gap of 100 bp
            *  108028 135702: contig of 27675 bp in length
            *  135703 135802: gap of 100 bp
            *  135803 170129: contig of 34327 bp in length
            *  170130 170229: gap of 100 bp
            *  170230 176671: contig of 6442 bp in length.

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                     /db_xref="taxon:9606"
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                     /clone_lib="RPCI-11 Human Male BAC"
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                     /note="assembly_fragment
                     clone_end:SP6
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    gap             /note="assembly_fragment"
                    8034..8133
    misc_feature    /estimated_length=100
                    8134..11152
    gap             /note="assembly_fragment"
                    11153..11252
    misc_feature    /estimated_length=100
                    11253..16925
    gap             /note="assembly_fragment"
                    16927..17026
    misc_feature    /estimated_length=100
                    17027..48247
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Query Match           4.7%;   Score 183;  DB 14;  Length 176671;
Best Local Similarity 100.0%;  Pred. No. 1.7e-94;
Matches 183;  Conservative   0;  Mismatches   0;   Indels   0;   Gaps   0;

Qy  1577 AGGCAACAGAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCTACCATCTGCTTGTGA 1636
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Db 76700 AGGCAACAGAAACAGACACAAAAATCAGAGTGTGCACCCGGGCCTACCATCTGCTTGTGA 76759

Qy  1637 AAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATATCCTAACCATTGGGA 1696
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 76760 AAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATATCCTAACCATTGGGA 76819

Qy  1697 CTGGAATGGGAGGAACAACAACTTGTATGCCATTAATTTATCCATGCAACAAAAGTCATTA 1756
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Db 76820 CTGGAATGGGAGGAACAACAACTTGTATGCCATTAATTTATCCATGCAACAAAAGTCATTA 76879

Qy  1757 AAG 1759
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Db 76880 AAG 76882
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RESULT 30
AC016512/c
LOCUS      AC016512            73656 bp    DNA    linear    HTG 13-JUL-2000
DEFINITION Homo sapiens clone RP11-11N21, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC016512
VERSION    AC016512.3  GI:9123838
KEYWORDS   HTG; HTGS_PHASE0.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE  1  (bases 1 to 73656)
AUTHORS    Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens, clone RP11-11N21
JOURNAL    Unpublished
REFERENCE  2  (bases 1 to 73656)
AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
           Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,R., Boukhgalter,B.,
           Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
           Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
           Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
           Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
           Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
           Lehoczky,J., Lieu,C., Locke,K., Locke,K., Macdonald,P., Marquis,N.,
           McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
           Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
           Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
           Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
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                        TITLE     Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
                                  Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
                        JOURNAL   Direct Submission
                                  Submitted (01-DEC-1999) Whitehead Institute/MIT Center for Genome
                                  Research, 320 Charles Street, Cambridge, MA 02141, USA
                        COMMENT   On Jul 13, 2000 this sequence version replaced gi:7144825.
                                  All repeats were identified using RepeatMasker.
                                  Smit, A.F.A. & Green, P. (1996-1997)
                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                  ----------------------Genome Center
                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                      Center code: WIBR
                                      Web site: http://www-seq.wi.mit.edu
                                      Contact: sequence submissions@genome.wi.mit.edu
                                  ----------------------Project Information
                                      Center project name: L3233
                                      Center clone name: 11_N_21
                                  ----------------------
                                * NOTE: This record contains 81 individual
                                * sequencing reads that have not been assembled into
                                * contigs. Runs of N are used to separate the reads
                                * and the order in which they appear is completely
                                * arbitrary. Low-pass sequence sampling is useful for
                                * identifying clones that may be gene-rich and allows
                                * overlap relationships among clones to be deduced.
                                * However, it should not be assumed that this clone
                                * will be sequenced to completion. In the event that
                                * the record is updated, the accession number will
                                * be preserved.
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                                *        1:      contig of 809 bp in length
                                *      810:      gap of 100 bp
                                *      910:      contig of 809 bp in length
                                *     1718:      gap of 100 bp
                                *     1719:      contig of 817 bp in length
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                                *     2636:      contig of 806 bp in length
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                                *     2736:      contig of 806 bp in length
                                *     3541:      gap of 100 bp
                                *     3542:      contig of 789 bp in length
                                *     3641:      gap of 100 bp
                                *     3642:      contig of 787 bp in length
                                *     4430:      gap of 100 bp
                                *     4431:      contig of 813 bp in length
                                *     4530:      gap of 100 bp
                                *     4531:      contig of 805 bp in length
                                *     5317:      gap of 100 bp
                                *     5318:      contig of 820 bp in length
                                *     5417:      gap of 100 bp
                                *     5418:      contig of 804 bp in length
                                *     6230:      gap of 100 bp
                                *     6231:      contig of 814 bp in length
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                                *     6331:      contig of 804 bp in length
                                *     7135:      gap of 100 bp
                                *     7136:      contig of 819 bp in length
                                *     7235:      gap of 100 bp
                                *     7236:      contig of 797 bp in length
                                *     8055:      gap of 100 bp
                                *     8056:      contig of 802 bp in length
                                *     8155:      gap of 100 bp
                                *     8156:      contig of 806 bp in length
                                *     8959:      gap of 100 bp
                                *     8960:      contig of 812 bp in length
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                                *     9874:      contig of 828 bp in length
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                                *     9974:      contig of 816 bp in length
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* 19971  20775: contig of 805 bp in length
* 20776  20875: gap of 100 bp
* 20876  21691: contig of 816 bp in length
* 21692  21791: gap of 100 bp
* 21792  22615: contig of 824 bp in length
* 22616  22715: gap of 100 bp
* 22716  23552: contig of 837 bp in length
* 23553  23652: gap of 100 bp
* 23653  24462: contig of 810 bp in length
* 24463  24562: gap of 100 bp
* 24563  25381: contig of 819 bp in length
* 25382  25481: gap of 100 bp
* 25482  26299: contig of 818 bp in length
* 26300  26399: gap of 100 bp
* 26400  27217: contig of 818 bp in length
* 27218  27317: gap of 100 bp
* 27318  28122: contig of 805 bp in length
* 28123  28222: gap of 100 bp
* 28223  29038: contig of 816 bp in length
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* 30054  30853: contig of 800 bp in length
* 30854  30953: gap of 100 bp
* 30954  31766: contig of 813 bp in length
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* 31867  32684: contig of 818 bp in length
* 32685  32784: gap of 100 bp
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* 33597  33696: gap of 100 bp
* 33697  34516: contig of 820 bp in length
* 34517  34616: gap of 100 bp
* 34617  35432: contig of 816 bp in length
* 35433  35532: gap of 100 bp
* 35533  36356: contig of 824 bp in length
* 36357  36456: gap of 100 bp
* 36457  37272: contig of 816 bp in length
* 37273  37372: gap of 100 bp
* 37373  38181: contig of 809 bp in length
* 38182  38281: gap of 100 bp
* 38282  39088: contig of 807 bp in length
* 39089  39188: gap of 100 bp
* 39189  39999: contig of 811 bp in length
* 40000  40099: gap of 100 bp
* 40100  40912: contig of 813 bp in length
* 40913  41012: gap of 100 bp
* 41013  41820: contig of 808 bp in length
* 41821  41920: gap of 100 bp
* 41921  42727: contig of 807 bp in length
* 42728  42827: gap of 100 bp
* 42828  43636: contig of 809 bp in length
* 43637  43736: gap of 100 bp
* 43737  44524: contig of 788 bp in length
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* 44625  45437: contig of 813 bp in length
* 45438  45537: gap of 100 bp
* 45538  46343: contig of 806 bp in length
* 46344  46443: gap of 100 bp
* 46444  47250: contig of 807 bp in length
* 47251  47350: gap of 100 bp
* 47351  48152: contig of 802 bp in length
* 48153  48252: gap of 100 bp
* 48253  49066: contig of 814 bp in length
* 49067  49166: gap of 100 bp
* 49167  49986: contig of 820 bp in length
* 49987  50086: gap of 100 bp
* 50087  50883: contig of 797 bp in length
* 50884  50983: gap of 100 bp
* 50984  51769: contig of 786 bp in length
* 51770  51869: gap of 100 bp
* 51870  52666: contig of 797 bp in length
* 52667  52766: gap of 100 bp
* 52767  53592: contig of 826 bp in length

* 53593  53692: gap of 100 bp
* 53693  54501: contig of 809 bp in length
* 54502  54601: gap of 100 bp
* 54602  55410: contig of 809 bp in length
* 55411  55510: gap of 100 bp
* 55511  56327: contig of 817 bp in length
* 56328  56427: gap of 100 bp
* 56428  57237: contig of 810 bp in length
* 57238  57337: gap of 100 bp
* 57338  58146: contig of 809 bp in length
* 58147  58246: gap of 100 bp
* 58247  59053: contig of 807 bp in length
* 59054  59153: gap of 100 bp
* 59154  59961: contig of 808 bp in length
* 59962  60061: gap of 100 bp
* 60062  60882: contig of 821 bp in length
* 60883  60982: gap of 100 bp
* 60983  61792: contig of 810 bp in length
* 61793  61892: gap of 100 bp
* 61893  62703: contig of 811 bp in length
* 62704  62803: gap of 100 bp
* 62804  63615: contig of 812 bp in length
* 63616  63715: gap of 100 bp
* 63716  64536: contig of 821 bp in length
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* 64637  65446: contig of 810 bp in length
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Matches  182;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     1638 AAAACTGGCTTAATCCAAATGACATTATTTTTGACCCTAATATCCTAACCATTGGGAC 1697
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Qy     1758 AG 1759
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Db    18618 AG 18617
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RESULT 31
BV204261

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DEFINITION  sqnm214563 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
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ACCESSION   BV204261
VERSION     BV204261.1  GI:48173869
KEYWORDS    STS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 201)
AUTHORS     Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
            Cantor,C.R. and Braun,A.
TITLE       Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
            Regions
JOURNAL     Genome Res. (2004) In press
COMMENT     Contact: Andreas Braun
            Pharmaceuticals division
            Sequenom, Inc.
            3595 John Hopkins Court, San Diego, CA 92121, USA
```

```
                    Tel: 18582029018
                    Fax: 18582029020
                    Email: abraun@sequenom.com
                    Primer A: No primer sequence submitted
                    Primer B: No primer sequence submitted
                    STS size: 201.
FEATURES            Location/Qualifiers
     source         1..201
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /clone_lib="Human DNA (Sequenom)"
     STS            <1..>201
ORIGIN

Query Match        3.3%;    Score 129;   DB 10;    Length 201;
Best Local Similarity  99.4%;   Pred. No. 9.8e-63;
Matches  179;    Conservative   0;   Mismatches   1;   Indels   0;   Gaps    0;

Qy   3560  TGCGGTACAAGGGCATCCGGCCCGGCTCCTGGCTACCCCAGCCAGCCGACCACCGAGA 3619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22  TGCGGTACAAGGGCATCCGGCCCGGCTCCTGGCTACCCCAGCCAGCCGACCACCGAGA 81

Qy   3620  AGCTCACCATGTGGGAGACTCGCAGACATCGAGCAGTCTACAGGCCATTAGGTTAACAGAAT 3679
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82  AGCTCACCATGTGGGAGACTYGCAGACATCGAGCAGTCTACAGGCCATTAGGTTAACAGAAT 141

Qy   3680  CATTAGCAATGCACCTGCTTCAGCAGTCTCAGGCCCTCTACTTCTCCAATTTGAAGTCCA 3739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142  CATTAGCAATGCACCTGCTTCAGCAGTCTCAGGCCCTCTACTTCTCCAATTTGAAGTCCA 201

RESULT 32
AC080113
LOCUS       AC080113            67611 bp    DNA     linear   HTG 24-SEP-2000
DEFINITION  Homo sapiens chromosome 5 clone RP11-28J13 map 5, LOW-PASS SEQUENCE
            SAMPLING.
ACCESSION   AC080113
VERSION     AC080113.1   GI:10281431
KEYWORDS    HTG; HTGS PHASE0.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 67611)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 5, clone RP11-28J13
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 67611)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Beda,P., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
            FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
            Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
            Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G.,
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            McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
            O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,T.,
            Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
            Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
            Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
            Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
            Zimmer,A. and zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT     All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -----------------------------Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -----------------------------Project Information
                Center project name: L1103
                Center clone name: 28_J_13
            -----------------------------
            * NOTE: This record contains 82 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            * -----------------------------
            *       1      714:  contig of 714 bp in length
            *     715      814:  gap of 100 bp
            *     815     1528:  contig of 714 bp in length
            *    1529     1628:  gap of 100 bp
            *    1629     2367:  contig of 739 bp in length
            *    2368     2467:  gap of 100 bp
            *    2468     3202:  contig of 735 bp in length
            *    3203     3302:  gap of 100 bp
            *    3303     4039:  contig of 737 bp in length
            *    4040     4139:  gap of 100 bp
            *    4140     4875:  contig of 736 bp in length
            *    4876     4975:  gap of 100 bp
            *    4976     5685:  contig of 710 bp in length
            *    5686     5785:  gap of 100 bp
            *    5786     6533:  contig of 748 bp in length
            *    6534     6633:  gap of 100 bp
            *    6634     7340:  contig of 707 bp in length
            *    7341     7440:  gap of 100 bp
            *    7441     8157:  contig of 717 bp in length
            *    8158     8257:  gap of 100 bp
            *    8258     8973:  contig of 716 bp in length
            *    8974     9073:  gap of 100 bp
            *    9074     9811:  contig of 738 bp in length
            *    9812     9911:  gap of 100 bp
            *    9912    10567:  contig of 656 bp in length
            *   10568    10667:  gap of 100 bp
            *   10668    11375:  contig of 708 bp in length
            *   11376    11475:  gap of 100 bp
            *   11476    12198:  contig of 723 bp in length
            *   12199    12298:  gap of 100 bp
            *   12299    13025:  contig of 727 bp in length
            *   13026    13125:  gap of 100 bp
            *   13126    13849:  contig of 724 bp in length
            *   13850    13949:  gap of 100 bp
            *   13950    14679:  contig of 730 bp in length
            *   14680    14779:  gap of 100 bp
            *   14780    15490:  contig of 711 bp in length
            *   15491    15590:  gap of 100 bp
            *   15591    16338:  contig of 748 bp in length
            *   16339    16438:  gap of 100 bp
            *   16439    17146:  contig of 708 bp in length
            *   17147    17246:  gap of 100 bp
            *   17247    17956:  contig of 710 bp in length
            *   17957    18056:  gap of 100 bp
            *   18057    18775:  contig of 719 bp in length
            *   18776    18875:  gap of 100 bp
            *   18876    19602:  contig of 727 bp in length
            *   19603    19702:  gap of 100 bp
            *   19703    20435:  contig of 733 bp in length
            *   20436    20535:  gap of 100 bp
```

```
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*  21364    22084: contig of 721 bp in length
*  22085    22184: gap of 100 bp
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*  22916    23015: gap of 100 bp
*  23016    23745: contig of 730 bp in length
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*  23846    24577: contig of 732 bp in length
*  24578    24677: gap of 100 bp
*  24678    25400: contig of 723 bp in length
*  25401    25500: gap of 100 bp
*  25501    26227: contig of 727 bp in length
*  26228    26327: gap of 100 bp
*  26328    27044: contig of 717 bp in length
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*  28791    29521: contig of 731 bp in length
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*  31190    31289: gap of 100 bp
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*  34502    34601: gap of 100 bp
*  34602    35334: contig of 733 bp in length
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*  36259    37010: contig of 752 bp in length
*  37011    37110: gap of 100 bp
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*  39526    39625: gap of 100 bp
*  39626    40339: contig of 714 bp in length
*  40340    40439: gap of 100 bp
*  40440    41161: contig of 722 bp in length
*  41162    41261: gap of 100 bp
*  41262    41981: contig of 720 bp in length
*  41982    42081: gap of 100 bp
*  42082    42807: contig of 726 bp in length
*  42808    42907: gap of 100 bp
*  42908    43648: contig of 741 bp in length
*  43649    43748: gap of 100 bp
*  43749    44467: contig of 719 bp in length
*  44468    44567: gap of 100 bp
*  44568    45265: contig of 698 bp in length
*  45266    45365: gap of 100 bp
*  45366    46081: contig of 716 bp in length
*  46082    46181: gap of 100 bp
*  46182    46908: contig of 727 bp in length
*  46909    47008: gap of 100 bp
*  47009    47739: contig of 731 bp in length
*  47740    47839: gap of 100 bp
*  47840    48565: contig of 726 bp in length
*  48566    48665: gap of 100 bp
*  48666    49390: contig of 725 bp in length
*  49391    49490: gap of 100 bp
*  49491    50216: contig of 726 bp in length
*  50217    50316: gap of 100 bp
*  50317    51006: contig of 690 bp in length

*  51007    51106: gap of 100 bp
*  51107    51816: contig of 710 bp in length
*  51817    51916: gap of 100 bp
*  51917    52656: contig of 740 bp in length
*  52657    52756: gap of 100 bp
*  52757    53479: contig of 723 bp in length
*  53480    53579: gap of 100 bp
*  53580    54315: contig of 736 bp in length
*  54316    54415: gap of 100 bp
*  54416    55154: contig of 739 bp in length
*  55155    55254: gap of 100 bp
*  55255    55985: contig of 731 bp in length
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*  56086    56811: contig of 726 bp in length
*  56812    56911: gap of 100 bp
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```
Query Match            3.3%;  Score 129;  DB 14;  Length 67611;
Best Local Similarity  100.0%;  Pred. No. 9.7e-63;
Matches  129;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   2913 AGTGAAGCCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGT 2972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30644 AGTGAAGCCCACGTTTATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGT 30703

Qy   2973 GGACTACATTGACTGACTGGAAGCCTTTCTTCTTTGATGTCTGGCAGCTCCGGGCAAGTACCCGAA 3032
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Qy   3033 TCGAGGCTT 3041
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Db  30764 TCGAGGCTT 30772
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LOCUS       AC080113              67611 bp    DNA     linear   HTG 24-SEP-2000
DEFINITION  Homo sapiens chromosome 5 clone RP11-28J13 map 5, LOW-PASS SEQUENCE
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ACCESSION   AC080113
VERSION     AC080113.1  GI:10281431
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 67611)
AUTHORS     Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE       Homo sapiens chromosome 5, clone RP11-28J13
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 67611)
AUTHORS     Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
            FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
            Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
            Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G.,
            Macdonald,P., Marquis,N., McCarthy,M., McSwan,P., McKernan,K.,
            McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
            O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K.,
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            Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,
            Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
            Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
            Zimmer,A. and Zody,M.
TITLE       Direct Submission
JOURNAL     Submitted (24-SEP-2000) Whitehead Institute/MIT Center for Genome
```

COMMENT

```
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
    Center: Whitehead Institute/ MIT Center for Genome Research
    Center code: WIBR
    Web site: http://www-seq.wi.mit.edu
    Contact: sequence submissions@genome.wi.mit.edu
------  Project Information
    Center project name: L11103
    Center clone name: 28_J_13
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* NOTE: This record contains 82 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*        1    714:  contig of 714 bp in length
*      715    814:  gap of 100 bp
*      815   1528:  contig of 714 bp in length
*     1529   1628:  gap of 100 bp
*     1629   2367:  contig of 739 bp in length
*     2368   2467:  gap of 100 bp
*     2468   3202:  contig of 735 bp in length
*     3203   3302:  gap of 100 bp
*     3303   4039:  contig of 737 bp in length
*     4040   4139:  gap of 100 bp
*     4140   4875:  contig of 736 bp in length
*     4876   4975:  gap of 100 bp
*     4976   5685:  contig of 710 bp in length
*     5686   5785:  gap of 100 bp
*     5786   6533:  contig of 748 bp in length
*     6534   6633:  gap of 100 bp
*     6634   7340:  contig of 707 bp in length
*     7341   7440:  gap of 100 bp
*     7441   8157:  contig of 717 bp in length
*     8158   8257:  gap of 100 bp
*     8258   8973:  contig of 716 bp in length
*     8974   9073:  gap of 100 bp
*     9074   9811:  contig of 738 bp in length
*     9812   9911:  gap of 100 bp
*     9912  10567:  contig of 656 bp in length
*    10568  10667:  gap of 100 bp
*    10668  11375:  contig of 708 bp in length
*    11376  11475:  gap of 100 bp
*    11476  12198:  contig of 723 bp in length
*    12199  12298:  gap of 100 bp
*    12299  13025:  contig of 727 bp in length
*    13026  13125:  gap of 100 bp
*    13126  13849:  contig of 724 bp in length
*    13850  13949:  gap of 100 bp
*    13950  14679:  contig of 730 bp in length
*    14680  14779:  gap of 100 bp
*    14780  15490:  contig of 711 bp in length
*    15491  15590:  gap of 100 bp
*    15591  16338:  contig of 748 bp in length
*    16339  16438:  gap of 100 bp
*    16439  17146:  contig of 708 bp in length
*    17147  17246:  gap of 100 bp
*    17247  17956:  contig of 710 bp in length
*    17957  18056:  gap of 100 bp
*    18057  18775:  contig of 719 bp in length
*    18776  18875:  gap of 100 bp
*    18876  19602:  contig of 727 bp in length
*    19603  19702:  gap of 100 bp
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*    23016  23745:  contig of 730 bp in length
*    23746  23845:  gap of 100 bp
*    23846  24577:  contig of 732 bp in length
*    24578  24677:  gap of 100 bp
*    24678  25400:  contig of 723 bp in length
*    25401  25500:  gap of 100 bp
*    25501  26227:  contig of 727 bp in length
*    26228  26327:  gap of 100 bp
*    26328  27044:  contig of 717 bp in length
*    27045  27144:  gap of 100 bp
*    27145  27875:  contig of 731 bp in length
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*    27976  28690:  contig of 715 bp in length
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*    28791  29521:  contig of 731 bp in length
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*    29622  30352:  contig of 731 bp in length
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*    30453  31189:  contig of 737 bp in length
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*    31290  32015:  contig of 726 bp in length
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*    32116  32847:  contig of 732 bp in length
*    32848  32947:  gap of 100 bp
*    32948  33671:  contig of 724 bp in length
*    33672  33771:  gap of 100 bp
*    33772  34501:  contig of 730 bp in length
*    34502  34601:  gap of 100 bp
*    34602  35334:  contig of 733 bp in length
*    35335  35434:  gap of 100 bp
*    35435  36158:  contig of 724 bp in length
*    36159  36258:  gap of 100 bp
*    36259  37010:  contig of 752 bp in length
*    37011  37110:  gap of 100 bp
*    37111  37854:  contig of 744 bp in length
*    37855  37954:  gap of 100 bp
*    37955  38696:  contig of 742 bp in length
*    38697  38796:  gap of 100 bp
*    38797  39525:  contig of 729 bp in length
*    39526  39625:  gap of 100 bp
*    39626  40339:  contig of 714 bp in length
*    40340  40439:  gap of 100 bp
*    40440  41161:  contig of 722 bp in length
*    41162  41261:  gap of 100 bp
*    41262  41981:  contig of 720 bp in length
*    41982  42081:  gap of 100 bp
*    42082  42807:  contig of 726 bp in length
*    42808  42907:  gap of 100 bp
*    42908  43648:  contig of 741 bp in length
*    43649  43748:  gap of 100 bp
*    43749  44467:  contig of 719 bp in length
*    44468  44567:  gap of 100 bp
*    44568  45265:  contig of 698 bp in length
*    45266  45365:  gap of 100 bp
*    45366  46081:  contig of 716 bp in length
*    46082  46181:  gap of 100 bp
*    46182  46908:  contig of 727 bp in length
*    46909  47008:  gap of 100 bp
*    47009  47739:  contig of 731 bp in length
*    47740  47839:  gap of 100 bp
*    47840  48565:  contig of 726 bp in length
*    48566  48665:  gap of 100 bp
*    48666  49390:  contig of 725 bp in length
*    49391  49490:  gap of 100 bp
*    49491  50216:  contig of 726 bp in length
*    50217  50316:  gap of 100 bp
```

```
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
    Center: Whitehead Institute/ MIT Center for Genome Research
    Center code: WIBR
    Web site: http://www-seq.wi.mit.edu
    Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
    Center project name: L11095
    Center clone name: 11_N_21
------- Summary Statistics
    Sequencing vector: Plasmid; n/a; 100% of reads
    Chemistry: Dye-terminator Big Dye; 100% of reads
    Assembly program: Phrap; version 0.960731
    Consensus quality: 147566 bases at least Q40
    Consensus quality: 155962 bases at least Q30
    Consensus quality: 159155 bases at least Q20
    Insert size: 170000; agarose-fp
    Insert size: 160929; sum-of-contigs
    Quality coverage: 3.7 in Q20 bases; agarose-fp
    Quality coverage: 3.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*       1       638:  contig of 638 bp in length
*       639     738:  gap of 100 bp
*       739    1280:  contig of 542 bp in length
*      1281    1380:  gap of 100 bp
*      1381    2021:  contig of 641 bp in length
*      2022    2121:  gap of 100 bp
*      2122    2830:  contig of 709 bp in length
*      2831    2930:  gap of 100 bp
*      2931    3970:  contig of 1040 bp in length
*      3971    4070:  gap of 100 bp
*      4071    4923:  contig of 853 bp in length
*      4924    5023:  gap of 100 bp
*      5024    6063:  contig of 1040 bp in length
*      6064    6163:  gap of 100 bp
*      6164    7446:  contig of 1283 bp in length
*      7447    7546:  gap of 100 bp
*      7547    9381:  contig of 1835 bp in length
*      9382    9481:  gap of 100 bp
*      9482   11219:  contig of 1738 bp in length
*     11220   11319:  gap of 100 bp
*     11320   12350:  contig of 1031 bp in length
*     12351   12450:  gap of 100 bp
*     12451   13291:  contig of 841 bp in length
*     13292   13391:  gap of 100 bp
*     13392   14939:  contig of 1548 bp in length
*     14940   15039:  gap of 100 bp
*     15040   17136:  contig of 2097 bp in length
*     17137   17236:  gap of 100 bp
*     17237   19620:  contig of 2384 bp in length
*     19621   19720:  gap of 100 bp
*     19721   22736:  contig of 3016 bp in length
*     22737   22836:  gap of 100 bp
*     22837   45780:  contig of 22944 bp in length
*     45781   45880:  gap of 100 bp
*     45881   48594:  contig of 2714 bp in length
*     48595   48694:  gap of 100 bp
*     48695   51084:  contig of 2390 bp in length
*     51085   51184:  gap of 100 bp
*     51185   53490:  contig of 2306 bp in length
*     53491   53590:  gap of 100 bp
*     53591   55545:  contig of 1955 bp in length
*     55546   55645:  gap of 100 bp
*     55646   57961:  contig of 2316 bp in length
```

```
*     50317   51006:  contig of 690 bp in length
*     51007   51106:  gap of 100 bp
*     51107   51816:  contig of 710 bp in length
*     51817   51916:  gap of 100 bp
*     51917   52656:  contig of 740 bp in length
*     52657   52756:  gap of 100 bp
*     52757   53479:  contig of 723 bp in length
*     53480   53579:  gap of 100 bp
*     53580   54315:  contig of 736 bp in length
*     54316   54415:  gap of 100 bp
*     54416   55154:  contig of 739 bp in length
*     55155   55254:  gap of 100 bp
*     55255   55985:  contig of 731 bp in length
*     55986   56085:  gap of 100 bp
*     56086   56811:  contig of 726 bp in length
*     56812   56911:  gap of 100 bp
```

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Query Match       3.1%;    Score 120;   DB 14;   Length 67611;
Best Local Similarity  100.0%;   Pred. No. 1.9e-57;
Matches 120;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    2105  AGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAAT 2164
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7642  AGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAAT 7583

Qy    2165  ATCCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAAAATTGTTGGTG 2224
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7582  ATCCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAAAATTGTTGGTG 7523
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```
RESULT 34
AC079975
LOCUS          AC079975          164529 bp    DNA     linear   HTG 22-NOV-2000
DEFINITION     Homo sapiens chromosome 1 clone RP11-11N21 map 1, WORKING DRAFT
               SEQUENCE, 37 unordered pieces.
ACCESSION      AC079975
VERSION        AC079975.2  GI:11276222
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1  (bases 1 to 164529)
AUTHORS        Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE          Homo sapiens chromosome 1, clone RP11-11N21
JOURNAL        Unpublished
REFERENCE      2  (bases 1 to 164529)
AUTHORS        Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
               Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
               Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
               Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
               DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
               FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
               Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
               Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
               Lamazzares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G.,
               Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
               McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
               Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
               O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K.,
               Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
               Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
               Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
               Strauss,N., Subramanian,A., Talamas,J., Tesfaye,J., Theodore,J.,
               Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
               Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
               Zimmer,A. and Zody,M.
TITLE          Direct Submission
JOURNAL        Submitted (20-SEP-2000) Whitehead Institute/MIT Center for Genome
               Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT        On Nov 22, 2000 this sequence version replaced gi:10198369.
               All repeats were identified using RepeatMasker:
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*              57962               
*              58061:  gap of 100 bp
*              58062   59375:  contig of 1314 bp in length
*              59376   gap of 100 bp
*              59475:  contig of 3603 bp in length
*              59476   63078:  gap of 100 bp
*              63079   contig of 2178 bp in length
*              63178:  gap of 100 bp
*              63179   65356:  contig of 2178 bp in length
*              65357   gap of 100 bp
*              65456:  contig of 3127 bp in length
*              65457   68583:  gap of 100 bp
*              68584   68683:  contig of 4391 bp in length
*              68684   gap of 100 bp
*              73074:  contig of 3501 bp in length
*              73075   73174:  gap of 100 bp
*              73175   76675:  contig of 4261 bp in length
*              76676   76775:  gap of 100 bp
*              76776   81036:  contig of 4261 bp in length
*              81037   81136:  gap of 100 bp
*              81137   86818:  contig of 5682 bp in length
*              86819   86918:  gap of 100 bp
*              86919   94761:  contig of 7843 bp in length
*              94762   94861:  gap of 100 bp
*              94862   102806:  contig of 7945 bp in length
*              102807  102906:  gap of 100 bp
*              102907  117954:  contig of 15048 bp in length
*              117955  118054:  gap of 100 bp
*              118055  130927:  contig of 12873 bp in length
*              130928  131027:  gap of 100 bp
*              131028  145686:  contig of 14659 bp in length
*              145687  145786:  gap of 100 bp
*              145787  162777:  contig of 16991 bp in length
*              162778  162877:  gap of 100 bp
*              162878  164529:  contig of 1652 bp in length.

FEATURES             Location/Qualifiers
source               1..164529
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1"
                     /clone="RP11-11N21"
                     /clone_lib="RPCI-11 Human Male BAC"
misc_feature         1..638
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
gap                  639..738
                     /estimated_length=100
misc_feature         739..1280
                     /note="assembly_fragment"
gap                  1281..1380
                     /estimated_length=100
misc_feature         1381..2021
                     /note="assembly_fragment"
gap                  2022..2121
                     /estimated_length=100
misc_feature         2122..2830
                     /note="assembly_fragment"
gap                  2831..2930
                     /estimated_length=100
misc_feature         2931..3970
                     /note="assembly_fragment"
gap                  3971..4070
                     /estimated_length=100
misc_feature         4071..4923
                     /note="assembly_fragment"
gap                  4924..5023
                     /estimated_length=100
misc_feature         5024..6063
                     /note="assembly_fragment"
gap                  6064..6163
                     /estimated_length=100
misc_feature         6164..7446
                     /note="assembly_fragment"
gap                  7447..7546
                     /estimated_length=100
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misc_feature         7547..9381
                     /note="assembly_fragment"
gap                  9382..9481
                     /estimated_length=100
misc_feature         9482..11219
                     /note="assembly_fragment"
gap                  11220..11319
                     /estimated_length=100
misc_feature         11320..12350
                     /note="assembly_fragment"
gap                  12351..12450
                     /estimated_length=100
misc_feature         12451..13291
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Query Match          2.9%;  Score 114;  DB 14;  Length 164529;
Best Local Similarity  100.0%;  Pred. No. 6.4e-54;
Matches  114;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      2255 CTCAGGTTATAAAGTCAGCCCGGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCA 2314
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87313 CTCAGGTTATAAAGTCAGCCCGGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCA 87372

Qy      .2315 TGGAAAAGAAAGAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAAGAGG 2368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87373 TGGAAAAGAAAGAGAAGAAACCAGAGTGCTTAACGGCACAGTAGAAGAAGAGG 87426
```

```
RESULT 35
AC016512
LOCUS        AC016512              73656 bp    DNA     linear   HTG 13-JUL-2000
DEFINITION   Homo sapiens clone RP11-11N21, LOW-PASS SEQUENCE SAMPLING.
ACCESSION    AC016512
VERSION      AC016512.3  GI:9123838
KEYWORDS     HTG; HTGS_PHASE0.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1  (bases 1 to 73656)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE        Homo sapiens, clone RP11-11N21
JOURNAL      Unpublished
REFERENCE    2  (bases 1 to 73656)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
             Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
             Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
             Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
             Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
             Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
             Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
             Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
             McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
             Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
             Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
             Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
             Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
             Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
TITLE        Direct Submission
JOURNAL      Submitted (01-DEC-1999) Whitehead Institute/MIT Center for Genome
             Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT      On Jul 13, 2000 this sequence version replaced gi:7144825.
             All repeats were identified using RepeatMasker:
             Smit, A.F.A. & Green, P. (1996-1997)
             http://ftp.genome.washington.edu/RM/RepeatMasker.html
             --------------- Genome Center
                 Center: Whitehead Institute/ MIT Center for Genome Research
                 Center code: WIBR
                 Web site: http://www-seq.wi.mit.edu
                 Contact: sequence_submissions@genome.wi.mit.edu
             --------------- Project Information
                 Center project name: L3233
                 Center clone name: 11_N_21
```

```
* ---------
* NOTE: This record contains 81 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
*       1    809: contig of 809 bp in length          * 28123  28222: gap of 100 bp
*     810    909: gap of 100 bp                        * 28223  29038: contig of 816 bp in length
*     910   1718: contig of 809 bp in length          * 29039  29138: gap of 100 bp
*    1719   1818: gap of 100 bp                        * 29139  29953: contig of 815 bp in length
*    1819   2635: contig of 817 bp in length          * 29954  30053: gap of 100 bp
*    2636   2735: gap of 100 bp                        * 30054  30853: contig of 800 bp in length
*    2736   3541: contig of 806 bp in length          * 30854  30953: gap of 100 bp
*    3542   3641: gap of 100 bp                        * 30954  31766: contig of 813 bp in length
*    3642   4430: contig of 789 bp in length          * 31767  31866: gap of 100 bp
*    4431   4530: gap of 100 bp                        * 31867  32684: contig of 818 bp in length
*    4531   5317: contig of 787 bp in length          * 32685  32784: gap of 100 bp
*    5318   5417: gap of 100 bp                        * 32785  33596: contig of 812 bp in length
*    5418   6230: contig of 813 bp in length          * 33597  33696: gap of 100 bp
*    6231   6330: gap of 100 bp                        * 33697  34516: contig of 820 bp in length
*    6331   7135: contig of 805 bp in length          * 34517  34616: gap of 100 bp
*    7136   7235: gap of 100 bp                        * 34617  35432: contig of 816 bp in length
*    7236   8055: contig of 820 bp in length          * 35433  35532: gap of 100 bp
*    8056   8155: gap of 100 bp                        * 35533  36356: contig of 824 bp in length
*    8156   8959: contig of 804 bp in length          * 36357  36456: gap of 100 bp
*    8960   9059: gap of 100 bp                        * 36457  37272: contig of 816 bp in length
*    9060   9873: contig of 814 bp in length          * 37273  37372: gap of 100 bp
*    9874   9973: gap of 100 bp                        * 37373  38181: contig of 809 bp in length
*    9974  10777: contig of 804 bp in length          * 38182  38281: gap of 100 bp
*   10778  10877: gap of 100 bp                        * 38282  39088: contig of 807 bp in length
*   10878  11696: contig of 819 bp in length          * 39089  39188: gap of 100 bp
*   11697  11796: gap of 100 bp                        * 39189  39999: contig of 811 bp in length
*   11797  12593: contig of 797 bp in length          * 40000  40099: gap of 100 bp
*   12594  12693: gap of 100 bp                        * 40100  40912: contig of 813 bp in length
*   12694  13490: contig of 797 bp in length          * 40913  41012: gap of 100 bp
*   13491  13590: gap of 100 bp                        * 41013  41820: contig of 808 bp in length
*   13591  14402: contig of 812 bp in length          * 41821  41920: gap of 100 bp
*   14403  14502: gap of 100 bp                        * 41921  42727: contig of 807 bp in length
*   14503  15304: contig of 802 bp in length          * 42728  42827: gap of 100 bp
*   15305  15404: gap of 100 bp                        * 42828  43636: contig of 809 bp in length
*   15405  16210: contig of 806 bp in length          * 43637  43736: gap of 100 bp
*   16211  16310: gap of 100 bp                        * 43737  44524: contig of 788 bp in length
*   16311  17114: contig of 804 bp in length          * 44525  44624: gap of 100 bp
*   17115  17214: gap of 100 bp                        * 44625  45437: contig of 813 bp in length
*   17215  18042: contig of 828 bp in length          * 45438  45537: gap of 100 bp
*   18043  18142: gap of 100 bp                        * 45538  46343: contig of 806 bp in length
*   18143  18958: contig of 816 bp in length          * 46344  46443: gap of 100 bp
*   18959  19058: gap of 100 bp                        * 46444  47250: contig of 807 bp in length
*   19059  19870: contig of 812 bp in length          * 47251  47350: gap of 100 bp
*   19871  19970: gap of 100 bp                        * 47351  48152: contig of 802 bp in length
*   19971  20775: contig of 805 bp in length          * 48153  48252: gap of 100 bp
*   20776  20875: gap of 100 bp                        * 48253  49066: contig of 814 bp in length
*   20876  21691: contig of 816 bp in length          * 49067  49166: gap of 100 bp
*   21692  21791: gap of 100 bp                        * 49167  49986: contig of 820 bp in length
*   21792  22615: contig of 824 bp in length          * 49987  50086: gap of 100 bp
*   22616  22715: gap of 100 bp                        * 50087  50883: contig of 797 bp in length
*   22716  23552: contig of 837 bp in length          * 50884  50983: gap of 100 bp
*   23553  23652: gap of 100 bp                        * 50984  51769: contig of 786 bp in length
*   23653  24462: contig of 810 bp in length          * 51770  51869: gap of 100 bp
*   24463  24562: gap of 100 bp                        * 51870  52666: contig of 797 bp in length
*   24563  25381: contig of 819 bp in length          * 52667  52766: gap of 100 bp
*   25382  25481: gap of 100 bp                        * 52767  53592: contig of 826 bp in length
*   25482  26299: contig of 818 bp in length          * 53593  53692: gap of 100 bp
*   26300  26399: gap of 100 bp                        * 53693  54501: contig of 809 bp in length
*   26400  27217: contig of 818 bp in length          * 54502  54601: gap of 100 bp
*   27218  27317: gap of 100 bp                        * 54602  55410: contig of 809 bp in length
*   27318  28122: contig of 805 bp in length          * 55411  55510: gap of 100 bp
*                                                      * 55511  56327: contig of 817 bp in length
*                                                      * 56328  56427: gap of 100 bp
*                                                      * 56428  57237: contig of 810 bp in length
*                                                      * 57238  57337: gap of 100 bp
*                                                      * 57338  58146: contig of 809 bp in length
*                                                      * 58147  58246: gap of 100 bp
*                                                      * 58247  59053: contig of 807 bp in length
*                                                      * 59054  59153: gap of 100 bp
*                                                      * 59154  59961: contig of 808 bp in length
*                                                      * 59962  60061: gap of 100 bp
*                                                      * 60062  60882: contig of 821 bp in length
*                                                      * 60883  60982: gap of 100 bp
```

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*        60983    61792:  contig of 810 bp in length
*        61793    61892:  gap of 100 bp
*        61893    62703:  contig of 811 bp in length
*        62704    62803:  gap of 100 bp
*        62804    63615:  contig of 812 bp in length
*        63616    63715:  gap of 100 bp
*        63716    64536:  contig of 821 bp in length
*        64537    64636:  gap of 100 bp
*        64637    65446:  contig of 810 bp in length
*        65447    65546:  gap of 100 bp

Query Match             2.6%;  Score 103;  DB 14;  Length 73656;
Best Local Similarity   100.0%;  Pred. No. 1.9e-47;
Matches  103;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2366 AGGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTTAAAGGCGACGTGCACGACATAG 2425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   32416 AGGACCCTTACCAGGGCACCATCGTGCTGGCCACTGTTAAAGGCGACGTGCACGACATAG 32475

Qy    2426 GCAAGAACATAGTTGGAGTAGTCCTTGGCGTGCAATAATTTCCG 2468
           ||||||||||||||||||||||||||||||||||||||||||||
Db   32476 GCAAGAACATAGTTGGAGTAGTCCTTGGCGTGCAATAATTTCCG 32518

RESULT 36
CQ750107/c
LOCUS       CQ750107           732 bp    DNA       linear    PAT 03-FEB-2004
DEFINITION  Sequence 36041 from Patent WO02068579.
ACCESSION   CQ750107
VERSION     CQ750107.1  GI:42380503
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE       Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
JOURNAL     Patent: WO 02068579-A 36041 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES    Location/Qualifiers
     source 1..732
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN

Query Match             2.4%;  Score 96;  DB 6;  Length 732;
Best Local Similarity   100.0%;  Pred. No. 2.5e-43;
Matches  96;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 GTCACCTGTGGAGAGCACGTCTTCTCTGCCCGGCCCCTGCGCAAGGAGGAGACTCGACA 61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     267 GTCACCTGTGGAGAGCACGTCTTCTCTGCCCGGCCCCTGCGCAAGGAGGAGACTCGACA 208

Qy      62 ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCCG 97
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Db     207 ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCCG 172

RESULT 37
BV599990
LOCUS       BV599990           731 bp    DNA       linear    STS 14-APR-2005
DEFINITION  S217P60970RH2.TO Noemie Pan troglodytes troglodytes STS genomic,
            sequence tagged site.
ACCESSION   BV599990
VERSION     BV599990.1  GI:62518904
KEYWORDS    STS.
SOURCE      Pan troglodytes troglodytes
ORGANISM    Pan troglodytes troglodytes
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REFERENCE   1  (bases 1 to 731)
AUTHORS     Mikkelsen,T.S., Hillier,W.L., Eichler,E.E., Zody,M.C. and
            Jaffe,D.B.
TITLE       Initial Sequence of the Chimpanzee Genome and Comparison with the
            Human Genome
JOURNAL     Unpublished (2005)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
COMMENT     Contact: Michael C. Zody
            Broad Institute of MIT and Harvard
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172580933
            Fax: 6172580903
            Email: mczody@broad.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 731
            Protocol:
            23,021,928 chimpanzee whole genome shotgun reads were aligned to
            the Human genome NCBI
            Build 34 (hg16,July 2003). Chimp WGS reads were from 9 donors,
            including Clint (Pan
            troglodytes verus), 3 other Pan troglodytes verus chimps
            (Donald,Karlien,Yvonne), 3 Pan
            troglodytes troglodytes chimps (Noemie,Masuku,Clara) and 2 chimps
            of unknown origin
            (Gon,Unknown Chimp). Common names:  Pan troglodytes verus is the
            western chimp and Pan
            troglodytes troglodytes is the central chimp. To be included in
            chimpanzee SNP discovery, a
            read must be at least 500bp in length, at least 50% of its base
            calls must have Phred
            score >= 20, at least 30% of its base calls must satisfy
            SNQS(30,25)(single strand NQS, the
            base in question has Phred score >= 30, the surrounding 10 bases in
            the read have Phred
            score >= 25), and the read must have at least 200 bp SNQS(30,25)
            bases. Reads not uniquely
            placed in the genome and read pairs whose two ends were not
            consistently placed were
            discarded. After above filtering, NQS(30,25) standard was applied
            to all pairs of
            overlapping reads to call NQS bases and SNPs. Alignments (between
            two reads) with less
            than 100 NQS bases or with SNP rate > 0.01 were discarded. To
            exclude alignment between two
            copies of a single read, comparisons between two reads that share
            95% of their genome
            alignments (>=95% bases of read A and >=95% bases of read B were
            placed at the same locus
            of human genome) were discarded.
FEATURES    Location/Qualifiers
     source 1..731
            /organism="Pan troglodytes troglodytes"
            /mol_type="genomic DNA"
            /sub_species="troglodytes"
            /db_xref="taxon:37011"
            /clone_lib="Noemie"
ORIGIN      <1. .>731

Query Match             2.4%;  Score 95;  DB 10;  Length 731;
Best Local Similarity   100.0%;  Pred. No. 9.7e-43;
Matches  95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     733 ATTTCAGGGACGATCGTTGATAAAAGTGGCGCGACTCTTTCCGGACACAGCAGGAGAGGGA 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 ATTTCAGGGACGATCGTTGATAAAAGTGGCGCGACTCTTTCCGGACACAGCAGGAGAGGGA 471

Qy     793 TTTGTCATCAGCGTGTCTCATCGATGAGAACCACTCTG 827
           ||||||||||||||||||||||||||||||||||||||
Db                                            827
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Db   472 TTTGTCATCAGCGTGTCTCATGAGAGACCACTCTG 506

RESULT 38
BV597233/c
LOCUS   BV597233   758 bp   DNA   linear   STS 14-APR-2005
DEFINITION   S216P61129FG4.TO Masuku Pan troglodytes troglodytes STS genomic,
                sequence tagged site.
ACCESSION   BV597233
VERSION   BV597233.1 GI:62536147
KEYWORDS   STS.
SOURCE   Pan troglodytes troglodytes
  ORGANISM   Pan troglodytes troglodytes
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Pan.
REFERENCE   1 (bases 1 to 758)
  AUTHORS   Mikkelsen,T.S., Hillier,W.L., Eichler,E.B., Zody,M.C. and
                Jaffe,D.B.
  TITLE   Initial Sequence of the Chimpanzee Genome and Comparison with the
                Human Genome
  JOURNAL   Unpublished (2005)
COMMENT   Contact: Michael C. Zody
                Broad Institute of MIT and Harvard
                320 Charles Street, Cambridge, MA 02141, USA
                Tel: 617580933
                Fax: 617580903
                Email: mczody@broad.mit.edu
                Primer A: No sequence submitted
                Primer B: No sequence submitted
                STS size: 758
                Protocol:
                23,021,928 chimpanzee whole genome shotgun reads were aligned to
                the Human genome NCBI
                Build 34 (hg16,July 2003). Chimp WGS reads were from 9 donors,
                including Clint (Pan
                troglodytes verus), 3 other Pan troglodytes verus chimps
                (Donald,Karlien,Yvonne), 2 Pan
                troglodytes troglodytes chimps (Noemie,Masuku,Clara) and 2 chimps
                of unknown origin
                (Gon,Unknown Chimp). Common names: Pan troglodytes verus is the
                western chimp and Pan
                troglodytes troglodytes is the central chimp. To be included in
                chimpanzee SNP discovery, a
                read must be at least 500bp in length, at least 50% of its base
                calls must have Phred
                score >= 20, at least 30% of its base calls must satisfy
                SNQS(30,25)(single strand NQS, the
                base in question has Phred score >= 30, the surrounding 10 bases in
                the read have Phred
                score >= 25), and the read must have at least 200 bp SNQS(30,25)
                bases. Reads not uniquely
                placed in the genome and read pairs whose two ends were not
                consistently placed were
                discarded. After above filtering, NQS(30,25) standard was applied
                to all pairs of
                overlapping reads to call NQS bases and SNPs. Alignments (between
                two reads) with less
                than 100 NQS bases or with SNP rate > 0.01 were discarded. To
                exclude alignment between two
                copies of a single read, comparisons between two reads that share
                95% of their genome
                alignments (>=95% bases of read A and >=95% bases of read B were
                placed at the same locus
                of human genome) were discarded.
FEATURES   Location/Qualifiers
     source   1..758
                     /organism="Pan troglodytes troglodytes"
                     /mol_type="genomic DNA"
                     /sub_species="troglodytes"
                     /db_xref="taxon:37011"
                     /clone_lib="Masuku"

STS
ORIGIN   <1..>758

Query Match   2.4%; Score 93; DB 10; Length 758;
Best Local Similarity   100.0%; Pred. No. 1.4e-41;
Matches   93; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   311 AGGAATACTTGCTGGCTGGCGGCAGATACATTCATTGAAACAAATACTTTTAGCAGCACTAGTA 370
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   427 AGGAATACTTGCTGGCTGGCGGCAGATACATTCATTGAAACAAATACTTTTAGCAGCACTAGTA 368

Qy   371 TTGCCCAAGCTGACTATGGCCTTGAACACTTGG 403
              |||||||||||||||||||||||||||||||||
Db   367 TTGCCCAAGCTGACTATGGCCTTGAACACTTGG 335

RESULT 39
DQ084519
LOCUS   DQ084519   3832 bp   mRNA   linear   MAM 28-JUN-2005
DEFINITION   Bos taurus 5-methyltetrahydrofolate-homocysteine methyltransferase
                (MTR) mRNA, complete cds.
ACCESSION   DQ084519
VERSION   DQ084519.1 GI:68160374
KEYWORDS   .
SOURCE   Bos taurus (cow)
  ORGANISM   Bos taurus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 3832)
  AUTHORS   Palin,M.F., Beaudry,D., Charest.R. and Girard,C.
  TITLE   Interactions of folic acid-vitamin B12-methionine: effects on liver
                metabolism and production of dairy cows
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 3832)
  AUTHORS   Palin,M.F., Beaudry,D., Charest,R. and Girard,C.
  TITLE   Direct Submission
  JOURNAL   Submitted (03-JUN-2005) Dairy and Swine Research and Development
                Centre, P.O. Box 90, 2000 Route 108 East, Lennoxville, Quebec J1M
                123, Canada
FEATURES   Location/Qualifiers
     source   1..3832
                     /organism="Bos taurus"
                     /mol_type="mRNA"
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                     /tissue_type="liver"
     gene   1..3832
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     CDS   22..3819
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                     /protein_id="AAY86762.1"
                     /db_xref="GI:68160375"
                     /translation="MAPTLQDLTPSAGMKKTLQDEIEAILQERIMVLDGGMGTMIQRH
                     KLSEEDFRGQEFKDHARPLKGNNDILSITQPNVIYQIHKEYLLAGADIIETNTFSSTS
                     IAQADYGLEHLAYRMNMCSAGVARKAAEDISLQTGIKRYVAGALGPTNKTLSVSPSVE
                     RPDYRNITFDELVEAYKEQAKGLLDGGVDILLIETIFPDTANAKAALFAVQKLFEEYV
                     PRPVFISGTIVDKSGRTLSGQTGEAFVISVSHADPLCIGLNCALGAAEMRPFIETIGK
                     CTTAYVLCYPNAGLPNTFGDYDETPHVMAMHLKDFAVDGLVNIVGGCCGTTPDHIREI
                     AEAVKNCKPRVPPATVFEGHMLLSGLEPFRIGPYTNFVNIGERCNVAGSRFAKLIMA
                     GNYEEALSVAKMQVEMGAQVLDINMDDGMLDGPSAMTRPCNFIASEPDIAKVPLCIDS
                     SNFAVIEAGLKCCQGKCIVNSISLKEGEDDFLEKARKIKKFGAAVVVMAFDEEGQATE
                     TDPKIRVCTRAYHLLLKKLGFNPNDILTIGTGMEHNLYAVNFINATKVIKE
                     TLPGAKVSGGLSNLSFSFRGMEAIREAMHGVFLYHAIKPGMDMGIVNAGSLPVYDDIH
                     EKLQLCEDLIWNRDPEATEKLLHYAQTQGKGGKKVIQTDEWRNGPLEBRLEYALVKG
                     IEKYIIEDTEEARLNQEKYPRPLNIIEGPLMNGMKIVGDLFGAGMFLPQVIKSARVM
                     KKAVGHLIPFMEKEREETKVLTGKIEDEDPYQGTIVLATVKGDVHDIGKNIVGVVLGC
                     NNFRVIDLGVMTPCDKILKAALDHKADIIGLSGLITPSLDEMIFVAKEMERLAIKIPL
                     LIGGATTSRTHTAVKIAPRYSAPVIHVLDASKSVVVCSQLLDENLKDEYFEEILEYE
                     DIRQDHYESLKERRYLTLRQARENGFHIDWLSEPPPVKPTFLGTRVFEDYDLQKLVDY

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                    EAYQEQAKGLLDGGVDILLIETIFDTANAKAALFALQKLFEENYASRPIFISGTIVD
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                    GLPNTFGQTDETPAMMAMHLKDFAVDGLVNVVGGCGSPTPDHIREIAEAVNCKPRVP
                    PDSVPEGHMLLSGLEPFRIGPYTNPVNIGRCNVAGSKKFAKLIMAGNYEBALSVAKV
                    QVEMGAQVLDINMDDGMLDGPSAMTKFCNFIASEPDIAKVPLCIDSSNFAVIEAGLKC
                    CQGKCIVNSISLKEGBEDFLEKARKIKKPGAAVVMAFDBEGQATETDVKVSVCTRAY
                    HLLVEKVGFNPNDIIFPDPNILTIGTGMEBHNLYAINFIHATRVIKETLPGVRISGGLS
                    NLSPAFRGMDAIREAMHGVPLYHAIKFGMDMGIVNAGSLPVYDDIHKDLLQLCEDLIW
                    NRDAEATEKLLRYAQTHGKGGKKVIQTDEWRNGSIEERLEYALVKGIEKHIVEDTEEA
                    RLNRBKYPRPLNIIEGPLMNGMKVVGDLFGAGKMFLPQVIKSARVMKKAVGHLIPFME
                    KEREBARVLNGSVEBEDPYQGTIVLATVKGDVHDIGKNIVGVVLGCNNFRVIDLGVMT
                    PCDKILQAALDHKADIIGLSGLITPSLDEMIFVAKEMERLAIKIPLLIGGATTSRTHT
                    AVKIAPRYSAPVIHVLDASKSVVVCSQLLDENLKDDYFEBILEBYEDIRQDHYESLKE
                    RKYLPLSQARKHSFHIDWLSEPHVKPTFIGTQVFEDYNLQKLVDYIDWKPFFPDVWQL
                    RGKYPNRGFPKIFNDKAVGEARKVYEDAQNMLSILISRKKLRARGVVGFWPAQSVQD
                    DIHLYAEGAVPQAAEPIATFYGLRQQAEKDSSSTDPYHCLSDFVAPLHSGVRDYLGLF
                    AVACFGVEELSKAYEDDGDDYSSIMVKALGDRLAEAFABELHERVRRELWAYCGSEQL
                    GVTDLRKLRYEGIRPAPGYPSQPDHTEKLTMWRLANIEQATGIRLTESLAMAPASAVS
                    GLYFSNVKSKYFAVGKISKDQIEDYALRKNMSVABVEKWLGPILGYDTD"

ORIGIN

Query Match              1.7%;   Score 65;  DB 9;  Length 4498;
Best Local Similarity  100.0%;   Pred. No. 4.2e-25;
Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2890 GATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTATTGGGACCCCAGGTCTTTGAA 2949
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3074 GATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTATTGGGACCCCAGGTCTTTGAA 3133

Qy   2950 GACTA 2954
               |||||
Db   3134 GACTA 3138


RESULT 41
AX611831
LOCUS       AX611831           63 bp    DNA      linear       PAT 17-FEB-2003
DEFINITION  Sequence 2856 from Patent WO02072882.
ACCESSION   AX611831
VERSION     AX611831.1  GI:28407260
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 2856 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1..63
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match              1.6%;   Score 63;  DB 6;  Length 63;
Best Local Similarity  100.0%;   Pred. No. 6.4e-24;
Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3544 GCAGACCTGCGGAAGGTTGCGGTACAAGGGCATCCGCCGGCTCCTGGCTACCCCAGCCAG 3603
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGACCTGCGGAAGGTTGCGGTACAAGGGCATCCGCCGGCTCCTGGCTACCCCAGCCAG 60

Qy   3604 CCC 3606
               |||
Db     61 CCC 63


RESULT 42
AC156661/c
```

Left column:

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variation       IDWKPFFPDVWQLRGKYPNRGFPKIFDDKTVGEBAKKVYDDAQNMLQALISQKKLQARG
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                LHSGIPDYLGLFAVACFGVEELSKAYEBECDDYSSIMVKALGDRLAEAPABELHERAR
                RELMGYCSGEQLAVADLRRLRYEGIRPAPGYPSQPDHTEKLTWRLADVEQRTGIRLT
                ESLAMAPASAVSGLYFSNLKSKYFAVGKISKDQIEDYASRKNMSVAEVEKWLGPILGY
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                /replace="g"
variation       409
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variation       3455
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ORIGIN

Query Match              1.7%;   Score 68;  DB 4;  Length 3832;
Best Local Similarity  100.0%;   Pred. No. 7.3e-27;
Matches   68;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2524 GACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTCCCTGGATGAAATG 2583
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2482 GACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTCCCTGGATGAAATG 2541

Qy   2584 ATTTTTGT 2591
               ||||||||
Db   2542 ATTTTTGT 2549


RESULT 40
AF034214
LOCUS       AF034214          4498 bp    mRNA     linear     ROD 20-JAN-1999
DEFINITION  Rattus norvegicus methionine synthase (MS) mRNA, complete cds.
ACCESSION   AF034214
VERSION     AF034214.1  GI:3978142
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 4498)
  AUTHORS   Yamada,K., Tobimatsu,T. and Toraya,T.
  TITLE     Cloning, sequencing, and heterologous expression of rat methionine
            synthase cDNA
  JOURNAL   Biosci. Biotechnol. Biochem. 62 (11), 2155-2160 (1998)
   PUBMED   9972236
REFERENCE   2  (bases 1 to 4498)
  AUTHORS   Yamada,K., Tobimatsu,T. and Toraya,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-NOV-1997) Bioscience and Biotechnology, Okayama
            University, 3-1-1 Tsushima-Naka, Okayama, Okayama 700, Japan
FEATURES             Location/Qualifiers
     source          1..4498
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Wistar"
                     /db_xref="taxon:10116"
                     /tissue_type="liver"
     CDS             284..4045
                     /EC_number="2.1.1.13"
                     /note="MS"
                     /codon_start=1
                     /product="methionine synthase"
                     /protein_id="AAD05384.1"
                     /db_xref="GI:3978143"
                     /translation="MKKTLQDEIEAILRKRIMVLDGGMGTMIQRYKLSEENFQGQEFK
                     DHSRPLKGNNDILSITQPDVIYQIHKEYLLAGADIIETNTFSSTSIAQADYGLEHLAY
                     RMNKKCSADVARKAAEBITLQTGVKRFVAGSLGPTNKTLSVSPSVERPDYRNITFDELV
```

```
LOCUS       AC156661              211299 bp    DNA     linear   HTG 01-JUL-2005
DEFINITION  Bos taurus clone CH240-66D4, WORKING DRAFT SEQUENCE, 19 unordered
            pieces.
ACCESSION   AC156661
VERSION     AC156661.2  GI:68265967
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 211299)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abranzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodei,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Derano,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,J., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
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            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,C., Minja,B., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarmpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Vales,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 211299)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-FEB-2005) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 211299)
  AUTHORS   Cow Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Jun 28, 2005 this sequence version replaced gi:58531381.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            --------- Genome Center
               Center: Baylor College of Medicine
               Center code: BCM
               Web site: http://www.hgsc.bcm.tmc.edu/
               Contact: hgsc-help@bcm.tmc.edu
            --------- Project Information
               Center project name: FDMA
               Center clone name: CH240-66D4
            --------- Summary Statistics
               Assembly program: Atlas 3.0;
               Consensus quality: 203895 bases at least Q40
               Consensus quality: 205492 bases at least Q30
               Consensus quality: 206916 bases at least Q20
               Estimated insert size: 206384; sum-of-contigs estimation
               Quality coverage: 7x in Q20 bases; sum-of-contig estimation
            * NOTE: Estimated insert size may differ from sequence length
            *       (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            *       consists of 19 contigs. The true order of the pieces
            *       is not known and their order in this sequence record is
            *       arbitrary. Gaps between the contigs are represented as
            *       runs of N, but the exact sizes of the gaps are unknown.
            *       This record will be updated with the finished sequence
            *       as soon as it is available and the accession number will
            *       be preserved.
            *           1: contig of 1769 bp in length
            *        1770: gap of 425 bp
            *        2194: gap of 28900 bp in length
            *        2195: contig of 28900 bp in length
            *       31094: gap of 50 bp
            *       31095: contig of 14239 bp in length
            *       31144: gap of 50 bp
            *       45383: contig of 14239 bp in length
            *       45384: gap of 50 bp
            *       45433: contig of 9866 bp in length
            *       45434: gap of 50 bp
            *       55299: contig of 9866 bp in length
            *       55300: gap of 50 bp
            *       55349: contig of 28689 bp in length
            *       55350: gap of 50 bp
            *       84038: contig of 28689 bp in length
            *       84039: gap of 50 bp
            *       84088: contig of 25745 bp in length
            *       84089: gap of 50 bp
            *      109833: contig of 25745 bp in length
            *      109834: gap of 50 bp
            *      109883: contig of 29072 bp in length
            *      109884: gap of 50 bp
            *      138955: contig of 29072 bp in length
            *      138956: gap of 50 bp
            *      139005: contig of 10043 bp in length
            *      139006: gap of 50 bp
            *      149048: contig of 10043 bp in length
            *      149049: gap of 50 bp
            *      149098: contig of 12698 bp in length
            *      149099: gap of 50 bp
            *      161796: contig of 12698 bp in length
            *      161797: gap of 50 bp
            *      161846: contig of 32178 bp in length
            *      161847: gap of 50 bp
            *      194024: contig of 32178 bp in length
            *      194025: gap of 50 bp
            *      194074: gap of 50 bp
            *      194075: contig of 1584 bp in length
            *      195658: gap of unknown length
            *      195659: contig of 3338 bp in length
            *      195758: gap of unknown length
            *      195759: contig of 3338 bp in length
            *      199096: gap of unknown length
            *      199097: contig of 1482 bp in length
            *      200578: gap of unknown length
            *      200579: contig of 1462 bp in length
            *      202040: gap of unknown length
            *      202041: contig of 1080 bp in length
            *      202140: gap of unknown length
            *      202141: contig of 1080 bp in length
            *      203220: gap of unknown length
            *      203221: contig of 1233 bp in length
            *      203320: gap of unknown length
            *      203321: contig of 1233 bp in length
            *      204553: gap of unknown length
            *      204554: contig of 1594 bp in length
            *      204653: gap of unknown length
            *      204654: contig of 1594 bp in length
            *      206247: gap of unknown length
            *      206248: contig of unknown length
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```
*  206348  207768: contig of 1421 bp in length
*  207769  207868: gap of unknown length
*  207869  209529: contig of 1661 bp in length
*  209530  209629: gap of unknown length
*  209630  211299: contig of 1670 bp in length.
FEATURES        Location/Qualifiers
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                /mol_type="genomic DNA"
                /db_xref="taxon:9913"
                /clone="CH240-66D4"
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     gap        45384..45433
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     gap        84039..84088
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     gap        109834..109883
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     gap        149049..149098
                /estimated_length=50
     gap        161797..161846
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     gap        199007..200578
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     gap        202041..202140
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ORIGIN
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Best Local Similarity 100.0%;  Pred. No. 2.1e-20;
Matches 57;  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2535 AGATATAATTGGCCGTGTCAGGACTCATCACTCCTTCCCTGGATGAAATGATTTTTGT 2591
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Db 204259 AGATATAATTGGCCGTGTCAGGACTCATCACTCCTTCCCTGGATGAAATGATTTTTGT 204203
```

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RESULT 43
AX611827
LOCUS       AX611827    55 bp   DNA   linear  PAT 17-FEB-2003
DEFINITION  Sequence 2852 from Patent WO02072882.
ACCESSION   AX611827
VERSION     AX611827.1  GI:28407256
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 2852 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES        Location/Qualifiers
 source         1..55
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN

Query Match     1.4%;  Score 55; DB 6; Length 55;
Best Local Similarity 100.0%;  Pred. No. 3.2e-19;
Matches 55;  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAATCATGGAAGAATATGAAGAGATATTAGACAGGACCATTATGAGTCTCTCAAGG 2839
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAATCATGGAAGAATATGAAGAGATATTAGACAGGACCATTATGAGTCTCTCAAGG 55

RESULT 44
AX611829
LOCUS       AX611829    55 bp   DNA   linear  PAT 17-FEB-2003
DEFINITION  Sequence 2854 from Patent WO02072882.
ACCESSION   AX611829
VERSION     AX611829.1  GI:28407258
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 2854 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES        Location/Qualifiers
 source         1..55
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN

Query Match     1.4%;  Score 55; DB 6; Length 55;
Best Local Similarity 100.0%;  Pred. No. 3.2e-19;
Matches 55;  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAATCATGGAAGAATATGAAGAGATATTAGACAGGACCATTATGAGTCTCTCAAGG 2839
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAATCATGGAAGAATATGAAGAGATATTAGACAGGACCATTATGAGTCTCTCAAGG 55

RESULT 45
AC154523/c
LOCUS       AC154523    194232 bp   DNA   linear  HTG 12-JAN-2005
DEFINITION  Mus musculus chromosome 13 clone RP24-65H12, WORKING DRAFT
            SEQUENCE, 9 unordered pieces.
ACCESSION   AC154523 AC133884
VERSION     AC154523.1  GI:56900149
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 194232)
  AUTHORS   Wilson,R.K.
  TITLE     The sequence of Mus musculus clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 194232)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-2004) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
```

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REFERENCE   3  (bases 1 to 194232)
AUTHORS     Wilson,R.K.
TITLE       Direct Submission
JOURNAL     Submitted (12-JAN-2005) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
COMMENT     On Dec 30, 2004 this sequence version replaced gi:28894649.

            -------------- Genome Center --------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu
            Contact: submissions@watson.wustl.edu
            -------------- Project Information --------------
            Center project name: M_BB0065H12
            Drafting center: WIBR

            -------------- Summary Statistics --------------
            Sequencing vector: M13; 0%
            Sequencing vector: plasmid; 100%
            Chemistry: Dye-primer ET; 0% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 190157 bases at least Q40
            Consensus quality: 191134 bases at least Q30
            Consensus quality: 191685 bases at least Q20

            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 9 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    1179: contig of 1179 bp in length
            *    1180    1279: gap of unknown length
            *    1280    2449: contig of 1170 bp in length
            *    2450    2549: gap of unknown length
            *    2550    4084: contig of 1535 bp in length
            *    4085    4184: gap of unknown length
            *    4185    6466: contig of 2282 bp in length
            *    6467    6566: gap of unknown length
            *    6567    8700: contig of 2134 bp in length
            *    8701    8800: gap of unknown length
            *    8801   24080: contig of 15280 bp in length
            *   24081   24180: gap of unknown length
            *   24181   54114: contig of 29934 bp in length
            *   54115   54214: gap of unknown length
            *   54215   87114: contig of 32900 bp in length
            *   87115   87214: gap of unknown length
            *   87215  194232: contig of 107018 bp in length.

FEATURES             Location/Qualifiers
     source          1..194232
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="13"
                     /clone="RP24-65H12"
     misc_feature    1..1179
                     /note="assembly_name:Contig24"
     gap             1180..1279
                     /estimated_length=unknown
     misc_feature    1280..2449
                     /note="assembly_name:Contig34"
     gap             2450..2549
                     /estimated_length=unknown
     misc_feature    2550..4084
                     /note="assembly_name:Contig36"
     gap             4085..4184
                     /estimated_length=unknown
     misc_feature    4185..6466
                     /note="assembly_name:Contig37"
     gap             6467..6566

     misc_feature    6567..8700
                     /note="assembly_name:Contig38"
     gap             8701..8800
                     /estimated_length=unknown
     misc_feature    8801..24080
                     /note="assembly_name:Contig39"
     gap             24081..24180
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     misc_feature    24181..54114
                     /note="assembly_name:Contig40"
     gap             54115..54214
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     misc_feature    54215..87114
                     /note="assembly_name:Contig41"
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                     /note="assembly_name:Contig42"
ORIGIN

Query Match             1.4%;    Score 54;   DB 14;   Length 194232;
Best Local Similarity 100.0%;   Pred. No. 1.2e-18;
Matches   54;           Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     2281 ATGAAGAAGGCTGTTGGCCACCTTATCCTTTCATGGAAAAAGAAGAGAAGAA 2334
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   140285 ATGAAGAAGGCTGTTGGCCACCTTATCCTTTCATGGAAAAAGAAGAGAAGAA 140232

RESULT 46
AC137163
LOCUS       AC137163              228824 bp    DNA     linear   HTG 19-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-unknown, WORKING DRAFT SEQUENCE, 3
            unordered pieces:
ACCESSION   AC137163
VERSION     AC137163.1  GI:25073033
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 228824)
AUTHORS     Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C. Allen.H., Alsbrooks,S., Anin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,B.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
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            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu.X., Ma.J.,
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ORIGIN

Query Match           1.4%;    Score 54;    DB 14;    Length 228824;
Best Local Similarity  100.0%;    Pred No. 1.2e-18;
Matches  54;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    2281 ATGAAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAAGAGAAGAA 2334
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   36551 ATGAAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAAGAGAAGAA 36604


RESULT 47
LOCUS       AC139941               236536 bp    DNA     linear   ROD 13-APR-2004
DEFINITION  Mus musculus chromosome 13, clone RP23-78M22, complete sequence.
ACCESSION   AC139941
VERSION     AC139941.9  GI:46359990
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 236536)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 13, clone RP23-78M22
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 236536)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
            Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
            Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
            Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
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            Vassliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 236536)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
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            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Soss,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wilczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 228824)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contig within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@cm.tmc.edu
            -------------- Project Information
            Center project name: KZZA
            Center clone name: CH230-unknown
            -------------- Summary Statistics
            Assembly program: Phrap; version 0.990329
            Consensus quality: 217440 bases at least Q40
            Consensus quality: 220237 bases at least Q30
            Consensus quality: 222469 bases at least Q20
            Estimated insert size: 222872; sum-of-contigs estimation
            Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
            * NOTE: Estimated insert size may differ from sequence length
            *       (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1  139431: contig of 139431 bp in length
            *  139431  139531: gap of unknown length
            *  139432           contig of unknown length
            *  139532  205030: contig of 65499 bp in length
            *  205031  205130: gap of unknown length
            *  205130           gap of unknown length
            *  205131  228824: contig of 23694 bp in length.
FEATURES             Location/Qualifiers
     source          1..228824
```

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           O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
           Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
           Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
           Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
           Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
           Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
           Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE    Direct Submission
  JOURNAL  Submitted (03-MAR-2004) Whitehead Institute/MIT Center for Genome
           Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE  4  (bases 1 to 236536)
  AUTHORS  Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
           Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
           Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
           Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
           DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
           Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
           Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
           Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
           Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
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           Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
           Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
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           Zimmer,A. and Zody,M.
  TITLE    Direct Submission
  JOURNAL  Submitted (13-APR-2004) Whitehead Institute/MIT Center for Genome
           Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT    On Apr 13, 2004 this sequence version replaced gi:44890997.
           All repeats were identified using RepeatMasker.
           Smit, A.F.A. & Green, P. (1996-1997)
           http://ftp.genome.washington.edu/RM/RepeatMasker.html
           --------  Genome Center
             Center: Whitehead Institute/MIT Center for Genome Research
             Center code: WIBR
             Web site: http://www-seq.wi.mit.edu
             Contact: sequence_submissions@broad.mit.edu
           --------  Project Information
             Center project name: L29136
             Center clone name: 78_M_22
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                     /map="13"
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                     clone_end:SP6"
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     repeat_region   171..317
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     misc_feature    455..460
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                     /rpt_family="RMER17C"

     repeat_region   2254..2561
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                     /rpt_family="RMER5"
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                     /rpt_family="rSINB1"
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                     /rpt_family="B1F"
     repeat_region   complement(12607..12820)
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     repeat_region   13030..13071
                     /rpt_family="B3"
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                     /note="single clone coverage"
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     repeat_region   14982..15042
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repeat_region    complement(18214..18306)
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Query Match        1.4%;    Score 54;   DB.9;   Length 236536;
Best Local Similarity 100.0%;  Pred. No. 1.2e-18;
Matches   54;   Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    2281 ATGAAGAAGGCTGTTGGCCACCTATCCCTTCATGGAAAAGAGAAGAAGA 2334
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Db   53174 ATGAAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAAGAGAAGAA 53227
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RESULT 48
AC113729
LOCUS   AC113729   244504 bp   DNA   linear   HTG 19-NOV-2002
DEFINITION Rattus norvegicus clone CH230-97A15, WORKING DRAFT SEQUENCE, 2
            unordered pieces.
ACCESSION   AC113729
VERSION   AC113729.5   GI:25072683
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1 (bases 1 to 244504)
AUTHORS   Anyalebechi,V., Aoyagi,A., Ayodeji,A., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chu,J.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
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            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
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            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
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            Lorensuhewa,L., Louiseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
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            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
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            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
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            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
TITLE   Direct Submission
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 244504)
AUTHORS   Worley,K.C.
TITLE   Direct Submission
JOURNAL   Submitted (05-MAR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3 (bases 1 to 244504)
AUTHORS   Rat Genome Sequencing Consortium.
TITLE   Direct Submission
JOURNAL   Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT   On Nov 19, 2002 this sequence version replaced gi:23265864.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat//). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            --------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            --------- Project Information
                Center project name: GSDI
                Center clone name: CH230-97A15
            --------- Summary Statistics
                Assembly program: Phrap; version 0.99029
                Consensus quality: 213541 bases at least Q40
                Consensus quality: 216589 bases at least Q30
                Consensus quality: 219247 bases at least Q20
                Estimated insert size: 221068; sum-of-contigs estimation
                Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            *   consists of 2 contigs. The true order of the pieces
            *   is not known and their order in this sequence record is
            *   arbitrary. Gaps between the contigs are represented as
            *   runs of N, but the exact sizes of the gaps are unknown.
            *   This record will be updated with the finished sequence
            *   as soon as it is available and the accession number will
            *   be preserved.
            *   1   235052: contig of 235052 bp in length
            *   235053   235152: gap of unknown length
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                     /note="clone_boundary
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ORIGIN        clone_end:Sp6"

Query Match     1.4%;    Score 54;   DB 14;   Length 244504;
Best Local Similarity  100.0%;    Pred. No. 1.2e-18;
Matches   54;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    2281 ATGAAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAAGAAGAAGAAGAA 2334
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RESULT 49
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LOCUS       AC121488              268715 bp    DNA     linear   HTG 13-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-unknown, WORKING DRAFT SEQUENCE, 6
            unordered pieces.
ACCESSION   AC121488
VERSION     AC121488.3  GI:24941249
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 268715)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
            Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
            Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
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            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 268715)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAY-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3 (bases 1 to 268715)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 13, 2002 this sequence version replaced gi:23364539.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            ------- Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu
            -------- Project Information
            Center project name: TUUQ
            Center clone name: CH230-unknown
            -------- Summary Statistics
            Assembly program: Phrap; version 0.990329
            Consensus quality: 247503 bases at least Q40
            Consensus quality: 250434 bases at least Q30
            Consensus quality: 252681 bases at least Q20
            Estimated insert size: 259015; sum-of-contigs estimation
            Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
            * NOTE: Estimated insert size may differ from sequence length.
            *       (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
            * NOTE: This sequence may represent more than one clone.
            * NOTE: This is a 'working draft' sequence. It currently
            *       consists of 6 contigs. The true order of the pieces
            *       is not known and their order in this sequence record is
            *       arbitrary. Gaps between the contigs are represented as
            *       runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            *       as soon as it is available and the accession number will
            *       be preserved.
            *      1     3413: contig of 3413 bp in length
            *      3414  3513: gap of unknown length
            *      3514 16165: contig of 12652 bp in length
            *     16166 16265: gap of unknown length
            *     16266 94984: contig of 78719 bp in length
            *     94985 95084: gap of unknown length
            *     95085 266072: contig of 170988 bp in length
            *    266073 266172: gap of unknown length
            *    266173 267497: contig of 1325 bp in length
            *    267498 267597: gap of unknown length
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ORIGIN

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SOURCE      Gallus gallus (chicken)
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            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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REFERENCE   1
  AUTHORS   Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J.,
            Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M.,
            Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
  TITLE     Full-length cDNAs from chicken bursal lymphocytes to facilitate
            gene function analysis
  JOURNAL   Genome Biol. 6 (1), R6 (2005)
   PUBMED   15642098
REFERENCE   2  (bases 1 to 5168)
  AUTHORS   Caldwell,R.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAY-2004) Caldwell R.B., GSF - Forschungszentrum,
            Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr.
            1, D-85764 Neuherberg, GERMANY
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     3'UTR

ORIGIN

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Job time : 18971 secs
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OM nucleic - nucleic search, using sw model

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                GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Bioacceleration Ltd.

Run on:   March 7, 2006, 01:41:09 ; Search time 2063 seconds
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                Gapop 60.0 , Gapext 60.0

Searched:       4996997 seqs, 3332346308 residues

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	1	3517	89.7	7122	4	AAF31100	Aaf31100 Methionin
	2	3517	89.7	7122	5	AAC91207	Aac91207 Human met
	3	3517	89.7	7122	14	AEA63658	Aea63658 Methionin
	4	3466	88.4	7224	4	AAF31101	Aaf31101 Methionin
	5	3390	86.5	3798	10	ADI39109	Adi39109 Homo sapi
	6	1349	34.4	3920	2	AAV34063	Aav34063 Human met
	7	308	7.9	4172	13	ADR07169	Adr07169 Full leng
	8	222	5.7	305	2	AAV88164	Aav88164 EST clone
	9	44	1.1	80	12	ADP49459	Adp49459 Oligonucl
	10	31	0.8	31	4	AAI29993	Aai29993 Human sin
	11	31	0.8	31	4	AAI29989	Aai29989 Human sin
	12	31	0.8	31	4	AAI29985	Aai29985 Human sin
	13	31	0.8	31	4	AAI29988	Aai29988 Human sin
	14	31	0.8	31	4	AAI29986	Aai29986 Human sin
	15	31	0.8	31	4	AAI29992	Aai29992 Human sin
	16	31	0.8	31	4	AAI29987	Aai29987 Human sin
	17	31	0.8	31	4	AAI29990	Aai29990 Human sin
	18	31	0.8	31	4	AAI29991	Aai29991 Human sin
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c	33	25	0.6	25	2	AAV34087	Aav34087 Methionin
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c	35	25	0.6	25	5	AAV34079	Aav34079 Methionin
	36	25	0.6	237	5	ABV61053	Abv61053 Human pro
	37	25	0.6	296	6	ABL86554	Abl86554 Human ova
	38	25	0.6	433	13	ACN52851	Acn52851 Cotton an
	39	25	0.6	475	13	ACN52668	Acn52668 Cotton an
	40	25	0.6	789	5	AAH03248	Aah03248 Human cDN
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	43	25	0.6	2050	12	ADK66235	Adk66235 Human NEO
	44	25	0.6	14231	5	ABA19751	Aba19751 Human ner
	45	25	0.6	142976	12	ABD32612	Abd32612 Human can
	46	25	0.6	151909	14	AEB96535	Aeb96535 Human CAB
	47	25	0.6	231222	10	ADL13693	Adl13693 Osteoarth
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	69	24	0.6	9417	14	AAX36849	Aax36849 Human XLI
	70	24	0.6	9417	8	ABX76234	Abx76234 Lung canc
	71	24	0.6	9417	14	ADV70098	Adv70098 Tumor-ass
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c	73	24	0.6	32249	4	AAI63718	Aai63718 Human kid
c	74	24	0.6	87495	14	AEB96528	Aeb96528 Human AP1
c	75	24	0.6	137908	11	ADP65634	Adp65634 Human seq
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	78	23	0.6	23	4	AAV34084	Aav34084 Methionin
	79	23	0.6	23	6	AAH49106	Aah49106 Human MTR
	80	23	0.6	23	6	ABX09548	Abx09548 Arteriosc
c	81	23	0.6	23	10	ADO57141	Ado57141 Human MTR
	82	23	0.6	385	10	ABT40755	Abt40755 Toxicity
	83	23	0.6	385	12	ADP71801	Adp71801 Renal tox
	84	23	0.6	385	13	ADV39794	Adv39794 Rat cardi
	85	23	0.6	421	6	ABK62924	Abk62924 Rat seque
	86	23	0.6	421	11	ADW21652	Adw21652 Rat hepat
	87	23	0.6	434	6	ABN73227	Abn73227 Bovine em
	88	23	0.6	434	6	ABN73317	Abn73317 Bovine em
	89	23	0.6	460	5	ABV56430	Abv56430 Human pro
	90	23	0.6	463	5	AAI89372	Aai89372 Human pol
c	91	23	0.6	474	9	ADA44975	Ada44975 Human pol
c	92	23	0.6	481	2	AAV99731	Aav99731 Human adu

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93		23	0.6	498	ADB55663	10	Adb55663	Toxicity-
94		23	0.6	498	ADV39607	13	Adv39607	Rat cardi
95	c	23	0.6	527	ADB55332	10	Adb55332	Toxicity-
96	c	23	0.6	1458	ADE63990	10	Ade63990	DNA encod
97	c	23	0.6	1458	ADE63994	10	Ade63994	Human gen
98		23	0.6	1492	ADW11288	14	Adw11288	Human C-t
99	c	23	0.6	1566	ABL41621	6	Abl41621	Human C-t
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101	c	23	0.6	1875	AAH33156	4	Aah33156	Human col
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104		23	0.6	2100	ACN42458	13	Acn42458	Human dia
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107		23	0.6	4840	ADQ23344	12	Adq23344	Human sof
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109		23	0.6	8847	ADO25304	12	Ado25304	Porcine u
110	c	23	0.6	9456	ADQ23327	12	Adq23327	Human sof
111	c	23	0.6	10480	ABL34201	6	Abl34201	Human imm
112	c	23	0.6	13288	ABA20468	5	Aba20468	Human ner
113	c	23	0.6	14117	ABL64107	6	Abl64107	Breast ca
114	c	23	0.6	17431	AAK90339	4	Aak90339	Human dig
115	c	23	0.6	17431	AAI57710	4	Aai57710	Human col
116	c	23	0.6	17431	ABS99887	10	Abs99887	Genomic D
117	c	23	0.6	17431	ADB93040	10	Adb93040	Human col
118	c	23	0.6	20486	ABL34611	6	Abl34611	Human met
119	c	23	0.6	20486	ADS99872	7	Ads99872	Complemen
120	c	23	0.6	23271	ACN37213	13	Acn37213	Human per
121	c	23	0.6	34245	ABD32614	13	Abd32614	Mouse can
122		23	0.6	98825	ADZ45062_09	14	Continuation (10 o
123	c	23	0.6	169659	ADQ59434	12	Adq59434	Human can
124	c	23	0.6	187851	ADZ13735	14	Adz13735	Human can
125	c	23	0.6	195102	ADV70461	13	Adv70461	Chicken g
126		22	0.6	22	AAV34085	2	Aav34085	Methionin
127		22	0.6	22	AAH49105	4	Aah49105	Human MTR
128		22	0.6	22	ABX09547	6	Abx09547	Arteriosc
129		22	0.6	121	ADK93800	12	Adk93800	Polynucle
130	c	22	0.6	194	ABL86939	6	Abl86939	Human ova
131		22	0.6	287	ABL85961	8	Abl85961	Human ova
132	c	22	0.6	324	ABK62734	6	Abk62734	Rat seque
133		22	0.6	324	ADB51132	10	Adb51132	Primary r
134		22	0.6	352	ACF85082	13	Acf85082	Human SIR
135		22	0.6	374	ABV99252	6	Abv99252	Marine sn
136		22	0.6	375	ADP72025	12	Adp72025	Renal tox
137		22	0.6	375	ADX25799	14	Adx25799	Novel cel
138		22	0.6	424	ABV13705	5	Abv13705	Human pro
139		22	0.6	436	ABV34818	5	Abv34818	Human pro
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142		22	0.6	482	AAI94479	4	Aai94479	Human neu
143	c	22	0.6	485	ACF83837	13	Acf83837	Human SIR
144		22	0.6	488	ACH37251	9	Ach37251	Human end
145		22	0.6	490	AAH71943	4	Aah71943	Human cer
146		22	0.6	490	AAH72697	4	Aah72697	Human cer
147		22	0.6	493	ACH33954	9	Ach33954	Human end
148		22	0.6	506	ADL39740	5	Adl39740	Human ova
149		22	0.6	518	ABL62708	6	Abl62708	Colon ade
150		22	0.6	550	AAH70743	4	Aah70743	Human cer
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152		22	0.6	569	ABZ34987	6	Abz34987	Human gen
153		22	0.6	569	ADE84813	10	Ade84813	Farnesyl
154		22	0.6	583	AAH08387	4	Aah08387	Human cDN
155		22	0.6	588	AAA16270	3	Aaa16270	Human col
156		22	0.6	598	ABV56139	5	Abv56139	Human pro
157		22	0.6	669	AAN90103	1	Aan90103	Human pre
158		22	0.6	688	ADT95691	11	Adt95691	Colon can
159		22	0.6	688	ADX42173	11	Adx42173	Human cDN
160		22	0.6	705	AAL24879	4	Aal24879	Human bre
161		22	0.6	759	ABK55355	6	Abk55355	Human col
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163	c	22	0.6	816	ABT42015	10	Abt42015	Toxicity
164		22	0.6	876	ADX59421	13	Adx59421	Plant ful
165	c	22	0.6	1028	ABK88911	6	Abk88911	Human agg
166	c	22	0.6	1031	ADI57327	10	Adi57327	Human GAB
167	c	22	0.6	1082	ADR20714	13	Adr20714	Human oes
168	c	22	0.6	1113	AAA51375	4	Aas51375	D. melano
169	c	22	0.6	1124	AAS33253	4	Aas33253	DNA encod
170	c	22	0.6	1136	ADB61368	10	Adb61368	Rheumatol
171	c	22	0.6	1211	AAC76729	3	Aac76729	Human ORF
172	c	22	0.6	1215	ADR83094	13	Adr83094	Human sca
173	c	22	0.6	1277	ABX05419	8	Abx05419	Human nov
174	c	22	0.6	1349	ADP04768	12	Adp04768	Sea squir
175	c	22	0.6	1352	AAV41918	2	Aav41918	Nucleotid
176	c	22	0.6	1471	ADK66919	10	Adk66919	Gene #9 f
177	c	22	0.6	1471	ADR28922	13	Adr28922	Human Hes
178	c	22	0.6	1471	ADR83406	13	Adr83406	Human hai
179	c	22	0.6	1471	ADX70426	14	Adx70426	Human tra
180	c	22	0.6	1518	AAX90449	4	Aax90449	Human sec
181	c	22	0.6	1518	AAS59278	6	Aas59278	Human CDN
182	c	22	0.6	1518	ABA90947	12	Aba90947	Human pol
183	c	22	0.6	1518	ADW09230	14	Adw09230	cDNA clon
184	c	22	0.6	1520	AAZ24901	13	Aaz24901	Human sec
185	c	22	0.6	1538	ADA45144	9	Ada45144	Human pol
186	c	22	0.6	1573	AAX35557	6	Aax35557	Secreted
187	c	22	0.6	1748	AEA36233	14	Aea36233	Human nuc
188	c	22	0.6	1791	ADX61621	13	Adx61621	Plant ful
189	c	22	0.6	1809	ADQ23540	12	Adq23540	Human sof
190	c	22	0.6	1809	ADQ22903	12	Adq22903	Human sof
191	c	22	0.6	1877	AAC79705	3	Aac79705	Human sec
192	c	22	0.6	1999	ABL62728	4	Abl62728	Colon ade
193	c	22	0.6	2274	ABL22784	4	Abl22784	Drosophil
194	c	22	0.6	2351	ADM03016	11	Adm03016	Human cDN
195	c	22	0.6	2595	AAH33385	4	Aah33385	Human col
196	c	22	0.6	2828	AEA62873	11	Aea62873	Rat trans
197	c	22	0.6	3033	ADX98503	14	Adx98503	Human hyp
198	c	22	0.6	3054	ADN00753	13	Adn00753	Human ROR
199	c	22	0.6	3115	AAC98113	3	Aac98113	Human col
200	c	22	0.6	3157	ACA48896	8	Aca48896	Prokaryot
201	c	22	0.6	3452	ADQ24824	12	Adq24824	Human sof
202	c	22	0.6	4182	ADL62107	6	Adl62107	Human ova
203	c	22	0.6	4256	ABL24674	4	Abl24674	Drosophil
204	c	22	0.6	4602	AAA51404	3	Aaa51404	Chromosom
205	c	22	0.6	5413	AAS46694	4	Aas46694	Tumour su
206	c	22	0.6	6045	AAH18244	4	Aah18244	Human cDN
207	c	22	0.6	6450	AAZ23433	6	Aaz23433	Human est
208	c	22	0.6	6450	ABK89695	6	Abk89695	Oestrogen
209	c	22	0.6	6450	ABK89703	6	Abk89703	Oestrogen
210	c	22	0.6	6450	ABV94431	6	Abv94431	Breast ca
211	c	22	0.6	6450	ABZ23389	6	Abz23389	Reverse c
212	c	22	0.6	6450	ABZ23388	8	Abz23388	Nucleotid
213	c	22	0.6	6450	ABX12085	8	Abx12085	cDNA enco
214	c	22	0.6	6450	ACC50140	8	Acc50140	Breast ca
215	c	22	0.6	6450	ABX93797	8	Abx93797	Human oes
216	c	22	0.6	6450	ADB81383	10	Adb81383	DNA seque
217	c	22	0.6	6450	ADD25499	10	Add25499	Binding d
218	c	22	0.6	6450	ADE12135	10	Ade12135	Human oes
219	c	22	0.6	6450	ADR76402	10	Adr76402	Human oes
220	c	22	0.6	6450	ADG89355	10	Adg89355	Novel hum
221	c	22	0.6	6450	ADF83093	12	Adf83093	Human tes
222	c	22	0.6	6450	ADF72329	12	Adf72329	Human and
223	c	22	0.6	6450	ADP07306	12	Adp07306	Human ESR
224	c	22	0.6	6450	ADP05662	12	Adp05662	Human nuc
225	c	22	0.6	6450	ADR24574	13	Adr24574	Breast ca
226	c	22	0.6	6450	ADR45377	13	Adr45377	Human oes
227	c	22	0.6	6450	ADR66804	13	Adr66804	Human pro
228	c	22	0.6	6450	ADR65901	13	Adr65901	Human ESR
229	c	22	0.6	6450	ADW86780	14	Adw86780	Human ESR
230	c	22	0.6	6450	ADY61188	14	Ady61188	Breast ca
231	c	22	0.6	6450	ADZ09607	12	Adz09607	Human bre
232	c	22	0.6	6450	AEB25746	12	Aeb25746	Human tes
233	c	22	0.6	6619	ADQ24081	12	Adq24081	Human sof
234	c	22	0.6	7171	ABN80216	6	Abn80216	Human che
235	c	22	0.6	7510	ABT04094	6	Abt04094	Human ova
236	c	22	0.6	8042	ABL32927	6	Abl32927	Human imm
237	c	22	0.6	8168	ABL32928	6	Abl32928	Human imm
238	c	22	0.6	8168	AAS63328	6	Aas63328	Chemical1

c	No.	Len	Score	Pos	Accession	Count	Description
c	239	22	0.6	8480	AAZ27521	2	Aaz27521 Interleuk
	240	22	0.6	8763	AAK89468	4	Aak89468 Human dig
c	241	22	0.6	9158	AAX03047	2	Aax03047 Human IL-
	242	22	0.6	9799	AAF97860	6	Aaf97860 Human neu
	243	22	0.6	10957	ABL33111	5	Abl33111 Human imm
c	244	22	0.6	11036	AAS45411	4	Aas45411 Human can
	245	22	0.6	11036	ABK28264	6	Abk28264 DNA trans
	246	22	0.6	12405	AAS45330	6	Aas45330 Chemicall
c	247	22	0.6	12405	ABK28169	6	Abk28169 DNA trans
	248	22	0.6	12774	AAK72738	4	Aak72738 Human imm
c	249	22	0.6	12774	ABA15302	5	Aba15302 Human ner
c	250	22	0.6	13182	ABX15028	10	Abx15028 Human gen
	251	22	0.6	13788	ABA19999	5	Aba19999 Human ner
c	252	22	0.6	17142	AAS45498	4	Aas45498 Chemical
	253	22	0.6	17142	ABL34107	6	Abl34107 Human imm
c	254	22	0.6	17142	ABK28430	4	Abk28430 DNA trans
	255	22	0.6	17200	AAL37025	4	Aal37025 DNA trans
	256	22	0.6	17200	ABX60013	12	Abx60013 cDNA enco
	257	22	0.6	17200	ADJ30763	8	Adj30763 Human mus
	258	22	0.6	17520	ABL32601	6	Abl32601 Human imm
c	259	22	0.6	19199	AAK70995	12	Aak70995 Human imm
	260	22	0.6	19338	AEA61189	14	Aea61189 Human DNA
	261	22	0.6	22475	ADQ97998	12	Adq97998 Human can
c	262	22	0.6	22478	ADA02849	8	Ada02849 Mouse Cbx
	263	22	0.6	22478	ADB72587	10	Adb72587 Mouse Cbx
	264	22	0.6	22478	ADC85328	10	Adc85328 Human Fgf
	265	22	0.6	22478	ADM74444	12	Adm74444 Murine ca
	266	22	0.6	22609	AAL35781	4	Aal35781 Human mus
	267	22	0.6	22609	ABX58769	8	Abx58769 cDNA enco
c	268	22	0.6	22609	ADJ29519	12	Adj29519 Human mus
c	269	22	0.6	24707	ABQ74933	9	Abq74933 Human tra
	270	22	0.6	24707	ADA24263	7	Ada24263 Human tra
	271	22	0.6	28444	ABK86948	6	Abk86948 Human glu
c	272	22	0.6	29764	AEB31548	14	Aeb31548 Glutathio
c	273	22	0.6	32193	AAL35782	4	Aal35782 Human mus
c	274	22	0.6	32193	ABX58770	8	Abx58770 cDNA enco
c	275	22	0.6	32193	ADJ29520	12	Adj29520 Human mus
	276	22	0.6	32203	ADZ59521	14	Adz59521 Secondary
	277	22	0.6	35000	ABT12817	6	Abt12817 Human REC
c	278	22	0.6	36445	ABL18116	4	Abl18116 Drosophil
	279	22	0.6	38054	ACN44994	11	Acn44994 Human gen
c	280	22	0.6	38054	ACN44994	11	Acn44994 Human gen
c	281	22	0.6	41765	AAK76675	7	Aak76675 Human imm
c	282	22	0.6	41787	AAK76676	4	Aak76676 Human imm
	283	22	0.6	41787	ABD33599	13	Abd33599 Human can
c	284	22	0.6	42016	ABD32962	13	Abd32962 Human can
	285	22	0.6	42334	ADA02588	9	Ada02588 Human ICS
c	286	22	0.6	42334	ADB72326	10	Adb72326 Human ICS
	287	22	0.6	42334	ADE95836	13	Ade95836 Human ICS
	288	22	0.6	43887	ABD33139	13	Abd33139 Murine ca
	289	22	0.6	52691	AAK84435	4	Aak84435 Human imm
	290	22	0.6	59475	ADQ59530	12	Adq59530 Human can
	291	22	0.6	61197	ACN45130	11	Acn45130 Human gen
c	292	22	0.6	65237	ABA90193_4	6	Continuation (5 of
c	293	22	0.6	65237	ABQ87681_4	8	Continuation (5 of
	294	22	0.6	65237	ABX33717_4	8	Continuation (5 of
	295	22	0.6	75252	ACN44450	11	Acn44450 Human gen
	296	22	0.6	76180	ABD33385	13	Abd33385 Human can
	297	22	0.6	79528	AAL50814	6	Aal50814 Human can
	298	22	0.6	79528	ADQ19802	12	Adq19802 Human sof
	299	22	0.6	89210	ADZ13911	14	Adz13911 Human can
c	300	22	0.6	91823	ADL13497	10	Adl13497 Osteoearth
	301	22	0.6	105413	ADI36512	12	Adi36512 Human kin
	302	22	0.6	110000	ABD32911_6	13	Continuation (7 of
c	303	22	0.6	110000	ADZ45062_03	14	Continuation (4 of
	304	22	0.6	110000	ADZ45062_03	14	Continuation (4 of
c	305	22	0.6	110096	ABN95044	5	Abn95044 Gene #154
	306	22	0.6	139573	ADH58564	10	Adh58564 Human Na+
c	307	22	0.6	156416	ABD32817	13	Abd32817 Human can
	308	22	0.6	169659	ADQ59434	12	Adq59434 Human can
	309	22	0.6	170245	ADP13586	12	Adp13586 Renal cel
	310	22	0.6	178024	ADQ97721	12	Adq97721 Human can
	312	22	0.6	180557	ABN85750	6	Abn85750 Human BAC
	313	22	0.6	185371	ABT10718	6	Abt10718 Human bre
	314	22	0.6	187851	ADZ13735	14	Adz13735 Human can
c	315	22	0.6	191150	ADM69029	12	Adm69029 Human pla
	316	22	0.6	191150	ABD33022	13	Abd33022 Human can
	317	22	0.6	245531	ADV35003	13	Adv35003 Murine CD
	318	22	0.6	251364	ADV34985	13	Adv34985 Murine CD
	319	22	0.6	251364	ADV34982	13	Adv34982 Murine CD
	320	22	0.6	251364	ADQ20017	12	Adq20017 Human sof
c	321	22	0.6	260160	ADC86916	10	Adc86916 Human GPC
	322	22	0.6	349989	AAV34089	2	Aav34089 Methionin
c	323	21	0.5	21	AAV34081	2	Aav34081 Methionin
	324	21	0.5	21	AAV34082	2	Aav34082 Methionin
c	325	21	0.5	21	AAF96203	4	Aaf96203 Human gen
	326	21	0.5	51	AAL27835	4	Aal27835 Human SNP
c	327	21	0.5	53	AAV29894	12	Aav29894 Target se
	328	21	0.5	121	ADK92447	5	Adk92447 Polynucle
	329	21	0.5	141	ADI68641	5	Adi68641 Human ova
c	330	21	0.5	141	ADI75004	5	Adi75004 Human ova
c	331	21	0.5	200	ADI75008	5	Adi75008 Human ova
	332	21	0.5	200	ADI68645	4	Adi68645 Human ova
	333	21	0.5	285	AAK72170	5	Aak72170 Human imm
c	334	21	0.5	290	ABV19408	5	Abv19408 Human pro
c	335	21	0.5	292	ABV07826	5	Abv07826 Human pro
c	336	21	0.5	301	ACF90242	13	Acf90242 Human SIR
c	337	21	0.5	310	ADV40197	13	Adv40197 Rat cardi
	338	21	0.5	315	ABX47201	8	Abx47201 Bovine ES
	339	21	0.5	327	ABX49772	8	Abx49772 Bovine ES
	340	21	0.5	337	AAL09791	5	Aal09791 Human bre
	341	21	0.5	339	ABV19636	6	Abv19636 Human pro
	342	21	0.5	355	ABL83749	5	Abl83749 Human mus
	343	21	0.5	360	AAL36865	5	Aal36865 Human mus
	344	21	0.5	360	ABX59853	12	Abx59853 cDNA enco
	345	21	0.5	360	ADJ30603	6	Adj30603 Human mus
c	346	21	0.5	371	ABL79958	8	Abl79958 Human ES
c	347	21	0.5	379	ABX37940	3	Abx37940 Bovine ES
c	348	21	0.5	385	AAC94443	3	Aac94443 Cat flea
c	349	21	0.5	388	AAD59584	10	Aad59584 Human end
	350	21	0.5	390	ABX44122	8	Abx44122 Bovine ES
c	351	21	0.5	390	ADI62653	10	Adi62653 Human apo
c	352	21	0.5	392	AAI80366	5	Aai80366 Human pol
	353	21	0.5	393	ABV13158	5	Abv13158 Human pro
	354	21	0.5	393	ABV37751	8	Abv37751 Human pro
	355	21	0.5	406	ABX54473	8	Abx54473 Bovine ES
	356	21	0.5	410	ADR60196	13	Adr60196 Cotton CD
	357	21	0.5	418	AAL18463	5	Aal18463 Human bre
c	358	21	0.5	418	ACN51983	13	Acn51983 Cotton an
c	359	21	0.5	422	ABV48501	8	Abv48501 Human pro
c	360	21	0.5	427	ABZ36470	8	Abz36470 Human GEN
c	361	21	0.5	431	ADQ24433	12	Adq24433 Human sof
c	362	21	0.5	437	ACH21497	9	Ach21497 Human adu
c	363	21	0.5	442	ABQ55883	5	Abq55883 Human ova
c	364	21	0.5	442	ABV10111	5	Abv10111 Human pro
c	365	21	0.5	444	ACN61251	13	Acn61251 Cotton gy
c	366	21	0.5	444	ABV49403	5	Abv49403 Human pro
c	367	21	0.5	446	ADL40245	5	Adl40245 Human ova
c	368	21	0.5	455	ADB55311	10	Adb55311 Toxicity-
c	369	21	0.5	457	AAS61528	6	Aas61528 Lung smal
c	370	21	0.5	457	ABA53342	4	Aba53342 Probe #16
c	371	21	0.5	457	AAI32948	4	Aai32948 Probe #15
	372	21	0.5	457	ABA23120	5	Aba23120 Human bon
	373	21	0.5	467	AAK27051	4	Aak27051 Human bon
	374	21	0.5	467	AAK01608	4	Aak01608 Human bra
	375	21	0.5	472	ABV00942	5	Abv00942 Human pro
c	376	21	0.5	472	ADE59577	4	Ade59577 Rat gene
c	377	21	0.5	472	AAK85582	5	Aak85582 Human imm
c	378	21	0.5	472	ADL40241	4	Adl40241 Human ova
c	379	21	0.5	472	ADT96089	11	Adt96089 Colon can
c	380	21	0.5	472	ADX42571	11	Adx42571 Human cDN
c	381	21	0.5	472	AAK32968	4	Aak32968 Human bon
c	382	21	0.5	478	AAK07213	4	Aak07213 Human bra
c	383	21	0.5	478	ABS32697	4	Abs32697 Human liv
c	384	21	0.5	478			

	#				Accession	Description
c	385	21	0.5	478	ABS07776	Abs07776 Human gen
	386	21	0.5	482	ACN79991	Acn79991 Breast ca
c	387	21	0.5	485	ABV99324	Abv99324 Marine sn
c	388	21	0.5	486	ABV40252	Abv40252 Human pro
c	389	21	0.5	486	ABV31283	Abv31283 Human pro
c	390	21	0.5	489	ABA21253	Aba21253 Human ner
	391	21	0.5	493	ABV40823	Abv40823 Human pro
c	392	21	0.5	501	ABV20622	Abv20622 Human pro
c	393	21	0.5	501	ABV26463	Abv26463 Human pro
	394	21	0.5	511	ABV34278	Abv34278 Human pro
c	395	21	0.5	511	ABV43139	Abv43139 Human pro
c	396	21	0.5	524	ADL40167	Adl40167 Human ova
	397	21	0.5	525	ABV55993	Abv55993 Human pro
c	398	21	0.5	525	ACN48293	Acn48293 Cotton pr
c	399	21	0.5	529	ADK82665	Adk82665 Rice endo
c	400	21	0.5	540	AAK63674	Aak63674 Human imm
c	401	21	0.5	559	AAH70901	Aah70901 Human cer
c	402	21	0.5	565	ADQ57734	Adq57734 Novel can
c	403	21	0.5	585	ADI74930	Adi74930 Human ova
c	404	21	0.5	585	ADI68566	Adi68566 Human ova
c	405	21	0.5	587	ABV22867	Abv22867 Human pro
c	406	21	0.5	587	ABV28697	Abv28697 Human pro
c	407	21	0.5	597	AAH87676	Aah87676 Peppermin
c	408	21	0.5	601	ADV15822	Adv15822 Human ost
c	409	21	0.5	601	ADV15365	Adv15365 Human ost
c	410	21	0.5	601	ADV15366	Adv15366 Human ost
c	411	21	0.5	601	ADV15821	Adv15821 Human ost
c	412	21	0.5	601	ADV15367	Adv15367 Human ost
c	413	21	0.5	601	ADV15823	Adv15823 Human ost
c	414	21	0.5	606	AAH09208	Aah09208 Human cDN
c	415	21	0.5	636	ACN86945	Acn86945 Breast ca
c	416	21	0.5	645	AAA75620	Aaa75620 Nucleotid
c	417	21	0.5	645	AAS20735	Aas20735 Human zal
c	418	21	0.5	645	ADH44678	Adh44678 Human zal
c	419	21	0.5	645	ADI01014	Adi01014 Human zal
c	420	21	0.5	645	ADP19837	Adp19837 Human zal
c	421	21	0.5	645	ADV96461	Adv96461 Human zal
c	422	21	0.5	674	AAF17977	Aaf17977 Human bre
c	423	21	0.5	674	AAI67220	Aai67220 B726P spl
c	424	21	0.5	674	AAS47407	Aas47407 Human cDN
c	425	21	0.5	674	ABS64008	Abs64008 Human bre
c	426	21	0.5	674	ABT33220	Abt33220 Human tum
c	427	21	0.5	674	ADL93127	Adl93127 Human bre
c	428	21	0.5	674	ADE44417	Ade44417 Human cDN
c	429	21	0.5	678	ADQ20094	Adq20094 Human sof
c	430	21	0.5	679	AAF14688	Aaf14688 Aspergill
c	431	21	0.5	679	ADU58729	Adu58729 Aspergill
c	432	21	0.5	679	ADZ96732	Adz96732 Aspergill
c	433	21	0.5	699	AAI84827	Aai84827 Human pol
c	434	21	0.5	733	ADP55241	Adp55241 Human PRO
c	435	21	0.5	735	ACF34515	Acf34515 Gene enco
c	436	21	0.5	772	AAF15058	Aaf15058 Trichoder
c	437	21	0.5	772	ADU59099	Adu59099 Trichoder
c	438	21	0.5	772	ADZ97102	Adz97102 Trichoder
c	439	21	0.5	806	AAI97414	Aai97414 Human neu
c	440	21	0.5	806	AAH03234	Aah03234 Human CDN
c	441	21	0.5	807	ABT43046	Abt43046 Human neu
c	442	21	0.5	838	ADX26034	Adx26034 Novel cel
c	443	21	0.5	896	AAH33122	Aah33122 Human col
c	444	21	0.5	908	ABV07580	Abv07580 Human pro
c	445	21	0.5	913	AAS36162	Aas36162 Human car
c	446	21	0.5	913	ABA20711	Aba20711 Human ner
c	447	21	0.5	913	ADE46856	Ade46856 Human car
c	448	21	0.5	913	ADJ08274	Adj08274 Human car
c	449	21	0.5	914	AAS36161	Aas36161 Human car
c	450	21	0.5	914	ABA20710	Aba20710 Human ner
c	451	21	0.5	914	ADE46855	Ade46855 Human car
c	452	21	0.5	914	ADJ08273	Adj08273 Human car
c	453	21	0.5	918	ABL90120	Abl90120 Human pol
c	454	21	0.5	918	ADP07687	Adp07687 Human sec
c	455	21	0.5	923	AAS32682	Aas32682 Human gen
c	456	21	0.5	931	AAS32683	Aas32683 Human gen
c	457	21	0.5	932	AAK84143	Aak84143 Human imm

	#					Accession	Description
c	458	21	0.5	998	13	ADT16529	Adt16529 Plant CDN
c	459	21	0.5	999	10	ADK41704	Adk41704 Maize ami
c	460	21	0.5	1108	4	AAF33113	Aaf33113 Human sec
c	461	21	0.5	1114	10	ADF82206	Adf82206 Leukaemia
c	462	21	0.5	1120	4	AAK65691	Aak65691 Human imm
c	463	21	0.5	1214	4	AAK78749	Aak78749 Human imm
c	464	21	0.5	1214	12	ADQ25563	Adq25563 Human sof
c	465	21	0.5	1239	2	ADM94267	Adm94267 Rice GTP
c	466	21	0.5	1243	8	ABX63096	Abx63096 Human CDN
c	467	21	0.5	1260	4	AAK71520	Aak71520 Human imm
c	468	21	0.5	1260	4	AAK71521	Aak71521 Human imm
c	469	21	0.5	1266	4	AAK71522	Aak71522 Human imm
	470	21	0.5	1266	13	ACN39840	Acn39840 Tumour-as
c	471	21	0.5	1292	6	ABQ93317	Abq93317 Human CDN
c	472	21	0.5	1312	10	ADI02590	Adi02590 Human can
c	473	21	0.5	1318	10	ADB37417	Adb37417 Human can
c	474	21	0.5	1318	13	ADR25077	Adr25077 Breast ca
c	475	21	0.5	1318	13	ADR14390	Adr14390 Human NF-
c	476	21	0.5	1318	13	ACN40099	Acn40099 Tumour-as
c	477	21	0.5	1318	13	ADP24031	Adp24031 PRO polyp
c	478	21	0.5	1318	13	ADY15813	Ady15813 DNA encod
c	479	21	0.5	1318	14	ADY61801	Ady61801 Human gen
c	480	21	0.5	1342	3	AAC98822	Aac98822 Human pan
c	481	21	0.5	1356	13	ABD15290	Abd15290 Pseudomon
c	482	21	0.5	1393	14	ADY18383	Ady18383 DNA encod
c	483	21	0.5	1413	6	ABQ76765	Abq76765 Human L1
c	484	21	0.5	1496	4	AAH15218	Aah15218 Human CDN
c	485	21	0.5	1521	13	AAL55798	Aal55798 cDNA enco
c	486	21	0.5	1521	13	ADR25589	Adr25589 Breast ca
c	487	21	0.5	1521	13	ADP55051	Adp55051 Human PRO
c	488	21	0.5	1559	12	AAA26377	Aaa26377 Human sec
c	489	21	0.5	1559	12	ADL71438	Adl71438 Novel hum
c	490	21	0.5	1569	6	AAS84119	Aas84119 DNA encod
c	491	21	0.5	1580	6	ABQ54264	Abq54264 Human ova
c	492	21	0.5	1583	6	ABS61424	Abs61424 Prostate
c	493	21	0.5	1616	6	ABL61093	Abl61093 Proteosom
c	494	21	0.5	1639	5	AAH64730	Aah64730 Human sec
c	495	21	0.5	1645	13	ADT17160	Adt17160 Plant CDN
c	496	21	0.5	1674	13	ADJ62777	Adj62777 Tumour-as
c	497	21	0.5	1674	13	ACN40026	Acn40026 Tumour-as
c	498	21	0.5	1681	4	AAF75080	Aaf75080 Human col
c	499	21	0.5	1762	8	ABZ18595	Abz18595 Group III
c	500	21	0.5	1778	4	AAS42859	Aas42859 Human G P
c	501	21	0.5	1791	10	ADF81426	Adf81426 Leukaemia
c	502	21	0.5	1803	12	ADQ24149	Adq24149 Human sof
c	503	21	0.5	1826	12	ADQ64818	Adq64818 Novel hum
c	504	21	0.5	1827	3	AAC93322	Aac93322 Human sec
c	505	21	0.5	1827	8	ABZ73648	Abz73648 Secreted
c	506	21	0.5	1827	8	ADA98140	Ada98140 Human sec
c	507	21	0.5	1827	8	ADA43996	Ada43996 Human sec
c	508	21	0.5	1827	10	ADC20292	Adc20292 Human sec
c	509	21	0.5	1827	10	ADF10667	Adf10667 Human sec
c	510	21	0.5	1827	10	ABT16848	Abt16848 Human sec
c	511	21	0.5	1827	10	ABZ67242	Abz67242 Human sec
c	512	21	0.5	1829	4	AAH33888	Aah33888 Human col
c	513	21	0.5	1853	13	ADT18784	Adt18784 Plant CDN
c	514	21	0.5	1861	10	ADL08456	Adl08456 Human can
c	515	21	0.5	1861	10	ADL08458	Adl08458 Human can
c	516	21	0.5	1868	5	ABV22237	Abv22237 Human pro
c	517	21	0.5	1868	5	ABV28075	Abv28075 Human pro
c	518	21	0.5	1918	4	AAF72744	Aaf72744 Human pro
c	519	21	0.5	1927	4	AAF72768	Aaf72768 Human pro
c	520	21	0.5	2000	7	ADZ74577	Adz74577 Arabidops
c	521	21	0.5	2023	5	ABV24752	Abv24752 Human pro
c	522	21	0.5	2056	4	AAS01496	Aas01496 Human sec
c	523	21	0.5	2056	4	AAH34935	Aah34935 Human col
c	524	21	0.5	2100	5	AAF24172	Aaf24172 Human sec
c	525	21	0.5	2166	4	AAD08390	Aad08390 Human sec
c	526	21	0.5	2166	4	ABZ73348	Abz73348 Secreted
c	527	21	0.5	2166	8	ADA97953	Ada97953 Human sec
c	528	21	0.5	2166	8	ADA43859	Ada43859 Human sec
c	529	21	0.5	2166	8	ADC20109	Adc20109 Human sec
c	530	21	0.5	2166	10	ADF10572	Adf10572 Human imm

Left block:

	No						Description
c	531	0.5	21	2177	13	ACN39839	Acn39839 Tumour-as
c	532	0.5	21	2222	5	ADM19255	Adm19255 Novel hum
c	533	0.5	21	2222	5	ADM19519	Adm19519 Novel hum
	534	0.5	21	2233	5	ABV23302	Abv23302 Human pro
	535	0.5	21	2233	5	ABV29149	Abv29149 Human pro
	536	0.5	21	2249	14	AEA61198	Aea61198 Human FLJ
	537	0.5	21	2265	8	ACC00053	Acc00053 Hydroxyme
	538	0.5	21	2265	10	ADD05245	Add05245 Glutaryl
	539	0.5	21	2334	4	AAH72822	Aah72822 Human cer
	540	0.5	21	2334	4	AAH72950	Aah72950 Human cer
	541	0.5	21	2341	10	ADG10448	Adg10448 Human STA
	542	0.5	21	2343	10	ADG10450	Adg10450 Human STA
	543	0.5	21	2350	4	AAH17973	Aah17973 Human cDN
	544	0.5	21	2465	10	ADB63124	Adb63124 Human cDN
	545	0.5	21	2515	10	AAL56514	Aal56514 cDNA sequ
	546	0.5	21	2519	10	ADD22468	Add22468 HLA-B46 T
	547	0.5	21	2519	10	ADI15984	Adi15984 Human PP
	548	0.5	21	2566	5	ABA19833	Aba19833 Human ner
	549	0.5	21	2600	13	ADW67774	Adw67774 Human sec
	550	0.5	21	2657	12	ADQ25396	Adq25396 Human sof
	551	0.5	21	2731	10	ADB62130	Adb62130 Human cDN
	552	0.5	21	2749	11	ACN90411	Acn90411 Breast ca
	553	0.5	21	2765	2	AAZ28810	Aaz28810 Rat membr
	554	0.5	21	2766	2	AAT75488	Aat75488 DNA for B
	555	0.5	21	2766	3	AAA71798	Aaa71798 B. stearo
	556	0.5	21	2771	4	AAK91225	Aak91225 Human dig
	557	0.5	21	2776	4	AAK91226	Aak91226 Human dig
	558	0.5	21	2804	11	ACN92346	Acn92346 Breast ca
	559	0.5	21	2809	13	ADR24479	Adr24479 Breast ca
	560	0.5	21	2846	2	AAV20806	Aav20806 Homo sapi
	561	0.5	21	2846	4	AAA91006	Aaa91006 Human VEG
	562	0.5	21	2937	2	AAC53340	Aac53340 Human sec
	563	0.5	21	2938	10	ADC51454	Adc51454 Human mac
c	564	0.5	21	3227	8	ABK35482	Abk35482 Human end
	565	0.5	21	3227	8	ABZ34754	Abz34754 Coding se
	566	0.5	21	3298	6	ABV76643	Abv76643 Human mic
	567	0.5	21	3352	12	ADQ22709	Adq22709 Human sof
c	568	0.5	21	3473	8	ABX76408	Abx76408 Lung canc
	569	0.5	21	3473	11	ADN39037	Adn39037 Cancer/an
	570	0.5	21	3523	8	ABX76407	Abx76407 Lung canc
	571	0.5	21	3523	9	ACC85484	Acc85484 Human alp
	572	0.5	21	3523	11	ADN39035	Adn39035 Cancer/an
c	573	0.5	21	3705	8	ACA42279	Aca42279 Prokaryot
	574	0.5	21	3705	10	ADI39093	Adi39093 Pseudomon
c	575	0.5	21	3748	4	AAS36163	Aas36163 Human car
	576	0.5	21	3748	5	ABA20712	Aba20712 Human ner
c	577	0.5	21	3748	10	ADE46857	Ade46857 Human car
	578	0.5	21	3748	13	ADJ08275	Adj08275 Human car
c	579	0.5	21	3762	11	ABD14844	Abd14844 Pseudomon
	580	0.5	21	3773	4	AAS36160	Aas36160 Human car
	581	0.5	21	3773	5	ABA20709	Aba20709 Human ner
	582	0.5	21	3773	10	ADE46854	Ade46854 Human car
	583	0.5	21	3773	13	ADJ08272	Adj08272 Human car
	584	0.5	21	3789	12	ADQ23381	Adq23381 Human sof
	585	0.5	21	3795	11	ABD15089	Abd15089 Pseudomon
c	586	0.5	21	3873	5	ABA19128	Aba19128 Human ner
c	587	0.5	21	3892	10	ADC27642	Adc27642 Human col
c	588	0.5	21	3952	12	ADQ22639	Adq22639 Human col
	589	0.5	21	3954	10	ADI39105	Adi39105 Caulobact
	590	0.5	21	3966	4	AAK90316	Aak90316 Human col
	591	0.5	21	3966	4	AAI57690	Aai57690 Human dig
	592	0.5	21	3966	10	ABS99867	Abs99867 Genomic D
c	593	0.5	21	3966	10	ADB93020	Adb93020 Human col
	594	0.5	21	4206	12	ADQ17424	Adq17424 Human sof
	595	0.5	21	4512	4	ABA07296	Aba07296 Human pan
	596	0.5	21	4512	4	AAK89941	Aak89941 Human dig
c.	597	0.5	21	4576	2	AAT96834	Aat96834 Intron 4
	598	0.5	21	4648	13	ADR06982	Adr06982 Full leng
	599	0.5	21	4660	14	ADZ70902	Adz70902 Human mat
	600	0.5	21	5013	4	AAK74879	Aak74879 Human imm
c	601	0.5	21	5317	5	ABL32608	Abl32608 Human imm
c	602	0.5	21	5389	6	AAF98711	Aaf98711 Human lat
c	603	0.5	21	5391	6	ABL32537	Abl32537 Human imm

Right block:

Description	Code					No	
Aas26619 Human gen	AAS26619	4	5470	0.5	21	604	
Abx73968 Human nov	ABX73968	4	5470	0.5	21	605	
Abl33423 Human imm	ABL33423	6	5559	0.5	21	606	c
Ads89678 Oligonucl	ADS89678	13	5605	0.5	21	607	c
Ads89404 Oligonucl	ADS89404	12	5605	0.5	21	608	c
Adq22854 Human sof	ADQ22854	12	5698	0.5	21	609	c
Aak67406 Human imm	AAK67406	4	5734	0.5	21	610	
Abk31191 Signal tr	ABK31191	6	6019	0.5	21	611	c
Abl70160 Chemical1	ABL70160	6	6019	0.5	21	612	c
Aas61104 Human gen	AAS61104	6	6019	0.5	21	613	c
Aak65406 Human imm	AAK65406	6	6065	0.5	21	614	c
Abl33475 Human imm	ABL33475	6	6101	0.5	21	615	c
Abl34449 Human met	ABL34449	6	6127	0.5	21	616	c
Abl70120 Chemical1	ABL70120	6	6127	0.5	21	617	c
Ads99710 Complemen	ADS99710	7	6127	0.5	21	618	c
Abq67140 Human ang	ABQ67140	6	6134	0.5	21	619	c
Aav42348 DNA encod	AAV42348	6	6143	0.5	21	620	c
Abk31407 Signal tr	ABK31407	6	6167	0.5	21	621	c
Abl70368 Chemical1	ABL70368	6	6167	0.5	21	622	c
Aas61330 Human gen	AAS61330	6	6167	0.5	21	623	c
Abl32089 Human imm	ABL32089	6	6283	0.5	21	624	c
Abl33986 Human imm	ABL33986	6	6403	0.5	21	625	c
Abq67120 Human ang	ABQ67120	6	6431	0.5	21	626	c
Aas46558 Tumour su	AAS46558	4	6432	0.5	21	627	c
Adb54290 Pretreate	ADB54290	10	6432	0.5	21	628	c
Adb54162 Pretreate	ADB54162	10	6432	0.5	21	629	c
Ade84124 Human lym	ADE84124	10	6432	0.5	21	630	c
Ade84200 Human lym	ADE84200	10	6432	0.5	21	631	c
Ads89316 Oligonucl	ADS89316	13	6432	0.5	21	632	c
Ads89590 Oligonucl	ADS89590	13	6432	0.5	21	633	c
Aba17328 Human ner	ABA17328	5	6455	0.5	21	634	c
Aas34621 Human DNA	AAS34621	5	6455	0.5	21	635	
Acf34507 Gene enco	ACF34507	8	6480	0.5	21	636	c
Adf76507 Novel hum	ADF76507	10	6480	0.5	21	637	c
Adh17148 Human cyc	ADH17148	12	6480	0.5	21	638	c
Adl82848 Human PRO	ADL82848	12	6480	0.5	21	639	c
Adp07302 Human CCN	ADP07302	12	6480	0.5	21	640	c
Ado20473 Human PRO	ADO20473	12	6480	0.5	21	641	c
Ado19115 Human PRO	ADO19115	12	6480	0.5	21	642	c
Ado19117 Human PRO	ADO19117	12	6480	0.5	21	643	c
Adp54150 Human PRO	ADP54150	13	6480	0.5	21	644	c
Adp23073 PRO polyp	ADP23073	13	6480	0.5	21	645	c
Ady14344 DNA encod	ADY14344	14	6480	0.5	21	646	c
Ady14346 DNA encod	ADY14346	14	6480	0.5	21	647	c
Aat78853 Human lec	AAT78853	2	6901	0.5	21	648	c
Ada26529 Human LCA	ADA26529	8	6901	0.5	21	649	c
Abq93533 Human Dis	ABQ93533	6	6930	0.5	21	650	c
Adr47378 Human DIS	ADR47378	13	6930	0.5	21	651	c
Abl32978 Human imm	ABL32978	6	6963	0.5	21	652	c
Aaa70106 Plasmodiu	AAA70106	3	7458	0.5	21	653	c
Aak72990 Human imm	AAK72990	4	7513	0.5	21	654	
Aal36017 Human mus	AAL36017	4	7513	0.5	21	655	
Abx59005 cDNA enco	ABX59005	8	7513	0.5	21	656	
Adj29755 Human mus	ADJ29755	13	7513	0.5	21	657	
Abk42648 Genomic s	ABK42648	4	7928	0.5	21	658	
Adb60804 Connectiv	ADB60804	9	8149	0.5	21	659	c
Abl33151 Human imm	ABL33151	6	8330	0.5	21	660	c
Adm66512 Human fib	ADM66512	12	8340	0.5	21	661	c
Abl29146 Drosophil	ABL29146	4	8605	0.5	21	662	c
Abl32535 Human imm	ABL32535	6	8648	0.5	21	663	c
Abk31355 Signal tr	ABK31355	6	8648	0.5	21	664	c
Abl70574 Chemical1	ABL70574	6	8648	0.5	21	665	c
Aas61257 Human gen	AAS61257	6	8648	0.5	21	666	c
Aas45504 Chemical1	AAS45504	4	8996	0.5	21	667	c
Abk28436 DNA trans	ABK28436	6	9293	0.5	21	668	c
Aas45320 Chemical1	AAS45320	6	9293	0.5	21	669	c
Abk39973 Human che	ABK39973	6	9293	0.5	21	670	c
Abk28159 DNA trans	ABK28159	6	9293	0.5	21	671	c
Aak80290 Human imm	AAK80290	4	9556	0.5	21	672	c
Adm20197 Alternati	ADM20197	5	9556	0.5	21	673	
Aal04217 Human rep	AAL04217	4	9969	0.5	21	674	c
Aak74868 Human lat	AAK74868	4	10296	0.5	21	675	c
Abl49301 Human pol	ABL49301	6	10467	0.5	21	676	c

	#					Accession	Description
c	677	21	0.5	10825	6	ABN80206	Abn80206 Human che
	678	21	0.5	10953	5	AAS29204	Aas29204 Genomic s
	679	21	0.5	10953	6	ABS68344	Abs68344 Human DNA
	680	21	0.5	10953	10	ADC25466	Adc25466 Human cDN
c	681	21	0.5	10989	8	AAD33870	Aad33870 Human tra
	682	21	0.5	10989	8	ABX95979	Abx95979 Human tra
c	683	21	0.5	13076	13	ADS89377	Ads89377 Oligonucl
c	684	21	0.5	13076	13	ADS89651	Ads89651 Oligonucl
	685	21	0.5	13337	4	ABK42742	Abk42742 Genomic s
	686	21	0.5	13337	5	AAS29203	Aas29203 Genomic s
	687	21	0.5	13337	5	ABA18582	Aba18582 Human ner
	688	21	0.5	13337	7	ABS68343	Abs68343 Human DNA
	689	21	0.5	13337	9	ADB60898	Adb60898 Connectiv
	690	21	0.5	13337	10	ADC25465	Adc25465 Human cDN
c	691	21	0.5	13418	4	AAK86473	Aak86473 Human imm
	692	21	0.5	13574	6	ABL33316	Abl33316 Human imm
	693	21	0.5	14537	4	AAS46356	Aas46356 Tumour su
	694	21	0.5	15122	6	ABL32775	Abl32775 Human imm
	695	21	0.5	15224	6	ABK31358	Abk31358 Signal tr
	696	21	0.5	15224	6	ABL70317	Abl70317 Chemicall
	697	21	0.5	15224	4	AAS61262	Aas61262 Human gen
	698	21	0.5	15914	4	AAK84889	Aak84889 Human imm
	699	21	0.5	15914	8	ABZ73768	Abz73768 Secreted
	700	21	0.5	15914	8	ADA98447	Ada98447 Human sec
	701	21	0.5	15914	8	ADA44234	Ada44234 Human sec
	702	21	0.5	15914	10	ADC20616	Adc20616 Human sec
	703	21	0.5	15914	10	ADF10823	Adf10823 Human sec
	704	21	0.5	15914	10	ABT16886	Abt16886 Human sec
	705	21	0.5	15914	10	ABZ67365	Abz67365 Human sec
	706	21	0.5	16736	4	ABL26478	Abl26478 Drosophil
	707	21	0.5	17717	4	AAK82007	Aak82007 Human imm
	708	21	0.5	17717	4	AAK82008	Aak82008 Human imm
	709	21	0.5	17719	4	AAK82006	Aak82006 Human imm
	710	21	0.5	17874	4	AAK71070	Aak71070 Human imm
	711	21	0.5	18389	4	AAK82632	Aak82632 Human imm
c	712	21	0.5	18389	4	AAK74864	Aak74864 Human imm
	713	21	0.5	19183	4	AAK64938	Aak64938 Human imm
	714	21	0.5	19183	4	AAL36434	Aal36434 Human mus
	715	21	0.5	19183	8	ABX59422	Abx59422 cDNA enco
	716	21	0.5	19183	12	ADJ30172	Adj30172 Human mus
	717	21	0.5	19701	4	AAK91227	Aak91227 Human dig
	718	21	0.5	19814	4	ABL70609	Abl70609 Chemicall
	719	21	0.5	20467	4	AAL36361	Aal36361 Human mus
	720	21	0.5	20467	8	AAL36360	Aal36360 Human mus
	721	21	0.5	20467	8	ABX59348	Abx59348 cDNA enco
	722	21	0.5	20467	8	ABX59349	Abx59349 cDNA enco
c	723	21	0.5	20467	12	ADJ30098	Adj30098 Human mus
	724	21	0.5	20467	12	ADJ30099	Adj30099 Human mus
	725	21	0.5	21000	13	ADT77194	Adt77194 Type II d
	726	21	0.5	21354	6	AAS46815	Aas46815 Tumour su
	727	21	0.5	21537	5	ABL33998	Abl33998 Human imm
	728	21	0.5	21602	13	ABD33092	Abd33092 Human can
	729	21	0.5	21890	4	ABL15986	Abl15986 Drosophil
	730	21	0.5	22313	4	ABL11964	Abl11964 Drosophil
c	731	21	0.5	23241	5	AAF97871	Aaf97871 Human neu
	732	21	0.5	23241	5	AAF97870	Aaf97870 Human neu
	733	21	0.5	23695	5	ABQ66982	Abq66982 Human ang
	734	21	0.5	24292	5	ABA15939	Aba15939 Human ner
	735	21	0.5	25000	6	ABL68348	Abl68348 Kidney ca
	736	21	0.5	26040	4	AAH27887	Aah27887 Nucleotid
	737	21	0.5	26354	12	ADQ97467	Adq97467 Human can
	738	21	0.5	27411	11	ACN44474	Acn44474 Human gen
	739	21	0.5	27411	14	ADZ12987	Adz12987 Human can
c	740	21	0.5	28313	4	AAL36829	Aal36829 Human mus
	741	21	0.5	28313	8	ABX59817	Abx59817 cDNA enco
	742	21	0.5	28313	12	ADJ30567	Adj30567 Human mus
	743	21	0.5	28470	4	AAK71445	Aak71445 Human imm
	744	21	0.5	28854	8	ABX95685	Abx95685 Human gen
	745	21	0.5	31168	5	AAS27804	Aas27804 DNA encod
	746	21	0.5	31168	4	ABA07295	Aba07295 Human pan
	747	21	0.5	31168	4	AAS42115	Aas42115 Genomic s
	748	21	0.5	31168	4	AAK89940	Aak89940 Human dig
c	749	21	0.5	31168	4	AAK64760	Aak64760 Human imm
	750	21	0.5	31168	10	ADB94607	Adb94607 Novel hum
	751	21	0.5	31277	11	ACN44854	Acn44854 Human gen
	752	21	0.5	31405	4	AAK83153	Aak83153 Human imm
	753	21	0.5	31405	4	AAK74865	Aak74865 Human imm
c	754	21	0.5	31405	4	AAK67293	Aak67293 Human imm
	755	21	0.5	31814	9	AAD47150	Aad47150 Human Ras
	756	21	0.5	31842	10	ADA02956	Ada02956 Human LCK
	757	21	0.5	31842	10	ADB72704	Adb72704 Human LCK
	758	21	0.5	31842	12	ADC85446	Adc85446 Human Lck
	759	21	0.5	31842	12	ADM74561	Adm74561 Human car
	760	21	0.5	31934	4	AAK82215	Aak82215 Human imm
c	761	21	0.5	31994	4	AAS30619	Aas30619 DNA encod
c	762	21	0.5	31994	4	AAS28165	Aas28165 Genomic s
c	763	21	0.5	31994	8	ACA03382	Aca03382 DNA encod
c	764	21	0.5	31994	10	ADB96730	Adb96730 Novel lun
c	765	21	0.5	31994	10	ADG41361	Adg41361 Human res
c	766	21	0.5	31994	11	ADI97135	Adi97135 Human res
c	767	21	0.5	32148	4	AAL04218	Aal04218 Human rep
c	768	21	0.5	32189	5	AAS30115	Aas30115 Human lun
c	769	21	0.5	32189	10	ADB33452	Adb33452 Human nov
c	770	21	0.5	32221	5	AAS30113	Aas30113 Human lun
c	771	21	0.5	32221	10	ADB33450	Adb33450 Human nov
c	772	21	0.5	33317	11	ACN44990	Acn44990 Human gen
c	773	21	0.5	34739	11	ACN45078	Acn45078 Human gen
c	774	21	0.5	34766	14	ADZ13291	Adz13291 Human can
c	775	21	0.5	35962	8	ABZ09958	Abz09958 Haematopo
	776	21	0.5	35962	8	ABZ10104	Abz10104 Haematopo
c	777	21	0.5	36785	4	AAK82208	Aak82208 Human imm
c	778	21	0.5	37590	4	AAS12439	Aas12439 DNA encod
c	779	21	0.5	37790	4	ADK41243	Adk41243 DNA regio
c	780	21	0.5	38166	12	ADK41244	Adk41244 DNA regio
c	781	21	0.5	43058	6	ABL64982	Abl64982 Lung canc
c	782	21	0.5	43058	6	ABL65219	Abl65219 Lung canc
c	783	21	0.5	43058	6	ABN97455	Abn97455 Gene #395
c	784	21	0.5	49561	4	AAK82012	Aak82012 Human imm
	785	21	0.5	49806	11	ACN44528	Acn44528 Mouse gen
	786	21	0.5	50849	6	ABN87883	Abn87883 Human glu
c	787	21	0.5	51001	12	ADJ10262	Adj10262 Human ger
	788	21	0.5	52302	10	ADA02738	Ada02738 Human CCN
	789	21	0.5	52302	10	ADB72476	Adb72476 Human CCN
	790	21	0.5	52302	10	ADC85218	Adc85218 Human Ccn
	791	21	0.5	52302	11	ADM74333	Adm74333 Human car
c	792	21	0.5	53122	11	ACN43998_6	Continuation (7 of
	793	21	0.5	55404	11	ACN44288	Acn44288 Mouse gen
	794	21	0.5	58366	10	ADC87618	Adc87618 Human GPC
	795	21	0.5	59446	10	AAD47904	Aad47904 Human tra
	796	21	0.5	62944	6	ABL68262	Abl68262 Kidney ca
	797	21	0.5	62944	6	ABL66947	Abl66947 Lung canc
	798	21	0.5	69648	12	ADQ97934	Adq97934 Human can
c	799	21	0.5	77777	12	ADQ94674	Adq94674 Human chr
	800	21	0.5	85920	14	ADZ13418	Adz13418 Human can
	801	21	0.5	93538	13	ABD33442	Abd33442 Murine ca
c	802	21	0.5	93538	13	ABD33444	Abd33444 Human can
	803	21	0.5	95514	9	ADA02564	Ada02564 Human RAS
	804	21	0.5	96596	10	ADB72302	Adb72302 Human RAS
	805	21	0.5	96596	10	ADE95812	Ade95812 Human RAS
	806	21	0.5	98638	12	ADQ97919	Adq97919 Human RAS
	807	21	0.5	98844	12	ADJ84099	Adj84099 Human WRN
	808	21	0.5	99960	3	AAZ50905	Aaz50905 Human TBC
c	809	21	0.5	101169	12	ADQ97584	Adq97584 Mouse can
c	810	21	0.5	110000	5	AAI61373_3	Continuation (4 of
c	811	21	0.5	110000	5	ADA13411_2	Continuation (3 of
	812	21	0.5	110000	10	ADG70447_2	Continuation (3 of
	813	21	0.5	110000	10	ADH10017_2	Continuation (3 of
	814	21	0.5	110000	10	ABZ77565_2	Continuation (3 of
	815	21	0.5	110000	10	ABQ84281_2	Continuation (3 of
	816	21	0.5	110000	11	ACN44150_3	Continuation (4 of
	817	21	0.5	110000	11	ACN43998_5	Continuation (6 of
	818	21	0.5	110000	11	ACN44934_0	Continuation
	819	21	0.5	110000	12	ADQ59446_2	Continuation (3 of
	820	21	0.5	110000	12	ADQ97266_2	Continuation (3 of
c	822	21	0.5	110000	12	ADQ97138_1	Continuation (2 of

Left block:

Flag	#	Len	Conc	Pos	GC	ID	Description
c	823	21	0.5	110000	12	ADQ97138_2	Continuation (3 of
	824	21	0.5	110000	14	ADZ13757_2	Continuation (3 of
	825	21	0.5	110000	14	ADZ12821_2	Continuation (3 of
c	826	21	0.5	110000	14	ADZ12617_0	Adz12617 Human can
	827	21	0.5	110000	14	ADZ46976_2	Continuation (3 of
	828	21	0.5	110000	12	ADQ18153	Adz42274 Human min
	829	21	0.5	112604	2	AAV52850	Adq18153 Human sof
	830	21	0.5	116624	13	ABD32886	Aav52850 Human eya
	831	21	0.5	117328	13	ABD33460	Abd32886 Mouse can
	832	21	0.5	119057	2	AAX90201	Abd33460 Murine ca
	833	21	0.5	119950	4	AAC89560	Aax90201 Human yes
	834	21	0.5	122108	12	ADP03055	Aac89560 Human his
	835	21	0.5	124987	13	ADS88553	Adp03055 Human hou
	836	21	0.5	124990	13	ADU60195	Ads88553 Human hou
	837	21	0.5	124990	12	ADH77123	Adu60195 Housekeep
c	838	21	0.5	126001	11	ACN44372	Adh77123 Human PAZ
	839	21	0.5	127238	12	ADQ97301	Acn44372 Mouse gen
	840	21	0.5	127722	13	ABD33584	Adq97301 Human ca
	841	21	0.5	127767	13	ADR67023	Abd33584 Murine ca
	842	21	0.5	127767	13	ADZ13356	Adr67023 Mouse can
	843	21	0.5	127767	14	ACN44674	Adz13356 Murine ca
	844	21	0.5	129042	11	ACN45054	Acn44674 Human gen
	845	21	0.5	133632	11	ADZ13285	Acn45054 Human gen
	846	21	0.5	133642	14	ACN44182	Adz13285 Human can
	847	21	0.5	134738	11	ADD50651	Acn44182 Human gen
	848	21	0.5	142299	10	ADV77909	Add50651 BAC seque
	849	21	0.5	142299	14	ADV15288	Adv77909 Human BAC
c	850	21	0.5	143776	13	AAL38336	Adv15288 Human ost
	851	21	0.5	143899	6	ADV15294	Aal38336 Genomic s
	852	21	0.5	144034	13	ADQ97526	Adv15294 Human ost
	853	21	0.5	151052	12	ADQ97965	Adq97526 Mouse can
	854	21	0.5	152096	12	ACA64961	Adq97965 Mouse can
	855	21	0.5	152151	8	ADP67269	Aca64961 Human BCR
c	856	21	0.5	152501	12	AEA61197	Adp67269 Human chr
	857	21	0.5	154875	14	AAD02697	Aea61197 Human MYH
c	858	21	0.5	160552	4	ACN44962	Aad02697 Human gly
	859	21	0.5	160921	11	ADJ19665	Acn44962 Human gen
	860	21	0.5	161484	13	ABD33232	Adj19665 Human PTP
	861	21	0.5	161531	13	ABT11173	Abd33232 Human can
c	862	21	0.5	168174	6	ABT11114	Abt11173 Human 5-1
	863	21	0.5	168273	11	ACN45088	Abt11114 Human 5-1
	864	21	0.5	175338	11	ADD50650	Acn45088 Mouse gen
	865	21	0.5	175590	10	ADD50650	Add50650 BAC seque
	866	21	0.5	175590	14	ADV77908	Add50650 BAC seque
	867	21	0.5	175590	14	ADV77908	Adv77908 Human BAC
	868	21	0.5	176001	12	ADK43203	Adv77908 Human BAC
	869	21	0.5	177866	10	ADQ97721	Adk43203 Human pro
	870	21	0.5	178024	10	ADL13931	Adq97721 Human can
c	871	21	0.5	180385	10	ADL13850	Adl13931 Osteoarth
c	872	21	0.5	180550	4	AAF92831	Adl13850 Osteoarth
c	873	21	0.5	183999	13	ADU76470	Aaf92831 Human ABC
	874	21	0.5	183999	12	ADK43195	Adu76470 Human ABC
	875	21	0.5	186739	10	ADL13825	Adk43195 Human pro
	876	21	0.5	192427	12	ADS56277	Adl13825 Osteoarth
	877	21	0.5	200620	11	ACN44598	Ads56277 Human pre
	878	21	0.5	212231	14	ADX80726	Acn44598 Human gen
	879	21	0.5	213300	11	ACN44754	Adx80726 Human RAL
	880	21	0.5	215221	11	ACN45150	Acn44754 Human gen
	881	21	0.5	217409	11	ACN44702	Acn45150 Human gen
	882	21	0.5	220224	6	ABK83497	Acn44702 Human gen
	883	21	0.5	227968	12	ADQ18538	Abk83497 Human cDN
c	884	21	0.5	227968	10	ADL13693	Adq18538 Human sof
c	885	21	0.5	231222	2	AAV57926	Adl13693 Osteoarth
	886	21	0.5	235033	2	AAV57903	Aav57926 Hereditar
	887	21	0.5	237326	12	ADL08109	Aav57903 Hereditar
	888	21	0.5	247682	11	ACN44650	Adl08109 Human gen
c	889	21	0.5	256157	13	ABD33570	Acn44650 Human gen
	890	21	0.5	256157	13	ABD33276	Abd33570 Human gen
	891	21	0.5	256190	12	ADQ97289	Abd33276 Human can
	892	21	0.5	257645	11	ACN44046	Adq97289 Human gen
c	893	21	0.5	260027	11	ACN44194	Acn44046 Human can
	894	21	0.5	275449	11	ACN44194	Acn44194 Human gen
	895	21	0.5				

Right block:

Flag	#	Len	Conc	Pos	GC	ID	Description
	896	20	0.5	294575	14	AEA61217	Aea61217 Human STK
c	897	20	0.5	294575	14	AEA61217	Aea61217 Human STK
	898	20	0.5	301477	13	ABD33362	Abd33362 Human can
c	899	20	0.5	301477	13	ABD33362	Abd33362 Human can
c	900	20	0.5	313287	13	ABD33100	Abd33100 Human can
c	901	20	0.5	313287	13	ABD33100	Abd33100 Human can
	902	20	0.5	321491	11	ACN44202	Acn44202 Human gen
	903	20	0.5	325791	4	AAS43104	Aas43104 Human Oes
c	904	20	0.5	334462	10	ADC24763	Adc24763 Human wil
c	905	20	0.5	335199	10	ADC24703	Adc24703 Human wil
c	906	20	0.5	349881	10	ADC86642	Adc86642 Human GPC
	907	20	0.5	28	2	AAQ75669	Aaq75669 Reverse t
c	908	20	0.5	28	2	AAT70114	Aat70114 PolyAB pr
c	909	20	0.5	28	2	AAT70112	Aat70112 PolyAB pr
c	910	20	0.5	30	2	AAT70113	Aat70113 PolyAB pr
c	911	20	0.5	30	13	ADR27781	Adr27781 MTR gene
	912	20	0.5	30	13	ADR27782	Adr27782 MTR gene
	913	20	0.5	31	13	ADV95692	Adv95692 Hepatitis
	914	20	0.5	31	13	ADV95694	Adv95694 Hepatitis
	915	20	0.5	51	13	ADV95693	Adv95693 Hepatitis
	916	20	0.5	51	4	AAL30069	Aal30069 Human SNP
	917	20	0.5	85	4	AAL32453	Aal32453 Human SNP
	918	20	0.5	132	12	ADG65306	Adg65306 Template
	919	20	0.5	133	6	ABL85667	Abl85667 Human ova
	920	20	0.5	133	5	ADI72651	Adi72651 Human ova
c	921	20	0.5	155	5	ADL37790	Adl37790 Human ova
c	922	20	0.5	168	13	ACF91490	Acf91490 Human SIR
	923	20	0.5	170	13	ADV40136	Adv40136 Rat cardi
c	924	20	0.5	171	6	ABL86116	Abl86116 Human ova
c	925	20	0.5	175	6	ABL86152	Abl86152 Human ova
c	926	20	0.5	180	6	ABL86075	Abl86075 Human ova
	927	20	0.5	190	6	ABL86303	Abl86303 Human ova
c	928	20	0.5	191	13	ACF90292	Acf90292 Human SIR
c	929	20	0.5	193	12	ADJ12811	Adj12811 DNA fragm
c	930	20	0.5	194	6	ABL86374	Abl86374 Human ova
	931	20	0.5	200	6	ABS72853	Abs72853 Human gen
c	932	20	0.5	201	6	ABL86155	Abl86155 Human ova
	933	20	0.5	201	8	ADA84000	Ada84000 Human POM
	934	20	0.5	201	13	ADS38091	Ads38091 Human aut
c	935	20	0.5	201	13	ADS38093	Ads38093 Human aut
	936	20	0.5	201	13	ADS39439	Ads39439 Human aut
c	937	20	0.5	208	13	ADS39438	Ads39438 Human aut
c	938	20	0.5	218	13	ADS39089	Ads39089 Human aut
c	939	20	0.5	224	6	ABL87778	Abl87778 Human ova
	940	20	0.5	228	6	AAC74365	Aac74365 Human sec
c	941	20	0.5	242	6	ABL86279	Abl86279 Human ova
	942	20	0.5	245	5	ADL43637	Adl43637 Human ova
	943	20	0.5	245	3	ADH69117	Adh69117 Human tum
	944	20	0.5	245	6	AAA57025	Aaa57025 Human col
	945	20	0.5	255	6	ABT12447	Abt12447 Orestes s
	946	20	0.5	260	6	ACD91741	Acd91741 Human col
	947	20	0.5	260	5	AAH81922	Aah81922 Rat diffe
	948	20	0.5	260	4	AAI22901	Aai22901 Probe #12
	949	20	0.5	260	4	ABA67993	Aba67993 Human foe
	950	20	0.5	260	5	ABV17990	Abv17990 Human pro
	951	20	0.5	260	4	AAI48200	Aai48200 Probe #16
	952	20	0.5	260	4	ABA35031	Aba35031 Probe #13
	953	20	0.5	261	4	AAK16387	Aak16387 Human bra
	954	20	0.5	262	6	ABS41744	Abs41744 Human liv
	955	20	0.5	266	6	AAI08565	Aai08565 Probe #85
	956	20	0.5	268	13	ABL83418	Abl83418 Human ova
c	957	20	0.5	269	4	ACF89627	Acf89627 Human SIR
c	958	20	0.5	277	5	ABX45802	Abx45802 Bovine ES
c	959	20	0.5	278	4	ABV17990	Abv17990 Human pro
c	960	20	0.5	279	12	AAL24094	Aal24094 Human bre
	961	20	0.5	291	5	ADQ21639	Adq21639 Human sof
	962	20	0.5	295	13	ABV61819	Abv61819 Human pro
	963	20	0.5	295	5	AAL15544	Aal15544 Human bre
	964	20	0.5	297	5	ADV39624	Adv39624 Rat cardi
	965	20	0.5	299	5	ABV61066	Abv61066 Human pro
c	966	20	0.5		5	ABV55175	Abv55175 Human pro
c	967	20	0.5		6	ABL86670	Abl86670 Human ova
c	968	20	0.5		4	AAK80628	Aak80628 Human imm

c	969	20	0.5	AAK67724	Aak67724 Human imm
c	970	20	0.5	AAK84088	Aak84088 Human imm
c	971	20	0.5	ADJ12789	Adj12789 DNA fragm
c	972	20	0.5	AAK85349	Aak85349 Human imm
c	973	20	0.5	AAS38991	Aas38991 Novel hum
c	974	20	0.5	ABL85650	Abl85650 Human ova
c	975	20	0.5	ADF90608	Adf90608 Human hep
c	976	20	0.5	ABV58014	Abv58014 Human pro
	977	20	0.5	AAL11061	Aal11061 Human bre
	978	20	0.5	AAK89039	Aak89039 Human dig
	979	20	0.5	AAS39638	Aas39638 Genomic s
	980	20	0.5	ADB32598	Adb32598 Human nov
c	981	20	0.5	ADD33011	Add33011 Human mit
c	982	20	0.5	ADP66311	Adp66311 Human cDN
	983	20	0.5	ABV54228	Abv54228 Human pro
	984	20	0.5	AAH69569	Aah69569 Human cer
	985	20	0.5	AAH73022	Aah73022 Human cer
	986	20	0.5	ABL85185	Abl85185 Human ova
c	987	20	0.5	ADD89921	Add89921 Murine DN
	988	20	0.5	ADS72585	Ads72585 Human kid
	989	20	0.5	ADW41439	Adw41439 cDNA elev
	990	20	0.5	AAS69983	Aas69983 DNA encod
	991	20	0.5	AAS80266	Aas80266 DNA encod
	992	20	0.5	AAL10919	Aal10919 Human bre
	993	20	0.5	ABV07938	Abv07938 Human pro
	994	20	0.5	ADE60435	Ade60435 Rat gene
	995	20	0.5	AAL24388	Aal24388 Human bre
c	996	20	0.5	AAK63668	Aak63668 Human imm
c	997	20	0.5	ABK53893	Abk53893 Human hea
	998	20	0.5	AAI84933	Aai84933 Human pol
c	999	20	0.5	ABV47779	Abv47779 Human pro
	1000	20	0.5	AAF65945	Aaf65945 Novel hum

ALIGNMENTS

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RESULT 1
AAF31100
ID   AAF31100 standard; cDNA; 7122 BP.
XX
AC   AAF31100;
XX
DT   27-APR-2001 (first entry)
XX
DE   Methionine synthase coding sequence #1.
XX
KW   Analyte-binding enzyme; analyte analysis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200102600-A2.
XX
PD   11-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018057.
XX
PR   06-JUL-1999;  99US-00347878.
PR   06-DEC-1999;  99US-00457205.
XX
PA   (GEAT ) GEN ATOMICS.
XX
PI   Yuan C;
XX
DR   WPI; 2001-071583/08.
XX
PT   Assaying method, useful for prognosis and diagnosis of disease, comprises
PT   contacting sample with a mutant analyte-binding enzyme and detecting
PT   binding.
XX
PS   Disclosure; Page; 187pp; English.
XX
CC   The present invention relates to a method for assaying an analyte in a
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CC   sample comprising: contacting the sample with a mutant analyte-binding
CC   enzyme which has binding affinity for the analyte or an immediate analyte
CC   enzymatic conversion product but has attenuated catalytic activity; and
CC   detecting resulting binding. The method is useful in monitoring
CC   biological systems/processes, or prognosis/diagnosis of disease caused by
CC   imbalances of the analytes. The present sequence is a coding sequence
CC   used in the present invention. Note: the present sequence is not shown in
CC   the specification, but was from Genbank, using information given in the
CC   specification
XX
SQ   Sequence 7122 BP; 2112 A; 1450 C; 1728 G; 1832 T; 0 U; 0 Other;
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Query Match             89.7%;  Score 3517;  DB 4;  Length 7122;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 3867;  Conservative    0;  Mismatches    0;  Indels    7;  Gaps    0;
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Qy           2 GTCACCTGTGGAGAGCACGTCTTCTGCGCGCCCTCGGCAAGGAGGAGACTCGACA 61
               ||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db         225 GTCACCTGTGGAGAGCACGTCTTCTGCGCCCGCCCTCGGCAAGGAGGAGACTCGACA 284

Qy          62 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAGAAAAACCCTCGGGG 121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         285 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAGAAAAACCCTCGGGG 344

Qy         122 ATGAGATCAATGCCATTCTGCAGAGAGGATTATGGTGCTGGATGGGGGATGGGGACCA 181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         345 ATGAGATCAATGCCATTCTGCAGAGAGGATTATGGTGCTGGATGGGGGATGGGGACCA 404

Qy         182 TGATCCAGCGGGAGAAGCTAAACGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         405 TGATCCAGCGGGAGAAGCTAAACGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 464

Qy         242 CCAGGCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTCATTACC 301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         465 CCAGGCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTCATTACC 524

Qy         302 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA 361
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         525 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA 584

Qy         362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 421
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Db         585 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 644

Qy         422 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGGAGGAGGTAACTCTCCAGACACAGAATTAAGA 481
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         645 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGGAGGAGGTAACTCTCCAGACACAGAATTAAGA 704

Qy         482 GGTTTGTGGCAGGGGCTTCGGGGTCCGGACTAATAAGACACTCTCTGTGTCCCATCTGTGG 541
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         705 GGTTTGTGGCAGGGGCTTCGGGGTCCGGACTAATAAGACACTCTCTGTGTCCCATCTGTGG 764

Qy         542 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGACAGG 601
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         765 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGACAGG 824

Qy         602 CCAAAGGACTTCGGATGGCGGGGTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC 661
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         885 CCAATGCCAAGGACCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC 944

Qy         662 CCAATGCCAAGGACCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC 721
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         705 GGCCTATCTTATTTCAGGGACGATCGTTGATAAAGTGGGCCGGACTCTTTCCGACAGA 781

Qy         722 GGCCTATCTTATTTCAGGGACGATCGTTGATAAAGTGGGCCGGACTCTTTCCGACAGA 781
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         945 GGCCTATCTTATTTCAGGGACGATCGTTGATAAAGTGGGCCGGACTCTTTCCGACAGA 1004

Qy         782 CAGGAGAGGGGATTTGTCATCAGCGTGTCTCATCGAGACCACTCTGCATTGGATTAAATT 841
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1005 CAGGAGAGGGGATTTGTCATCAGCGTGTCTCATCGAGACCACTCTGCATTGGATTAAATT 1054

Qy         842 GTGCTTTGGGTGCAGCTGAGATGAGACCCTTTATTGAAAAATGTACACAG 901
```

Db 2145 ATGATGATATCCATAAGGAGACTTCTGCGAGTCTCGTCGTGAAGATCTCATCTGAAATAAGACC 2204
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Qy 1982 CTGAGGCCACTGACTGAGAAGCTCTTACGTTACGTTACGTTACGTTACGTGGACTATGGACGAAAAG 2041

Db 2205 CTGAGGCCACTGACTGAGAAGCTCTTACGTTACGTTATGCCAGACTCAAGGCACAGAGGCAGGAGAAAG 2264
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Qy 2042 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGACGCCTTGAGTATGCCCTTG 2101

Db 2265 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTTG 2324
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Qy 2102 TGAACGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTAAACCAAAAA 2161

Db 2325 TGAACGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTAAACCAAAAAAA 2384
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Qy 2162 AATATCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAAATTGTTG 2221

Db 2385 AATATCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAAATTGTTG 2444
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Qy 2222 GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGTTA 2281

Db 2445 GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2504
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Qy 2282 TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAAGAGAAACCAGAG 2341

Db 2505 TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAAGAGAAACCAGAG 2564
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Qy 2342 TGCTTAACGGACAGTGAGAAGAGGACCCTTACCAGGGCACCATCGTGCTGGCCACTG 2401

Db 2565 TGCTTAACGGACAGTGAGAAGAGGACCCTTACCAGGGCACCATCGTGCTGGCCACTG 2624
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2402 TTAAAGGGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA 2461

Db 2625 TTAAAGGGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA 2684
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Qy 2462 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCATGTGATGGCTGTCAGGACTCATCACTCCCTCCCTGAGATGAAA 2521

Db 2685 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCATGTGATGGCTGTCAGGACTCATCACTCCCTCCCTGAGATGAAA 2744
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Qy 2522 TTGACCACAAAGCAGATATAATTGGCCGTGTCAGGACGTCAGGACTAGTTGGATGGAG 2581

Db 2745 TTGACCACAAAGCAGATATAATTGGCCGTGTCAGGACGTCAGGACTAGTTGGATGGAG 2804
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Qy 2582 TGATTTTTGTTGTGCCAAGGAAATGAGAGATTAGCTATAAGATTCCATTGTTGATTGGAG 2641

Db 2805 TGATTTTTGTTGTGCCAAGGAAATGAGAGATTAGCTATAAGATTCCATTGTTGATTGGAG 2864
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Qy 2642 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATAATAGTCCGAGATACAGTGCACCTG 2701

Db 2865 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGTCCGAGATAATAGTCCGAGATACAGTGCACCTG 2924
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Qy 2702 TAATCCATGTCCTGACGCGTCCAAGAGTGGTGTTCCCAGTCGTGTTGTAGATGAAA 2761

Db 2925 TAATCCATGTCCTGACGCGTCCAAGAGTGGTGTTCCCAGTCGTGTTGTAGATGAAA 2984
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Qy 2762 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAGAAATATTAGACAGGACC 2821

Db 2985 ATCTAAAGGATGAATACTTTGAGGAAATCATGGAGAATATTAGACAGGACC 3044
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Qy 2822 ATTATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT 2881

Db 3045 ATTATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT 3104
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Qy 2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGACCCAGG 2941

Db 3105 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG 3164
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Qy 2942 TCTTTGAAGACTATGACCTGCGAGATAGTGAATGCTGGAAGCTTTCTTTG 3001

Db 3165 TCTTTGAAGACTATGACCTGCGAGATAGTGAATGCTGGAAGCCTTTCTTTG 3224
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Qy 3002 ATGTCTGGCAGCTCCGGGGCAAGTACCCGGGGCAATGCAGAATCGGAATCTGAATCTGAAATAAAGACA 3061

Db 3225 ATGTCTGGCAGCTCCGGGGCAAGTACCCGGGGCAATGCAGAATCGGAATCTGAATCTGAAATAAAGACA 3284

Db 1065 GTGCTTGGGTGGCAGCTGAAATGAGACCTTTATTGAAAATGTACAACAG 1124
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Qy   902 CCTATGTCCTCGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA 961

Db 1125 CCTATGTCCTCGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA 1184
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Qy   962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGCTTGGTGCTCAATATAG 1021

Db 1185 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGCTTGGTGCTCAATATAG 1244
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Qy 1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1081

Db 1245 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1304
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Qy 1082 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTC 1141

Db 1305 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTC 1364
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1142 TAGAGCCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCGTGTAATG 1201

Db 1365 TAGAGCCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCGTGTAATG 1424
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Qy 1202 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACATATGAGAAGCCTTGT 1261

Db 1425 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACATATGAGAAGCCTTGT 1484
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Qy 1262 GTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATG 1321

Db 1485 GTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATG 1544
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Qy 1322 GCAATGCTAGATGTGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAG 1381

Db 1545 GCAATGCTAGATGTGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAG 1604
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Qy 1382 ACATCGCAAAGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGGT 1441

Db 1605 ACATCGCAAAGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGGT 1664
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Qy 1442 TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACG 1501

Db 1665 TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACG 1724
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Qy 1502 ACTTCTTCTTGGAGAAGATTAAAAGATGGAGCTGTCATGGTTCATGGCTT 1561

Db 1725 ACTTCTTCTTGGAGAAGATTAAAAGATGGAGCTGTCATGGTTCATGGGCTT 1784
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Qy 1562 TTGATGAAGAGGACAGGCAACAGCAATCAGAGTGTCGCACCCGGGCCT 1621

Db 1785 TTGATGAAGAGGACAGGCAACAGCAATCAGAGTGTCGCACCCGGGGCCT 1844
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1622 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCAAATGACATTATTTTGACCCTAATA 1681

Db 1845 ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA 1904
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Qy 1682 TCCTAACCATTGGAATGGAATGGAACAACTTGTATGCCATTAATTTATCCATG 1741

Db 1905 TCCTAACCATTGGGAATGGAATGGAACAACTTGTATGCCATTAATTTATCCATG 1964
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1742 CAACAAAGTCATTAAAGAACAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 1801

Db 1965 CAACAAAGTCATTAAAGAACAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 2024
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1802 TGTCCTTCTTCCTTCCTCCGAGGAATGCAATGCAAGCAATGCATGGGGTTTTCCTTT 1861

Db 2025 TGTCCTTCTTCCTTCCTCCGAGGAATGCAATGCAAGCAATGCATGGGGTTTTCCTTT 2084
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Qy 1862 ACCATGCAATCAAGTCTGGGCATGGACATGGAGATAGTGAATGCTGGAAACCTCCCTGTGT 1921

Db 2085 ACCATGCAATCAAGTCTGGGCATGGACATGGAGATAGTGAATGCTGGAAACCTCCCTGTGT 2144
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1922 ATGATGATATCCATAAGGAGACTTCTGCGAGTCTCGTCGTGAAGATCTCATCTGAAATAAAGACC 1981

OS   Homo sapiens.
XX
PN   WO200071754-A1.
XX
PD   30-NOV-2000.
XX
PF   24-MAY-2000; 2000WO-US014354.
PR   25-MAY-1999; 99US-00318448.
XX
PA   (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI   Johnson WG, Stenroos ES;
XX
DR   WPI; 2001-025174/03.
XX
PT   Diagnosing a developmental disorder, e.g. schizophrenia, by forming
PT   datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
PT   and environmental variables affecting an individual and then comparing
PT   these DS with reference DS.
XX
PS   Disclosure; Page 115-117; 156pp; English.
XX
CC   The present invention provides a novel method of estimating the
CC   susceptibility of an individual to a developmental disorder using genetic
CC   and environmental variables. The method can be used in the diagnosis,
CC   prevention and treatment of disorders such as schizophrenia, spina bifida
CC   cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
CC   attention deficit disorder, obsessive compulsive disorder, chronic
CC   multiple tic syndrome and learning disorders such as dyslexia
XX
SQ   Sequence 7122 BP; 2112 A; 1450 C; 1728 G; 1832 T; 0 U; 0 Other;

Query Match   89.7%;   Score 3517;   DB 5;   Length 7122;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 3867;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy   2 GTCACCTGTGGAGAGCAGCGTCTTCTCCTGCGCGCCCTCTGCGGCAAGGAGGAGACTCGACA   61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 GTCACCTGTGGAGAGCAGCGTCTTCTCCTGCGCGCCCTCTGCGGCAAGGAGGAGACTCGACA   284

Qy   62 ACATGTCACCCGCGCTCCAAGACACCTGTCGCAACCCGAAGGTCTGAAGAAACCCTGCGGG   121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 ACATGTCACCCGCGCTCCAAGACACCTGTCGCAACCCGAAGGTCTGAAGAAACCCTGCGGG   344

Qy   122 ATGAAGATCAATGCCATTCTGCGAGAAGAGGATTATGGTGCTCGATGGGGGATGGGGACCA   181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 ATGAAGATCAATGCCATTCTGCGAGAAGAGGATTATGGTGCTCGATGGGGGATGGGGACCA   404

Qy   182 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG   241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG   464

Qy   242 CCAGGCCGCTGAAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTATTACC   301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 CCAGGCCGCTGAAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC   524

Qy   302 AAATCCATAAGGAATACTTGCTGGCTGGCTGGCTGGCTCAGATATCATTGAAACAAATACTTTTAGCA   361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 AAATCCATAAGGAATACTTGCTGGCTGGCTGGCTGGCTCAGATATCATTGAAACAAATACTTTTAGCA   584

Qy   362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT   421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT   644

Qy   422 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGAAAAGCTGCCGACTAATAAGACTCTCGTGTCCCATCTGTGG   481
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Db   645 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGAAAAGCTGCCGACTAATAAGACTCTCGTGTCCCATCTGTGG   704

Qy   482 GGTTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG   541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 GGTTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG   764

Qy   3062 AAACAGTAGGTGGAGAGGCCAGGAAGGTTCACGATGATGCCCACAATATGCTGAACACAC   3121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3285 AAACAGTAGGTGGAGAGGCCAGGAAGGTTCACGATGATGCCCACAATATGCTGAACACAC   3344

Qy   3122 TGATTAGTCAAAGAAACTCCGGGCCCGGGGTGTGGTTGGGTTCGGCCAGCACACAGAGTA   3181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3345 TGATTAGTCAAAGAAACTCCGGGCCCGGGGTGTGGTTGGGTTCGGCCAGCACACAGAGTA   3404

Qy   3182 TCCAAGACGACATTCACCTGTACGCAGAGAGCTGCTGTGCCCCAGGCTGCGAGAGCCCATAG   3241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3405 TCCAAGACGACATTCACCTGTACGCAGAGAGCTGCTGTGCCCCAGGCTGCGAGAGCCCATAG   3464

Qy   3242 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACT   3301
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Db   3465 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACT   3524

Qy   3302 ACTGGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT   3361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3525 ACTGGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT   3584

Qy   3362 TTGCGTTGCCTGCTTGGGTAGAGAGCTGAGCAAGGCCTATGAGGATGATGTGACG   3421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3585 TTGCCGTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGATGTGACG   3644

Qy   3422 ACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCACCGGCCTGGCGAGAGCCTTTGCAGAAG   3481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3645 ACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCCTGGCGAGAGCCTTTGCAGAAG   3704

Qy   3482 AGCTCCATGAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGTGAGCAGCTGGACG   3541
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Db   3705 AGCTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGACG   3764

Qy   3542 TCGCAGACCTGCGAAGGTTGGCGAAGGTTGGGGTACAAGGGCATCGCCCCGGCTCCTGGGCTACCCCAGCC   3601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3765 TCGCAGACCTGCGCGCAGGCTGCGGGTACAAGGGCATCGCCCCGGCTCCTGGGCTACCCCAGCC   3824

Qy   3602 AGCCCGACCACCACCGAGAAGCTCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACAG   3661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3825 AGCCCGACCACCACCGAGAAGCTCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCAGTCTACAG   3884

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACT   3721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3885 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACT   3944

Qy   3722 TCTCCAATTTGAAGTCGTGTGGGGAAGATTTTCCAAGGATCCAGGTTGAGG   3781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3945 TCTCCAATTTGAAGTCGTGTGGGGAAGATTTTCCAAGGATCCAGGTTGAGG   4004

Qy   3782 ATTATGCATTGAGGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGCTTGGACCCCATTT   3841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4005 ATTATGCATTGAGGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGCTTGGACCCCATTT   4064

Qy   3842 TGGGATATGATACAGACTAACTTTTTTTTTTTTT   3875
           ||||||||||||||||||||||||||||||||||||
Db   4065 TGGGATATGATACAGACTAACTTTTTTTTTTTTTT   4098

RESULT 2
AAC91207
ID   AAC91207 standard; DNA; 7122 BP.
XX
AC   AAC91207;
XX
DT   20-MAR-2001 (first entry)
XX
DE   Human methionine synthase gene SEQ ID NO: 2.
XX
KW   Human; schizophrenia; developmental disorder; spina bifida cystica;
KW   Tourette's syndrome; bipolar illness; autism; conduct disorder;
KW   attention deficit disorder; obsessive compulsive disorder;
KW   chronic multiple tic syndrome; learning disorder; polymorphism; ds.
XX

```
Qy  542  AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG  601
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  765  AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG  824

Qy  602  CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG  661
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  825  CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG  884

Qy  662  CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC  721
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  885  CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC  944

Qy  722  GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCCGACAGA  781
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  945  GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCCGACAGA  1004

Qy  782  CAGGAGGAGGGATTTGTCATCGACGTGTCTCATGGAGAACACCTCTGCCATTGGATTAAAT  841
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1005 CAGGAGGAGGGATTTGTCATCGACGTGTCTCATGGAGAACACCTCTACATTGGATTAAAT  1064

Qy  842  GTGCTTGGGTGCAGCTGAGATGAGACCTTTATTGAAAATAATTGCAAAATGTACAACAG  901
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Db  1065 GTGCTTGGGTGCAGCTGAAATGAGACCTTTATTGAAAATGGAAAATGTACAACAG  1124

Qy  902  CCTATGTCCTCGTTATCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA  961
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1125 CCTATGTCCTCGTTATCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA  1184

Qy  962  CGCCTTCTATGATGCCAAGGCACCTAAAGGATTTGCTATGACTCATATCATATATATAG  1021
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Db  1185 CGCCTTCTATGATGCCAAGGCACCTAAAGGATTTGCTATGACTCATATCATATATATAG  1244

Qy  1022 TTGGAGGATGCGTGTGGGTCAACACCAGATCACACCAGATCACACCAGGGAAATGGCTTGT  1081
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1245 TTGGAGGATGCGTGTGGGTCAACACCAGATCACACCAGATCACACCAGGGAAATGGCTTGT  1304

Qy  1082 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGCTGGTC  1141
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1305 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGTCTGGTC  1364

Qy  1142 TAGAGCCCTTCAGGATTGACCGTACACCAACTTGTTAACACTTGTGTGAGCGCTGTAATG  1201
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1365 TAGAGCCCTTCAGGATTGACCGTACACCAACTTGTTAACACTTGTGTGAGCGCTGTAATG  1424

Qy  1202 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGAAACATGAGAGAAGCCTTGT  1261
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1425 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGAAACATGAGAGAAGCCTTGT  1484

Qy  1262 GTGTTGCCAAAGTGCAGGTGGAAATGGAGCCCCAGGTGTTGAAATGGATGTCAACATGATGATG  1321
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1485 GTGTTGCCAAAGTGCAGGTGGAAATGGAGCCCCAGGTGTTGAAATGGATGTCAACATGATGATG  1544

Qy  1322 GCAATGCTAGATGGTCCAAGTGCAATGACCAGATTTGTCAATAGCATTAGTCTGAAGGAGGACCAG  1381
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1545 GCAATGCTAGATGGTCCAAGTGCAATGACCAGATTTGTCAATAGCATTAGTCTGAAGGAGGAGGACCAG  1604

Qy  1382 ACATCGCAAAGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGT  1441
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1605 ACATCGCAAAGTACCTTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGT  1664

Qy  1442 TAAAGTGCTGCCAAGGGAAGTGGTTGTGCAATGGAAGTGTCAAGGGCTCATGAATAGCATTAGTCTGCAATATAATTT  1501
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1665 TAAAGTGCTGCCAAGGGAAGTGGTTGTGCAATGGAAGTGTCAAGGGCTCATGGCTCAATATAATTT  1724

Qy  1502 ACTTCTTGGAGAAGGAGGCCAGGAGTGGTCATGGCTTGCTCATGGTTGGTCATGGTTAAAAAGTGGGAAATGGGAGAT  1561
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1725 ACTTCTTGGAGAAGGAGGCCAGGAGTGGTCATGGCTTTAAAAAGTGGGAAATGGGAGAT  1784

Qy  1562 TTGATGAAGAGGACAACAGAGCAACAGAAATCAGAGTGTGTCACCCGGCCT  1621
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1785 TTGATGAAGAGGACAACAGAGCAACAGAAATCAGAGTGTGTCACCCGGCCT  1844

Qy  1622 ACCATCTGCTTGTGAAAAACTGGGCTTTAATCAAATGACATTATTTTTGACCCTAATA  1681
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1845 ACCATCTGCTTGTGAAAAACTGGGCTTTAATCAAATGACATTATTTTTGACCCTAATA  1904

Qy  1682 TCCTAACCATTGGGACTGGAATGGAGGAACAACTGTATGCCATTAATTTTATCCATG  1741
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1905 TCCTAACCATTGGGACTGGAATGGAGGAACAACTGTATGCCATTAATTTTATCCATG  1964

Qy  1742 CAACAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT  1801
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1965 CAACAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT  2024

Qy  1802 TGTCCTTCTCCTTCCGGAGAATGGAAGCCATTCGAGAAGCAATGCAATGGGGTTTCTTT  1861
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2025 TGTCCTTCTCCTTCCGGAGAATGGAAGCCATTCGAGAAGCAATGCAATGGGGTTTCTTT  2084

Qy  1862 ACCATGCAATCAAGTCTGGCATGGACATGAGAGTAGTGAATGCTGAAACCTCCCTGTGT  1921
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2085 ACCATGCAATCAAGTCTGGCATGGACATGAGAGTAGTGAATGCTGAAACCTCCCTGTGT  2144

Qy  1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCGTGAAGATCTCATCTGAATAAAGACC  1981
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2145 ATGATGATATCCATAAGGAACTTCTGCAGCTCGTGAAGATCTCATCTGAATAAAGACC  2204

Qy  1982 CTGAGGCCACTGAGAAGTCTTCTACGTTATGCCAGACTCAAGGCACAGAGGAGGAAAG  2041
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2205 CTGAGGCCACTGAGAAGTCTTCTACGTTATGCCAGACTCAAGGCACAGAGGAGGAAAG  2264

Qy  2042 TCATTCAGACTGATGAGTGGAGAAACATATTATTGAGGATTATTGAGGATATGCCCCTG  2101
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2265 TCATTCAGACTGATGAGTGGAGAAACATATTATTGAGGATTATTGAGGATATGCCCCTG  2324

Qy  2102 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAA  2161
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2325 TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAA  2384

Qy  2162 AATATCCCGACCTCTCAATATAATTGAAGGACACCCTGATGAATGAAATTGTTG  2221
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2385 AATATCCCGACCTCTCAATATAATTGAAGGACACCCTGATGAATGAAATTGTTG  2444

Qy  2222 GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA  2281
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2445 GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA  2504

Qy  2282 TGAAGAAGGCTGTGTGGCCACCTTATCCTTTCATGGAAAAGAAGAAACCAGAG  2341
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2505 TGAAGAAGGCTGTGTGGCCACCTTATCCTTTCATGGAAAAGAAGAAACCAGAG  2564

Qy  2342 TGCTTAACGGACAGTAGAAGAAGAGGACCCTGCCGGGCCACCATCGTGTCTGGCCACTG  2401
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2565 TGCTTAACGGACAGTAGAAGAAGAGGACCCTGCCGGGCCACCATCGTGTCTGGCCACTG  2624

Qy  2402 TTAAAGGGACGTGCACGACGACCAGCAAGAACATAGTTGGAGTAGTCCTGCAATA  2461
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2625 TTAAAGGGACGTGCACGACGACCAGCAAGAACATAGTTGGAGTAGTCCTGCAATA  2684

Qy  2462 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATGATAAGATAAGTGTCTC  2521
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2685 ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATGATAAGATAAGTGTCTC  2744

Qy  2522 TTGACCACAAAGCAGTATATAATTTGACCAGGACTCATCGTCGAGATGAAA  2581
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2745 TTGACCACAAAGCAGTATATAATTTGACCAGGACTCATCGTCGAGATGAAA  2804

Qy  2582 TGATTTTGTTGTGCCAAGGAAATGGAAAGATTAGCTATAAGGATTCCATTGTTGATTGGAG  2641
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2805 TGATTTTGTTGTGCCAAGGAAATGGAAAGATTAGCTATAAGGATTCCATTGTTGATTGGAG  2864

Qy  2642 GAGCAACCACTTCAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  2701
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2865 GAGCAACCACTTCAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  2924

Qy  2702 TAATCCATGCTCCTGCAGCGCTCCCAAGAGTGTGTTCCCGCCTGTTGTCGTGTTAGATGAAA  2761
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3842 TGGGATATGATACAGACTAACTTTTTTTTTTTT        3875
          |||||||||||||||||||||||
Db   4065 TGGGATATGATACAGACTAACTTTTTTTTTTTTTTT     4098
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RESULT 3
AEA63658
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ID   AEA63658 standard; DNA; 7122 BP.
XX
AC   AEA63658;
XX
DT   08-SEP-2005  (first entry)
XX
DE   Methionine synthase, MTR, DNA sequence, SEQ ID 2.
XX
KW   Neuroleptic; Nootropic; Tranquilizer; folate metabolism;
KW   psychiatric disorder; schizophrenia; autism;
KW   attention deficit hyperactivity disorder; obsessive-compulsive disorder;
KW   gene; ds; Methionine synthase; chromosome 1.
XX
OS   Homo sapiens.
XX
PN   US6912492-B1.
XX
PD   28-JUN-2005.
XX
PF   23-MAY-2000; 2000US-00577266.
XX
PR   25-MAY-1999;  99US-0136198P.
XX
PA   (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI   Johnson WG, Stenroos ES;
XX
DR   WPI; 2005-442724/45.
XX
PT   Estimating the susceptibility of an individual to have offspring that
PT   develop a developmental disorder comprises analyzing the nucleic acids
PT   and/or proteins for genes involved in folate, pyridoxine, and/or
PT   cobalamin metabolism.
XX
PS   Disclosure; SEQ ID NO 2; 84pp; English.
XX
CC   The present invention relates to a method (M1) for estimating the
CC   susceptibility of an individual to have offspring that develop a
CC   developmental disorder. The method comprises analyzing the nucleic acids
CC   and/or proteins from the biological sample, where analyzing results in a
CC   partial or full genotype of the alleles of two or more genes involved in
CC   folate, pyridoxine, and/or cobalamin metabolism. The present sequence is
CC   one such gene involved in folate metabolism. The method is also useful
CC   for diagnosing, preventing, and treating developmental disorders, e.g.
CC   schizophrenia, autism, attention deficit hyperactivity disorder, or
CC   obsessive-compulsive disorder. The protein encoded by the present
CC   sequence is also known as 5-methyltetrahydrofolate-homocysteine S-
CC   methyltransferase. The present sequence is located on chromosome 1q43.
XX
SQ   Sequence 7122 BP; 2112 A; 1450 C; 1728 G; 1832 T; 0 U; 0 Other;
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Query Match             89.7%;  Score 3517;  DB 14;  Length 7122;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 3867;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      2 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCCTTCGCCAAGGAGGAGGAGACTCGACA     61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCCCTTCGCCAAGGAGGAGGAGACTCGACA    284

Qy     62 ACATGTCACCCGCGCTCCAAGAACCGTCGCAACCGAGGTCGAAGAAACCCTGCGGG      121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 ACATGTCACCCGCGCTCCAAGAACCGTCGCAACCGAGGTCGAAGAAACCCTGCGGG      344

Qy    122 ATGAGATCAATGCCATTCTGCGAGAAGAGGATTATGGTGCTGCTGAATGGTGAGGGGACCA    181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  (cont.)
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Db   2925 TAATCCATGTCCTGGACGCGGTCCAAGAGTGTGGTCGTGTGTTCCAGCTGTTAGATGAAA    2984

Qy   2762 ATCTAAAGGATGAATCATTTGAGGAAATCATGAGGAAATGATGAGAATATTAGACAGGACC    2821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2985 ATCTAAAGGATGAATCATTTGAGGAAATCATGAGGAAATGATGAGAATATTAGACAGGACC    3044

Qy   2822 ATTATGAGTCTCTCAAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGTT    2881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3045 ATTATGAGTCTCTCAAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT    3104

Qy   2882 TCCAAATGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG    2941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3105 TCCAAATGGATTGGCGTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG    3164

Qy   2942 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG    3001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3165 TCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG    3224

Qy   3002 ATGTCTGGCAGCTCCGGGGCAAGTACCGGGAATCGAGGCTTCCCAAGATATTAACGACA    3061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3225 ATGTCTGGCAGCTCCGGGGCAAGTACCGGGAATCGAGGCTTTCCCAAGATATTAACGACA    3284

Qy   3062 AAACAGTAGTGGAGAGGCCAGGAAGGTCACGATGAGTGCCACAAATATGCTGAACACAC    3121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3285 AAACAGTAGTGGAGAGGCCAGGAAGGTCACGATGAGTGCCACAAATATGCTGAACACAC    3344

Qy   3122 TGATTAGTCAAAAGAAACTCCGGGCCCGGGGGTGTGGTTGGGGTTCTGGCCAGCACAGAGTA    3181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3345 TGATTAGTCAAAAGAAACTCCGGGCCCGGGGGTGTGGTTGGGGTTCTGGCCAGCACAGAGTA    3404

Qy   3182 TCCAAGACGACATTCACCTGTACGCAGAGGCTGCGTGTGCCCAGGCTGCGAGCCCATAG    3241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3405 TCCAAGACGACATTCACCTGTACGCAGAGGCTGCGTGTGCCCAGGCTGCGAGCCCATAG    3464

Qy   3242 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACCGGAGCCATACT    3301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3465 CCACCTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACCGGAGCCATACT    3524

Qy   3302 ACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGCATCCGTGACTACCTGGCGCTGT    3361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3525 ACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGCATCCGTGACTACCTGGCGCTGT    3584

Qy   3362 TTGCCGTGCCGCTTTGGGTGAGAGAGCTGAGCAAGGCCTATGAGGATGGATGGTGACG    3421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3585 TTGCCGTGCCGCTTTGGGTGAGAGAGCTGAGCAAGGCCTATGAGGATGGATGGTGACG    3644

Qy   3422 ACTACAGCAGCATCATGGTCAAGGGCGCTGGGGACCGGGCCTGGCAGAGAAG    3481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3645 ACTACAGCAGCATCATGGTCAAGGGCGCTGGGGACCGGGCCTGGCAGAGAAG    3704

Qy   3482 AGCTCCATGAAAAGAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGCTGGCAGCTCGACG    3541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3705 AGCTCCATGAAAAGAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGCTGGCAGCTCGACG    3764

Qy   3542 TCGCAGACCTGCGAAGGTTGCGTACAAGGGCATCCGCCGGCTCCTGCGTACCCCAGCC    3601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3765 TCGCAGACCTGCGCAGCTGCGGTACAAGGGCATCCGCCGGCTCCTGCGTACCCCAGCC    3824

Qy   3602 AGCCCGACCACCACCGAGAAGCTCACCATGTGGAGACTCGAGACATCGAGCAGTCTCACAG    3661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3825 AGCCCGACCACCACCGAGAAGCTCACCATGTGGAGACTCGAGACATCGAGCAGTCTTCACAG    3884

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCGACTCTCACT    3721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3885 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCGACTCTCACT    3944

Qy   3722 TCTCCAATTTGAAGTCCAAATATTTTTGCTGTGTGGGGGAGATTTCCAAGGATCAGGTTGAGG    3781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3945 TCTCCAATTTGAAGTCCAAATATTTTTGCTGTGTGGGGGAGATTTCCAAGGATCAGGTTGAGG    4004

Qy   3782 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCCATTT    3841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4005 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCCATTT    4064
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Db   345 ATGAGATCATGCCATTCTGCAGAAGAGAGATTATGGTGCTGGAGGGATGGGGGACCA 404

Qy   182 TGATCCAGCGGGAGAAGCTAAACGAAGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG
         |||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 TGATCCAGCAGCGGGAGAAGCTAAACGAAGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 464

Qy   242 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC 524

Qy   302 AAATCCATAAGGAATACTTGCTGCTGGGGCAGATATCATTGAAACAAATACTTTAGCA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 AAATCCATAAGGAATACTTGCTGCTGGGGCAGATATCATTGAAACAAATACTTTAGCA 584

Qy   362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 644

Qy   422 GCTCTGCAGGAGTGCCAGAAAAGTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   645 GCTCTGCAGGAGTGCCAGAAAAGTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGA 704

Qy   482 GGTTGTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCGTGTG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 GGTTGTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCGTGTG 764

Qy   542 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   765 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 824

Qy   602 CCAAAGGACTTCTGATGCGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   825 CCAAAGGACTTCTGATGCGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG 884

Qy   662 CCAATGCCAAGGCAGCAGCCTTGTTTGCACTCCCAAAATCTTTTGAGGAGAAATATGCTCCCC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   885 CCAATGCCAAGGCAGCAGCCTTGTTTGCACTCCCAAAATCTTTTGAGGAGAAATATGCTCCCC 944

Qy   722 GGGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCCGGACTCTTCCGGACAGA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   945 GGGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCCGGACTCTTCCGGACAGA 1004

Qy   782 CAGGAGAGGGATTTGTCATCAGCGTGTCTCATCAGGAGAACCACCTCTGCATTGGATTAAAT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1005 CAGGAGAGGGATTTGTCATCAGCGTGTCTCATCAGGAGAACCACCTCTGCATTGGATTAAAT 1064

Qy   842 GTGCTTGGGTGGTCAGCTGAGTGAGAGACCTTTATTGAAAATAATTGGAAAATGTACAACAG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1065 GTGCTTGGGTGGTCAGCTGAGTGAGAGACCTTTATTGAAAATAATTGGAAAATGTACAACAG 1124

Qy   902 CCTATGTCCTGTATCCCAAATGAGGTCTTCCCAAACACCTTTGGTGACTATGATGAAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1125 CCTATGTCCTGTATCCCAAATGAGGTCTTCCCAAACACCTTTGGTGACTATGATGAAA 1184

Qy   962 CGCCTTCATGATGGCCAAGCACCTAAAGATTTTGCTATGGATGGCTTGGTCAATATAG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1185 CGCCTTCATGATGGCCAAGCACCTAAAGATTTTGCTATGGATGGCTTGGTCAATATAG 1244

Qy  1022 TTGGAGGATGCTGTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1245 TTGGAGGATGCTGTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1304

Qy  1082 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1305 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTC 1364

Qy  1142 TAGAGCCCTTCAGGATTGACCGTACACCAACTTGTTAACATTGGAAGCGCTGTAATG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1365 TAGAGCCCTTCAGGATTGACCGTACACCAACTTGTTAACATTGGAAGCGCTGTAATG 1424

Qy  1202 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAAACTATGAAGAAGCCTTGT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1425 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAAACTATGAAGAAGCCTTGT 1484


Qy  1262 GTGTTGCCAAAGTGCAGGTGCAAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1485 GTGTTGCCAAAGTGCAGGTGCAAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATG 1544

Qy  1322 GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1545 GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAG 1604

Qy  1382 ACATCGCAAAGGTACCTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1605 ACATCGCAAAGGTACCTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGT 1664

Qy  1442 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAGGAGGAACG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1665 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAGGAGGACG 1724

Qy  1502 ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCATGGTCATGGCTT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1725 ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCATGGTCATGGCTT 1784

Qy  1562 TTGATGAAGAAGGACAGGCAACAGAACACAGACACAAAAATCAGAGTTGTGCACCCGGGCCT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1785 TTGATGAAGAAGGACAGGCAACAGAACACAGACACAAAAATCAGAGTTGTGCACCCGGGCCT 1844

Qy  1622 ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCTTAATA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1845 ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCTTAATA 1904

Qy  1682 TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTTATCCATG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1905 TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTTATCCATG 1964

Qy  1742 CAACAAAAGTCATTAAAGAGAACATTACCTGAGCCAGAATAAGTGAGGTCTTCCAACT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1965 CAACAAAAGTCATTAAAGAGAACATTACCTGAGCCAGAATAAGTGAGGTCTTCCAACT 2024

Qy  1802 TGTCCTTCCCTTCCGGAGGAATGCAGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2025 TGTCCTTCCCTTCCGGAGGAATGCAGCCATTCGAGAAGCAATGCATGGGGTTTTCCTTT 2084

Qy  1862 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGAAACCTCCCTGTGT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2085 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGAAACCTCCCTGTGT 2144

Qy  1922 ATGATGATATCCATAAGGAGACTTCTGCAGCTGTCGTGAAGATCTCATCTGAATAAGACC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2145 ATGATGATATCCATAAGGAGACTTCTGCAGCTGTCGTGAAGATCTCATCTGAATAAAGACC 2204

Qy  1982 CTGAGGCCACTGAGAGCTCTACGTTATGCCCAGACTCAAGGCACAGAGGACGGGAGAAAG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2205 CTGAGGCCACTGAGAGCTCTACGTTATGCCCAGACTCAAGGCACAGAGGACGGGAGAAAG 2264

Qy  2042 TCATTCAGACTGATGAGTGGAGAAATGGCCTTGTGTCGAAGAACGCCTTGAGTGATGCCCTTG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2265 TCATTCAGACTGATGAGTGGAGAAATGGCCTTGTGTCGAAGAACGCCTTGAGTGATGCCCTTG 2324

Qy  2102 TGAAGGGCATTGAAAAACATATTATTGAGGATACTAGTGAAACCAAAAAA
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2325 TGAAGGGCATTGAAAAACATATTATTGAGGATACTAGTGAAACCAAAAAA 2384

Qy  2162 AATATCCCCGACCTCTCAATAATAATTGAAGAGCCCTGATGATGAAAATTGTTG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2385 AATATCCCCGACCTCTCAATAATAATTGAAGAGCCCTGATGATGAAAATTGTTG 2444

Qy  2222 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGTTATAAAGTCAGCCCCGGGTTA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2445 GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGTTATAAAGTCAGCCCCGGGTTA 2504

Qy  2282 TGAAGAAGGCTGTTGGCCACCTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAGAAGAAACCAGAG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2505 TGAAGAAGGCTGTTGGCCACCTTGGCCACCTTATCCCTTTCATGGAAAAAGAAAGAAGAAACCAGAG 2564
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RESULT 4
AAF31101
ID   AAF31101 standard; cDNA; 7224 BP.
XX
AC   AAF31101;
XX
DT   27-APR-2001 (first entry)
XX
DE   Methionine synthase coding sequence #2.
XX
KW   Analyte-binding enzyme; analyte analysis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200102600-A2.
XX
PD   11-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018057.
XX
PR   06-JUL-1999; 99US-00347878.
PR   06-DEC-1999; 99US-00457205.
XX
PA   (GEAT) GEN ATOMICS.
XX
PI   Yuan C;
XX
DR   WPI; 2001-071583/08.
XX
PT   Assaying method, useful for prognosis and diagnosis of disease, comprises
PT   contacting sample with a mutant analyte-binding enzyme and detecting
PT   binding.
XX
PS   Disclosure; Page; 187pp; English.
XX
CC   The present invention relates to a method for assaying an analyte in a
CC   sample comprising: contacting the sample with a mutant analyte-binding
CC   enzyme which has binding affinity for the analyte or an immediate analyte
CC   enzymatic conversion product but has attenuated catalytic activity; and
CC   detecting resulting binding. The method is useful in monitoring
CC   biological systems/processes, or prognosis/diagnosis of disease caused by

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CC   imbalances of the analytes. The present sequence is a coding sequence
CC   used in the present invention. Note: the present sequence is not shown in
CC   the specification, but was from Genbank, using information given in the
CC   specification
XX
SQ   Sequence 7224 BP; 2108 A; 1491 C; 1761 G; 1864 T; .0 U; 0 Other;

Query Match             88.4%;  Score 3466;  DB 4;  Length 7224;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 3866; Conservative    0; Mismatches    8; Indels    0; Gaps    0;

Qy         2 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACA 61
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       333 GTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACA 392

Qy        62 ACATGTCACCCGGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG 121
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       393 ACATGTCACCCGGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAAGAAAACCCTGCGGG 452

Qy       122 ATGAGATCAATGCCATTCTGCAGAGAGAGGATTATGGTGCTGGGATGGAGGGGACCA 181
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       453 ATGAGATCAATGCCATTCTGCAGAGAGAGGATTATGGTGCTGGGATGGAGGGGACCA 512

Qy       182 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCAGGTCAGGAATTTAAAGATCATG 241
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       513 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCAGGTCAGGAATTTAAAGATCATG 572

Qy       242 CCAGGCCGCTGAAAGGCCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC 301
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       573 CCAGGCCGCTGAAAGGCCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC 632

Qy       302 AAATCCATAAGGAATACTTGCTCGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA 361
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       633 AAATCCATAAGGAATACTTGCTCGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCA 692

Qy       362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 421
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       693 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 752

Qy       422 GCTCTGCAGGAGTGGCCCAGAAAAGCTGCCAGGAGGTAACTCTCCAGACAGGAATTAAGA 481
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 GCTCTGCAGGAGTGGCCCAGAAAAGCTGCCAGGAGGTAACTCTCCAGACAGGAATTAAGA 812

Qy       482 GGTTTGTGGGTGCAGGGGCTCTCGGGTCCGACTAATAAGACACTTCCTCTGTCCCATCTGTGG 541
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       813 GGTTTGTGGGTGCAGGGGCTCTCGGGTCCGACTAATAAGACACTTCCTCTGTCCCATCTGTGG 872

Qy       542 AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 601
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       873 AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 932

Qy       602 CCAAAGGACTTCTGATGCGGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG 661
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 CCAAAGGACTTCTGATGCGGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG 992

Qy       662 CCAATGCCAAGGCAGCGCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC 721
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 CCAATGCCAAGGCAGCGCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC 1052

Qy       722 GGCCTATCTTTATTTCAGGGAGCGATCGTTGTTGATAAAAGTGGGCGGACTCTTTCCGACACAG 781
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1053 GGCCTATCTTTATTTCAGGGAGCGATCGTTGTTGATAAAAGTGGGCGGACTCTTTCCGACACAG 1112

Qy       782 CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGGAGCAACCACTCTGCCATTGGATTTAAATT 841
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1113 CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGGAGCAACCACTCTGCCATTGGATTTAAATT 1172

Qy       842 GTGCTTTGGGTGCACTGACGATGAACCTTTTTGACTCCAAATCTTTTGAGGAGAAAATTGACAAACAG 901
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1173 GTGCTTTGGGTGCACTGACGATGAACCTTTTTGACTCCAAATCTTTTGAGGAGAAAATTGACAAACAG 1232

Qy       902 CCTATGTCCTCTGTTATCCCAATGCAGCGTCTTCCCAACACCTTTGGTGACTATGATGAAA 961
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1233 CCTATGTCCTCTGTTATCCCAATGCAGCGTCTTCCCAACACCTTTGGTGACTATGATGAAA 1292
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG 1021

Qy      1293 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG 1352
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1022 TTGGAGGATCGTGTGGTCAACACCAGATCATATCAGGGGAAATTGCTGAAGCTGTGAAAA 1081

Qy      1353 TTGGAGGATCGTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA 1412
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1082 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCGGTC 1141

Qy      1413 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGTC 1472
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1142 TAGAGCCCTTCAGGATTGGACGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATG 1201

Qy      1473 TAGAGCCCTTCAGGATTGGACGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATG 1532
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1202 TTGCAGGATCAAGGAAGTTTGCTAAACTCATGCTGCAGAAAACTATGAGAAGCCTTGT 1261

Qy      1533 TTGCAGGATCAAGGAAGTTTGCTAAACTCATGCTGCAGAAAACTATGAGAAGCCTTGT 1592
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1262 GTGTTGCCAAAGTGCAGGTGGAAATGGCAGCCCAGGTGTTGGAATGGTCAACATGGATGATG 1321

Qy      1593 GTGTTGCCAAAGTGCAGGTGGAAATGGCAGCCCAGGTGTTGGAATGGTCAACATGGATGATG 1652
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1322 GCATGTCTAGATGGTCCAAGTGCAATGACTCGACTCCTCCAAATTTCGTCGATTGAAGCTGGGT 1381

Qy      1653 GCATGTCTAGATGGTCCAAGTGCAATGACTCGACTCCTCCAAATTTCGTCGATTGAAGCTGGGT 1712
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1382 ACATGCAAAGGTACCTTCTGTGCATCGAAGTGCCCAAATTTCTGCAATTTGCTCTCAAGATAGCA 1441

Qy      1713 ACATGCAAAGGTACCTTCTGTGCATCGAAGTGCCCAATTTTGTGCAATTTGCTCTCAAGATAGCA 1772
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1442 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTGTCTGATGAAGGAAGGAGGAGGACG 1501

Qy      1773 TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTGTCTGATGAAGGAAGGAGGAGGACG 1832
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1502 ACTTCTTGGAGAAGGGCCAGGAGAGATTAAAAGTATGGCTGCTATGGTCATGGCTT 1561

Qy      1833 ACTTCTTGGAGAAGGGCCAGGAGAGATTAAAAGTATGGCTGCTATGGTCATGGCTT 1892
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1562 TTGATGAAGAGGACAGGCAACAGACAGAACAGAGACACACAGAGTGTGCACCCGGGCCT 1621

Qy      1893 TTGATGAAGAGGACAGGCAACAGACAGAACAGAGACACACAGAGTGTGCACCCGGGCCT 1952
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1622 ACCATCTGCTTGTGTGAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAATA 1681

Qy      1953 ACCATCTGCTTGTGTGAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCTAATA 2012
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1682 TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTTATCCATG 1741

Qy      2013 TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTTATCCATG 2072
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1742 CAACAAAAGTCATTAAGAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 1801

Qy      2073 CAACAAAAGTCATTAAGAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACT 2132
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1802 TGTCCTTCTCCTTCCGGAGAATGGAAGCCATTGAGAAGCAATGCATGGGTTTTCCTTT 1861

Qy      2133 TGTCCTTCTCCTTCCGGAGAATGGAAGCCATTGAGAAGCAATGCATGGGTTTTCCTTT 2192
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1862 ACCATGCAATCAAGTCTGGCATGGACATGGGATAGTGAAATGCTGAAACCTCCCGTGT 1921

Qy      2193 ACCATGCAATCAAGTCTGGCATGGACATGGGATAGTGAAATGCTGAAACCTCCCGTGT 2252
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1922 ATGATGATCCATAAGAGAACTTCTGCAGCTCTCGTGAAGATCTCATCTCGGAATAAGACC 1981

Qy      2253 ATGATGATCCATAAGAGAACTTCTGCAGCTCTCGTGAAGATCTCATCTCGGAATAAAGCAACC 2312
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1982 CTGAGGCCACTGACAGTCTTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAG 2041

Qy      2313 CTGAGGCCACTGACAGTCTTTACGTTATGCCCAGACTCAAGGCACAGGAGGGAAGAAAG 2372
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2042  TCATTCAGACTGATGAGTGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTTG  2101        Qy  3122  TGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGGTTCTGGCCAGCACAGAGTA  3181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2373  TCATTCAGACTGATGAGTGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTTG  2432        Db  3453  TGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGGTTCTGGCCAGCACAGAGTA  3512

Qy  2102  TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA  2161        Qy  3182  TCCAAGACGACATTCACCTGTACGACGAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAG  3241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2433  TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAA  2492        Db  3513  TCCAAGACGACATTCACCTGTACGACGAGAGGCTGCTGTGCCCCAGGCTGCGAGAGCCCATAG  3572

Qy  2162  AATATCCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAAAATTGTTG  2221        Qy  3242  CCACTTTCTATGGGTTAAGGCAACAGGCTGCGAGAAGACTCGCCAGCACGAGCCATACT  3301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2493  AATATCCCCGACCTCTCAATATAATTGAAGACCCCTGATGAATGAAAATTGTTG  2552        Db  3573  CCACTTTCTATGGGTTAAGGCAACAGGCTGCGAGAAGACTCGCCAGCACGAGCCATACT  3632

Qy  2222  GTGATCTTTTTGGAGCTGGAAAAATGTTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTTA  2281        Qy  3302  ACTGCCTCTCAGACTTCATCGTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2553  GTGATCTTTTTGGAGCTGGAAAAATGTTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTTA  2612        Db  3633  ACTGCCTCTCAGACTTCATCGTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3692

Qy  2282  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAGAGAAAACCAGAG  2341        Qy  3362  TTGCCGTTGCCTTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG  3421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2613  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAAGAGAGAAAACCAGAG  2672        Db  3693  TTGCCGTTGCCTTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG  3752

Qy  2342  TGCTTAACGGCACAGTAGAAGAGAGACCCTTACCAGGGCACCCATCGTGCTGGCCACTG  2401        Qy  3422  ACTACAGCAGCATCATGGTCAAGGCGCTGGAGGGACCGGCTCGCGCAGAGGCCTTTGCAGAAG  3481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2673  TGCTTAACGGCACAGTAGAAGAGAGACCCTTACCAGGGCACCCATCGTGCTGGCCACTG  2732        Db  3753  ACTACAGCAGCATCATGGTCAAGGCGCTGGAGGGACCGGCTCGCGCAGAGGCCTTTGCAGAAG  3812

Qy  2402  TTAAAGGCGACCTGCACGACAATAGGCAAGAACATAGTTGAGTCCATGTAGTCCTTGGCTGCAATA  2461        Qy  3482  AGCTCCATGAAAAGAGTTCGCCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGACG  3541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2733  TTAAAGGCGACCTGCACGACAATAGGCAAGAACATAGTTGAGTCCATGTAGTCCTTGGCTGCAATA  2792        Db  3813  AGCTCCATGAAAAGAGTTCGCCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGACG  3872

Qy  2462  ATTTCCGAGTTATTGATTTGGCCTGTCATGAGTCCATGTGATAAGATACTGAAAAGTGCTC  2521        Qy  3542  TCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGGCCTACCCCCAGCC  3601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2793  ATTTCCGAGTTATTGATTTGGCCTGTCATGAGTCCATGTGATAAGATACTGAAAAGTGCTC  2852        Db  3873  TCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGGCCTACCCCCAGCC  3932

Qy  2522  TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGGATGAAA  2581        Qy  3602  AGCCCGACCACCACCGAGAAGCTCACCATGCAATGACAATGGCCACCTGCTTCAGCGTCTCACT  3661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2853  TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGGATGAAA  2912        Db  3933  AGCCCGACCACCACCGAGAAGCTCACCATGCAATGACAATGGCCACCTGCTTCAGCGTCTCACT  3992

Qy  2582  TGATTTTTGTTGCCAAGGAGAATGGAGAATTAGCTATAAGGATTCATTGTTGATTGGAG  2641        Qy  3662  GCATTAGGTTAACAGAATCATTAGCAATGACACCTGCTTCAGCGTCTCACT  3721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2913  TGATTTTTGTTGCCAAGGAGAATGGAGAATTAGCTATAAGGATTCATTGTTGATTGGAG  2972        Db  3993  GCATTAGGTTAACAGAATCATTAGCAATGACACCTGCTTCAGCGTCTCACT  4052

Qy  2642  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTAGACACCTG  2701        Qy  3722  TCTCCAATTTGAAGTCCAAAATATTTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG  3781
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2973  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTAGACACCTG  3032        Db  4053  TCTCCAATTTGAAGTCCAAAATATTTTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG  4112

Qy  2702  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTGTTCCCAGCTGTTGAGATGAAA  2761        Qy  3782  ATTATGCATTGAGGAAGAACATATCTGTGGCTGGCTTGAGGTTGAGAAAATGGCTTGACCCATTT  3841
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3033  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTGTTCCCAGCTGTTGAGATGAAA  3092        Db  4113  ATTATGCATTGAGGAAGAACATATCTGTGGCTGGCTTGAGGTTGAGAAAATGGCTTGACCCATTT  4172

Qy  2762  ATCTAAAGGATGAATACTTTGAGGAAATCATGAAGAAATATGAAGATATTAGACACGGACC  2821        Qy  3842  TGGGATAATGATACAGACTAACTTTTTTTTTTTTTTT  3875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                      |||||||||||||||||||||||||||||||||||||
Db  3093  ATCTAAAGGATGAATACTTTGAGGAAATCATGAAGAAATATGAAGATATTAGACACGGACC  3152        Db  4173  TGGGATAATGATACAGACTAACTTTTTTTTTTTTTTTTTTT  4206

Qy  2822  ATTATGAGTCTCTCAAGGAGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT  2881
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3153  ATTATGAGTCTCTCAAGGAGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT  3212

Qy  2882  TCCAAATGGATTGGCTGTCTGAACCTGCACCCAGTGAAGCCCACGTTTATTGGGACCCCAGG  2941
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3213  TCCAAATGGATTGGCTGTCTGAACCTCACCCCAGTGAAGCCCACGTTTATTGGGACCCCAGG  3272

Qy  2942  TCTTTGAAGACTATGACCTGCAGAAGCTGGTCGACTACATTGACTGACAAGCCTTTCTTTG  3001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3273  TCTTTGAAGACTATGACCTGCAGAAGCTGGTCGACTACATTGACTGACAAGCCTTTCTTTG  3332

Qy  3002  ATGTCTGCAGCTCCGGGGCAAGTACCCGGCTTCCCCAAGATATTTAACGACA  3061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3333  ATGTCTGCAGCTCCGGGGCAAGTACCCGGCTTCCCCAAGATATTTAACGACA  3392

Qy  3062  AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGTCCACCAAATATGCTGAACACAC  3121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3393  AAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGTCCACCAAATATGCTGAACACAC  3452
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RESULT 5
ADI39109

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XX
PN   WO200307386-A2.
XX
PD   23-OCT-2003.
XX
PF   16-APR-2003; 2003WO-EP004010.
PR   17-APR-2002; 2002DE-01017058.
XX
PA   (BADI ) BASF AG.
XX
PI   Kroeger B, Zelder O, Klopprogge C, Schroeder H, Haefner S;
XX
DR   WPI; 2003-877106/81.
DR   P-PSDB; ADI39110.
XX
PT   Fermentative production of sulfur-containing compounds, particularly L-
PT   methionine, useful as feed additives, by using Coryneform bacteria that
PT   overexpress methionine synthase.
XX
PS   Claim 5; SEQ ID NO 43; 304pp; German.
XX
CC   This invention describes a novel method for the fermentative production
CC   of methionine by growing a sulphur-producing Coryneform bacteria that
CC   expresses at least one heterologous nucleic acid encoding a protein with
CC   methionine synthase (MetH) activity. Methionine accumulates in the medium
CC   or the cells. The method can be used to produce an L-methionine-
CC   containing animal feed additive by culturing an L-Met-producing
CC   microorganism, removing water from the resulting broth, removing 0-100%
CC   of the biomass formed and drying the product to produce the feed additive
CC   in powdered or granular form. The nucleic acid encoding MetH has sequence
CC   homology less than 100% with respect to the metH coding sequence of
CC   Corynebacterium glutamicum ATCC 13032. Optionally at least one other gene
CC   in the methionine biosynthesis pathway (e.g. aspartate kinase,
CC   glyceraldehyde-3-phosphate dehydrogenase or 3-phosphoglycerate kinase) is
CC   also amplified or mutated so that it is not affected by metabolites. Also
CC   at least one metabolic pathway that reduces production of methionine is
CC   at least partly switched off (e.g. homoserine kinase, threonine
CC   dehydratase or threonine synthase). The method is especially used to
CC   produce L-methionine, useful as an additive for animal feeds. More
CC   generally sulphur-containing fine chemicals are useful in human and
CC   animal nutrition, cosmetics and pharmaceuticals. This sequence encodes a
CC   metH protein described in the disclosure of the invention.
XX
SQ   Sequence 3798 BP; 1082 A; 809 C; 982 G; 925 T; 0 U; 0 Other;

Query Match              86.5%;  Score 3390;  DB 10;  Length 3798;
Best Local Similarity    99.8%;
Matches   3790;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    64 ATGTCACCCGGCTCCAAGACCTGTCGCAACCCGAGAGGTCTGAAGAAAACCCTGCGGGAT 123
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGTCACCCGGCTCCAAGACCTGTCGCAACCCGAGAGGTCTGAAGAAAACCCTGCGGGAT  60

Qy   124 GAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGAGGGGATGGGGGACCATG 183
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGAGGGGATGGGGGACCATG 120

Qy   184 ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATGCC 243
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATGCC 180

Qy   244 AGGCCGCTGAAAGGCAACAATGCACATGACATTTAAGTATATAACTCAGCCTGATGTCATTTACCAA 303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGGCCGCTGAAAGGCAACAATGCACATGACATTTAAGTATATAACTCAGCCTGATGTCATTTACCAA 240

Qy   304 ATCCATAAGGAATACTTGCTCTGGGGGCAGATATCATTGAAACAAATACTTTTAGCAGC 363
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATCCATAAGGAATACTTGCTCTGGGGGCAGATATCATTGAAACAAATACTTTTAGCAGC 300

Qy   364 ACTAGTATTGCCCAAGCTGACTATGCCCTTGAACACTTGGCCTACCGGATGAACATGTGC 423
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACTAGTATTGCCCAAGCTGACTATGCCCTTGAACACTTGGCCTACCGGATGAACATGTGC 360

Qy   424 TCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAGAGAGG 483
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTTCCAGACAGGAATTAGAGAGG 420

Qy   484 TTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCGTGTGGAA 543
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCGTGTGGAA 480

Qy   544 AGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGACAGGCC 603
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGACAGGCC 540

Qy   604 AAAGGACTTCTGGATGGCGGGGTTGATATCTTCACTCATTGAAACTATTTTGATACTGCC 663
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGGACTTCTGGATGGCGGGGTTGATATCTTCACTCATTGAAACTATTTTGATACTGCC 600

Qy   664 AATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGG 723
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCCGG 660

Qy   724 CCTATCTTTATTTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTCCGACAGACA 783
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CCTATCTTTATTTCAGGGACGATCGTTGATAAAGTGGGCGGACTCTTCCGACAGACA 720

Qy   784 GGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACCTCGCATTGGATTAAATTGT 843
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACCTCGCATTGGATTAAATTGT 780

Qy   844 GCTTTGGGTGCAGCTGAGATGAGACCCTTTATTGAAAATTGGAAAATGTACAACAGCC 903
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GCTTTGGGTGCAGCTGAGATGAGACCCTTTATTGAAAATTGGAAAATGTACAACAGCC 840

Qy   904 TATGTCCTCTGTTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAACG 963
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TATGTCCTCTGTTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAACG 900

Qy   964 CCTTCTATGATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAGTT 1023
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CCTTCTATGATGATGGCCAAGCACCTAAAGGATTTGCTATGGATGGCTTGGTCAATATAGTT 960

Qy  1024 GGAGGATGCTGTGGGTCAACACAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1083
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GGAGGATGCTGTGGGTCAACACAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAAAT 1020

Qy  1084 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGCTGGTCTA 1143
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTGAAGGACATATGTTACTGCTGGTCTA 1080

Qy  1144 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGGCTGTAATGTT 1203
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGGCTGTAATGTT 1140

Qy  1204 GCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATCATGAAGAGCCTTGTGT 1263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACTATCATGAAGAGCCTTGTGT 1200

Qy  1264 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATGGGC 1323
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGATGATGGGC 1260

Qy  1324 ATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGAC 1383
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGAC 1320

Qy  1384 ATCGCAAAGGTACCTTTGTCATCGACTCCTCCAATTTGTGTGATTGATTGAAGCTGGGTTA 1443
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ATCGCAAAGGTACCTTTGTCATCGACTCCTCCAATTTGTGTGATTGATTGAAGCTGGGTTA 1380

Qy  1444 AAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCGAAGGAGGAGGAGGACGAC 1503
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 AAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCGAAGGAGGAGGAGGACGAC 1440
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Qy  1504 TTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGCGTGGTCATGGCTTTT 1563
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 TTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGCGTGGTCATGGCTTTT 1500

Qy  1564 GATGAAGAAGGACAGGCAACAGAACAGAAAATCAGAGTGCACCGGGCCTAC 1623
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 GATGAAGAAGGACAGGCAACAGAACAGAAAATCAGAGTGCACCGGGCCTAC 1560

Qy  1624 CATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATATC 1683
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 CATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCTAATATC 1620

Qy  1684 CTAACCATTGGGACTGGAATGGAGGAACACAACTGTATGCCATTAATTTATCCATGCA 1743
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 CTAACCATTGGGACTGGAATGGAGGAACACAACTGTATGCCATTAATTTATCCATGCA 1680

Qy  1744 ACAAAAGTCATTAAAGAAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTG 1803
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 ACAAAAGTCATTAAAGAAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAACTTG 1740

Qy  1804 TCCTTCTCCTTCCGGAGGAATGGAAGCCATTCGAGAGAATGCTGGAAACCTCCTGTGTAT 1863
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TCCTTCTCCTTCCGGAGGAATGGAAGCCATTCGAGAGAATGCTGGAAACCTCCTGTGTAT 1800

Qy  1864 CATGCAATCAAGTCTGCATGGACATGGAGATAGTGAATGCTGGAAGATCTCCATCTGTGAAGAT 1923
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CATGCAATCAAGTCTGCATGGACATGGAGATAGTGAATGCTGGAAGATCTCCATCTGTGAAGAT 1860

Qy  1924 GATGATATCCATAAGGAACTTCTGCAGCTCTGTGTGAAGATCTCATCTGGAATAAAGACCCT 1983
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GATGATATCCATAAGGAACTTCTGCAGCTCTGTGTGAAGATCTCATCTGGAATAAAGACCCT 1920

Qy  1984 GAGGGCCACTGAGAAGTCTGAGAAGTCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAAGTC 2043
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 GAGGGCCACTGAGAAGTCTGAGAAGTCTCTTACGTTATGCCCAGACTCAAGGCACAGGAGGAAGAAAGTC 1980

Qy  2044 ATTCAGACTGATGAGTGGAGAAAATGGCCCTGTCGAAGAACCGCTTGAGTATGCCCTTGTG 2103
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 ATTCAGACTGATGAGTGGAGAAAATGGCCCTGTCGAAGAACCGCTTGAGTATGCCCTTGTG 2040

Qy  2104 AAGGGCCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAA 2163
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 AAGGGCCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAAA 2100

Qy  2164 TATCCCGACCTCTCAATAATATTGAAGACCCCTGATGAATGAATTGTTGGT 2223
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TATCCCGACCTCTCAATAATATTGAAGACCCCTGATGAATGAATTGTTGGT 2160

Qy  2224 GATCTTTTTGGAGCTGCACGACATAGGCAAGAACATAGTTCGAGTAGTCCTTGGCTGCAATAAT 2283
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GATCTTTTTGGAGCTGCACGACATAGGCAAGAACATAGTTCGAGTAGTCCTTGGCTGCAATAAT 2220

Qy  2284 AAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAATAAGAAAGAGAAACCAGAGTG 2343
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAATAAGAAAGAGAAACCAGAGTG 2280

Qy  2344 CTTAACGGCACAGTAGAAGAGAGAAGCCCTGTTACCAGGGCACCATGTGTCCTGGCCACTGTT 2403
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CTTAACGGCACAGTAGAAGAGAGAAGCCCTGTTACCAGGGCACCATGTGTCCTGGCCACTGTT 2340

Qy  2404 AAAGGGCGACGTGCACGGACATAGGCAAGAACATAGTTCGAGTAGTCCTTGGCTGCAATAAT 2463
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 AAAGGGCGACGTGCACGGACATAGGCAAGAACATAGTTCGAGTAGTCCTTGGCTGCAATAAT 2400

Qy  2464 TTCCGAGTTATTGATTTAGGAGTCATCCATGTGATAAGAGCTGAAAGTCTGCTTCTT 2523
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TTCCGAGTTATTGATTTAGGAGTCATCCATGTGATAAGAGCTGAAAGTCTGCTTCTT 2460

Qy  2524 GACCACAAAGCAGCAGATAATATTGGCCTGTCGAGGACTCATCACTCACTTCCCTGATGAAATG 2583
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 GACCACAAAGCAGCAGATAATATTGGCCTGTCGAGGACTCATCACTCACTTCCCTGATGAAATG 2520

Qy  2584 ATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGA 2643
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 ATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGA 2580
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Qy  2644 GCAACCACTTCAAAAACCCACACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTA 2703
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 GCAACCACTTCAAAAACCCACACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTA 2640

Qy  2704 ATCCATGTCCTTGGACGCGTCAAAGACGTGTGGTGTTCCCAGCTGTTAGATGAGAAAT 2763
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 ATCCATGTCCTTGGACGCGTCAAAGACGTGTGGTGTTCCCAGCTGTTAGATGAGAAAT 2700

Qy  2764 CTAAAGGATGAATACTTTGAGGAAATCATGGAAGAGATAATGAAGATTAGCAGGAGACCAT 2823
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTAAAGGATGAATACTTTGAGGAAATCATGGAAGAGATAATGAAGATTAGCAGGAGACCAT 2760

Qy  2824 TATGAGTCTCTCAAGGAGGAGAGAGATACTTACCCCTTAAGTCAAGCCAGAAAAAGTGGTTTC 2883
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TATGAGTCTCTCAAGGAGGAGAGAGATACTTACCCCTTAAGTCAAGCCAGAAAAAGTGGTTTC 2820

Qy  2884 CAAATGATTGGCTGTTCTGCGAAGCTGGTGGACTACATTGACTGGGAAGCCTTTCTTTGAT 2943
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 CAAATGATTGGCTGTTCTGCGAAGCTGGTGGACTACATTGACTGGGAAGCCTTTCTTTGAT 2880

Qy  2944 TTTGAAGACTATGACCTGCAGAAGCTGGTGACTACATTGACTGGTGGAAACCTCCGTGTAT 3003
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TTTGAAGACTATGACCTGCAGAAGCTGGTGACTACATTGACTGGTGGAAACCTCCGTGTAT 2940

Qy  3004 GTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACAAA 3063
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 GTCTGGCAGCTCCGGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACAAA 3000

Qy  3064 ACAGTAGGTGGAGAGGCCAGGAAGGTCTACAGTGATGCCCACAATATGCTGAACACACTG 3123
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ACAGTAGGTGGAGAGGCCAGGAAGGTCTACAGTGATGCCCACAATATGCTGAACACACTG 3060

Qy  3124 ATTAGTCAAAAGAAACTCCGGGCCCCGGGGGTGTGGTTCGGGCCCCAGCACAGAGTATCC 3183
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 ATTAGTCAAAAGAAACTCCGGGCCCCGGGGGTGTGGTTCGGGCCCCAGCACAGAGTATCC 3120

Qy  3184 CAAGACGACATTCACCTGTACGGAGGCTGCTGTGTGCCCAGGCTGCGAGAGCCCCATAGCC 3243
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 CAAGACGACATTCACCTGTACGGAGGCTGCTGTGTGCCCAGGCTGCGAGAGCCCCATAGCC 3180

Qy  3244 ACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGAGGAGCCATACTAC 3303
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 ACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGAGGAGCCATACTAC 3240

Qy  3304 TGCCTCTCAGACTTCATCGCTTGCATTCGGGCATCCTGGGCTACTTGGGCCTCTGTTT 3363
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 TGCCTCTCAGACTTCATCGCTTGCATTCGGGCATCCTGGGCTACTTGGGCCTCTGTTT 3300

Qy  3364 GCCGTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCATGGATGGTGACGAC 3423
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GCCGTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCATGGATGGTGACGAC 3360

Qy  3424 TACAGCGCATCATGGTCAAGGCGCTGGGGAGCGGCCTTTGCAGAGAGAG 3483
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TACAGCGCATCATGGTCAAGGCGCTGGGGAGCGGCCTTTGCAGAGAGAG 3420

Qy  3484 CTCCATGAAAAGAGTTGCCGAAGGTTGCGGTTGCTGGCCGAGAACTGTGGGCCTCACTGTGGGCAGCTGGACGTC 3543
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 CTCCATGAAAAGAGTTGCCGAAGGTTGCGGTTGCTGGCCGAGAACTGTGGGCCTCACTGTGGGCAGCTGGACGTC 3480

Qy  3544 GCAGACCTGCGAAGGTTGCGGTTGCAGGGCATCCGCCGCTCCCCAGCCAG 3603
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GCAGACCTGCGAAGGTTGCGGTTGCAGGGCATCCGCCGCTCCCCAGCCAG 3540

Qy  3604 CCCGACCACCACCGAGAGCTCACCATGTGCGAGACTCGCAGACTCTACAGC 3663
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CCCGACCACCACCGAGAGCTCACCATGTGCGAGACTCGCAGACTCTACAGC 3600

Qy  3664 ATTAGGTTAACAGAATCATTAGCAATGGCACCTCGCTTCAGCAGTCTCACTTC 3723
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3601 ATTAGGTTAACAGAATCATTAGACAATGGCACCTGCTTCAGCAGTCTCAGCCCTCTACTTC 3660
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Qy   3724 TCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT 3783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT 3720

Qy   3784 TATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATTTTTG 3843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATGCATTGAGGAAGAACACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATTTTG 3780

Qy   3844 GGATATGATGATACAGACTAA 3861
          ||||||||||||||||||||
Db   3781 GGATATGATGATACAGACTAA 3798
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Query Match     34.4%;  Score 1349;  DB 2;  Length 3920;
Best Local Similarity   99.0%;  Pred. No. 0;
Matches 2649;  Conservative   0;  Mismatches  26;  Indels   0;  Gaps   0;

Qy     1 GGTCACCTGTGGAGAGCACGTCTTCTCTGCGCCCTCTGCCAAGGAGGAGGACTCGAC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GGTCACCTGTGGAGAGCACGTCTTCTCTGCGCCCTCTGCGCAAGGAGGAGGACTCGAC 60

Qy    61 AACATGTCACCCGCTCCAAGACCTGTCGCAAGACCTGTCGCGAAGGTCTGAAGAAACCCTGCGG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AACATGTCACCCGCTCCAAGACCTGTCGCAAGACCTGTCGCGAAGGTCTGAAGAAACCCTGCGG 120

Qy   121 GATGAGATCAATGCCATTCTGCAGAAGAGAGATTATGGTGTCGTGGATGGGAGGGATGGGGACC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GATGAAATCAATGCCATTCTCCAGAAGAGAGATTATGTGTCGTGGATGGGAGGGATGGGGACC 180

Qy   181 ATGATCCAGGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCAT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATGATCCAGGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCAT 240

Qy   241 GCCAGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTAC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCCAGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTAC 300

Qy   301 CAAATCCATAAGGAATACTTGCTGCTGGGCAGATATCATTGAAACAAATACTTTTAGC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CAAATCCATAAGGAATACTTGCTGCTGGGCAGATATCATTGAAACAAATACTTTTAGC 360

Qy   361 AGCACTAGTATTGCCCAAGCTGACTATGGCCTTGACACTGCCGATGACAATG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGCACTAGTATTGCCCAAGCTGACTATGGCCTTGACACTGCCGATGACAATG 420

Qy   421 TGCTCTGCAGGAGTGGCCAGAAAAGTGCGCCGAGGAGTAACTCTCCAGACAGGAATTAAG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGCTCTGCAGGAGTGGCCAGAAAAGTGCGCCGAGGAGTAACTCTCCAGACACGAATTAAG 480

Qy   481 AGGTTGTGGCAGGGGCTCTGGGTCCGACTAATAGACACTCTCTGGTCCCCATCTGTG 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGGTTTCTGGCAGGGGCTCTGGGTCCGACTAATAGACACTCTCTGGTCCCCATCTGTG 540

Qy   541 GAAAGGCCGATTATAGGAACATCACATTGATGAGCTTGTTGAAGCATACCAAGAGCAG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GAAAGGCCGATTATAGGAACATCACATTGATGAGCTTGTTGAAGCATACCAAGAGCAG 600

Qy   601 GCCAAAGGACTTCTGATGCGGGGTTGATATCTTACTCACTGAAACTATTTTGATACT 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GCCAAAGGACTTCTGATGCGGGGTTGATATCTTACTCACTGAAACTATTTTGATACT 660

Qy   661 GCCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GCCAATGCCAAGGCAGCCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCC 720

Qy   721 CGGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGGGACTCTTCCGGACAG 780
         ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db   721 CGGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGCCCGACACTCTTCCGGACAG 780

Qy   781 ACAGGAGAGGATTTGTCATCACGGTGTCTCATGGAGAACCACTCTGCATTGGATTAAAT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ACAGGAGAGGATTTGTCATCACGGTGTCTCATGGAGAACCACTCTGCATTGGATTAAAT 840

Qy   841 TGTGCTTGGGTGCAGCTGAGATGAACACCTTTATTGAAATAATTGGAAAATGTACAACA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TGTGCTTGGGTGCAGCTGAGATGAACACCTTTATTGAAATAATTGGAAAATGTACAACA 900

Qy   901 GCCTATGTCCTCGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTCGACTATGATGAA 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GCCTATGTCCTCGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTCGACTATGATGAA 960
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  961 ACGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATA 1020
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  961 ACCCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATA 1020

 1021 GTTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAA 1080
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1021 GTTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAA 1080

 1081 AATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGT 1140
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1081 AATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGT 1140

 1141 CTAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCTGTAAT 1200
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1141 CTAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCTGTAAT 1200

 1201 GTTGCAGGATCAAGGAAGTTGCTAAACTGCAGAAACTGAGAAACTATGAAGAAGCCTTG 1260
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1201 GTTGCAGGATCAAGGAAGTTGCTAAACTGCAGAAACTGAGAAACTATGAAGAAGCCTTG 1260

 1261 TGTGTTGCCAAAGTGCAGGTGAAATGGGAGCCCAGTGTGTTGGATGTCAACATGGATGAT 1320
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1261 TGTGTTGCCAAAGTGCAGGTGAAATGGGAGCCCAGTGTGTTGGATGTCAACATGGATGAT 1320

 1321 GGCATGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCA 1380
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1321 GGCATGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCA 1380

 1381 GACATCGCAAAGGTACCTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGG 1440
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1381 GACATCGCAAAGGTACCTTGTGCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGG 1440

 1441 TTAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAGGAGGAGGAC 1500
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1441 TTAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAGGAGGAGGAC 1500

 1501 GACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCT 1560
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1501 GACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCT 1560

 1561 TTTGATGAAGAAGACAGGCAACAACAGAAACAGACAAAAAATCAGAGTGTGCACCCGGGCC 1620
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1561 TTTGATCAAGAAGACAGGCAACAACAGAAACAGACAAAAAATCAGAGTGTGCACCCGGGCC 1620

 1621 TACCATCGTGCTTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAAT 1680
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1621 TACCATCTCCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTCACCCTAAT 1680

 1681 ATCCTAACCATTGGGACTGGAATGGAGGAGAACCAACTTGTATGCCATTAATTTTATCCAT 1740
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1681 ATCCTAACCATTGGGACTGGAATGGAGGAGAACCAACTTGTATGCCATTAATTTTATCCAT 1740

 1741 GCAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAAC 1800
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1741 GCAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTTCCAAC 1800

 1801 TTGTCCTTCCTTCCGAGGAATGGAGAAGCCATTCGAGAAGCAATGCATGGGGTTTTTCCTT 1860
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1801 TTGTCCTTCCTTCCGAGGAATGGAGAAGCCATTCGAGAAGCAATGCATGGGGTTTTTCCTT 1860

 1861 TACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGAAAACCTCCCTGTG 1920
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1861 TACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGAAAACCTCCCTGTG 1920

 1921 TATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGTGAAGATCTCATCTGGAATAAAGAC 1980
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1921 TATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGTGAAGATCTCATCTGGAATAAAGAC 1980

 1981 CCTGAGGGCCACTGAGAAGCTCTTACGTTATGCCCAAGACTCAAGGCACAGGAGGGAGAGAAA 2040
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1981 CCTGAGGGCCACTGAGAAGCTCTTACGTTATGCCCAAGACTCAAGGCACAGGAGGGAGAGAAA 2040
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 2041 GTCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGCCCTTGAGTATGCCCTT 2100
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2041 GTCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACGCCCTTGAGTATGCCCTT 2100

 2101 GTGAACGGGCATTGAAAAAACATATTATTGAGGATACTGAGGAAGTTAAACCAAAAA 2160
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2101 GTCAAGGGCATTGAAAAAACATATTATTGAGGATACTGAGGAAGTTAAACCAAAAA 2160

 2161 AAATATCCCGACCTTCAATATAATTGAAGGACCCCTGATGAATGAAAAATTGTT 2220
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2161 AAATATCCCGACCTTCAATATAATTGAAGGACCCCTGATGAATGAAAAATTGTT 2220

 2221 GGTGATCTTTTGGAGCTGGAAAAATGTTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTT 2280
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2221 GGTGATCTTTTGGAGCTGGAAAAATGTTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTT 2280

 2281 ATGAAGAGGCTGTTGGCCCACCTTTCATGGAAAAAGAAGAGAAACCAGA 2340
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2281 ATGAAGAGGCTGTTGGCCCACCTTTCATGGAAAAAGAAGAGAAACCAGA 2340

 2341 GTGCTTAACGGCACAGTAGAGAAGAAGGACCCTTACCAGGGCACCATCGTGCTGGCCACT 2400
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2341 GTCCTTAACGGCACAGTAGAGAAGAAGGACCCTTACCAGGGCACCATCGTGCTGGCCACT 2400

 2401 GTTAAAGGCGACGTGCACGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTT 2460
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2401 GTTAAAGGCGACGTGCACGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTT 2460

 2461 AATTTCCGAGTTATTGATTTTAGGAGTCATGACTCCATGTGATAAGACTGAAAGCTGCT 2520
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2461 AATTTCCGAGTTATTGATTTTAGGAGTCATGACTCCATGTGATAAGACTGAAAGCTGCT 2520

 2521 CTTGACCACAAAGCAGATAATAATTGGCCTGTCAGGACTCATCACTCCTTCCTGGATGAA 2580
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2521 CTTGACCACAAAGCAGATAATAATTGGCCTGTCAGAACTCATCACTCCTTCCTGGATGAA 2580

 2581 ATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGA 2640
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2581 ATGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGA 2640

 2641 GGAGCAACCACTTCAAAAACCCACACAGCAGTTAA 2675
      ||||||||||||||||||||||||||||||||||
 2641 GGAGCAACCACTTCAAAAACCCACACAGCAGTTAA 2675
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RESULT 7
ADR07169
ID   ADR07169 standard; cDNA; 4172 BP.
XX
AC   ADR07169;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Full length human cDNA useful for treating neurological disease Seq 675.
XX
KW   gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
KW   osteoporosis; neurological disease; Alzheimer's disease;
KW   Parkinson's disease; dementia; short memory; cancer;
KW   sense or motor function; emotional reaction; fear response; panic;
KW   osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW   tranquiliser.
XX
OS   Homo sapiens.
XX
PN   EP1447413-A2.
XX
PD   18-AUG-2004.
XX
PF   12-FEB-2004; 2004BP-00003145.
XX
PR   14-FEB-2003; 2003JP-00102207.
PR   09-MAY-2003; 2003JP-00131452.
XX
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PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI   Wakamatsu A, Ishii K, Nagai K, Irie R;
XX
DR   WPI; 2004-583265/57.
DR   P-PSDB; ADR09125.
XX
PT   New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT   Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS   Claim 1; SEQ ID NO 675; 2686pp; English.
XX
CC   This invention relates to novel, isolated full length human cDNA
CC   molecules and the encoded proteins thereof. Specifically, it refers to
CC   cDNA clones obtained by an oligo-capping method, where none of these
CC   clones are identical to any known human mRNAs. The present invention
CC   describes an immunoassay to identify agonists and antagonists, as well as
CC   antibodies, antisense molecules and siRNAs that can all be used to bind
CC   to and modulate expression of the cDNA molecules. As such, these
CC   molecules are useful for diagnostic markers or therapeutic targets for
CC   the various diseases or morbid states. In particular, they are useful in
CC   gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC   disease, Parkinson's disease, dementia, short memory and various cancers,
CC   as well as for maintaining equilibrium of sense or motor function, and
CC   for treating emotional reaction, fear response and panic. Accordingly,
CC   they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC   cytostatic and tranquiliser activities. This polynucleotide is a full
CC   length human cDNA sequence of the invention. NOTE: This sequence is not
CC   given in the sequence listing of the specification but can be obtained on
CC   CD-ROM from the European Patent Office, Vienna Sub-office.
XX
SQ   Sequence 4172 BP; 1175 A; 835 C; 980 G; 1182 T; 0 U; 0 Other;

Query Match   7.9%; Score 308; DB 13; Length 4172;
Best Local Similarity 99.5%; Pred. No. 9.2e-113;
Matches 408; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   3467 AGGCCTTTGAGAAGAGTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCA 3526
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1015 AGGCCTTTGAGAAGAGTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCA 1074

Qy   3527 GTGAGCAGCTGGACGTGCGAGACCTGCGAGAGGTTGCGGTACAAGGGCATCCGCCCGGCTC 3586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1075 GTGAGCAGCTGGACGTGCGAGACCTGCGAGAGGCTGCGGTACAAGGGCATCCGCCCGGCTC 1134

Qy   3587 CTGGCTACCCCGACCAGCCAGCGACCACCACCCAGGAGAGCTCACCATGTGGAGACTCGCAGACA 3646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1135 CTGGCTACCCCGACCAGCCAGCGACCACCACCCAGGAGAGCTCACCATGTGGAGACTTGCAGACA 1194

Qy   3647 TCGAGCAGTCACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAG 3706
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1195 TCGAGCAGTCACAGGCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAG 1254

Qy   3707 TCTCAGGCCCTCTACTTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGAAGATTTCCA 3766
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1255 TCTCAGGCCCTCTACTTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGAAGATTTCCA 1314

Qy   3767 AGGATCAGGTTGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAAT 3826
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1315 AGGATCAGGTTGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAAT 1374

Qy   3827 GGCTTGACCCCATTTTGGGATATGATACAGACTAACTTTTTTTTTTTT 3876
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1375 GGCTTGACCCCATTTTGGGATATGATACAGACTAACTTTTTTTTTTTT 1424

RESULT 8
AAV88164
ID   AAV88164 standard; cDNA; 305 BP.
XX
AC   AAV88164;
XX

DT   12-FEB-1999 (first entry)
XX
DE   EST clone GA64.
XX
KW   Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW   tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW   chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW   receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS   Homo sapiens.
XX
PN   WO9845437-A2.
XX
PD   15-OCT-1998.
XX
PF   10-APR-1998;   98WO-US006956.
XX
PR   10-APR-1997;   97US-00837312.
XX
PA   (GEMY) GENETICS INST INC.
XX
PI   Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI   Spaulding V, Agostino MJ;
XX
DR   WPI; 1999-070078/06.
XX
PT   New polynucleotides encoding human secreted proteins - derived from e.g.
PT   human blood, kidney, foetal lung, placenta, testes, brain, ovary,
PT   pituitary, retina and colon cDNA libraries.
XX
PS   Claim 1; Page 304; 641pp; English.
XX
CC   The present sequence represents an expressed sequence tag (EST), and is a
CC   polynucleotide of the invention. The polynucleotides of the invention are
CC   all secreted EST sequences isolated from a variety of human tissue
CC   sources. The EST sequences and proteins encoded by them are predicted to
CC   have useful biological activities which would make them suitable for
CC   treating, preventing or ameliorating medical conditions in humans and
CC   animals, although no supporting data is given. Suggested activities
CC   include nutritional activity, immune stimulating or suppressing activity,
CC   haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC   activity. The EST sequences are also stated to be useful for gene therapy
XX
SQ   Sequence 305 BP; 89 A; 63 C; 77 G; 76 T; 0 U; 0 Other;

Query Match   5.7%; Score 222; DB 2; Length 305;
Best Local Similarity 99.6%; Pred. No. 2.7e-78;
Matches 272; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   2751 GTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAGAAATATGAAGATAT 2810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22   GTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAGAAATATGAAGATAT 81

Qy   2811 TAGACAGGACCATTATGAGTCTCTCAAGGAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAG 2870
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82   TAGACAGGGCCATTATGAGTCTCTCAAGGAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAG 141

Qy   2871 AAAAGTGGTTCAAATGATTGGCTGTCTGAACCTGCTGAACCTCAGTGAAGCCCACGTTTAT 2930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   142 AAAAGTGGTTCCAAATGATTGGCTGTCTGAACCTGCTGAACCTCAGTGAAGCCCACGTTTAT 201

Qy   2931 TGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGAGCTGGTGGACTACATTGACTGGAA 2990
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   202 TGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAA 261

Qy   2991 GCCTTTCTTTGATGTCTGGCAGTCCGGGGCAA 3023
          ||||||||||||||||||||||||||||||||
Db   262 GCCTTTCTTTGATGTCTGGCAGTCCGGGGCAA 294

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RESULT 9
ADP49459
ID   ADP49459 standard; DNA; 80 BP.
XX
AC   ADP49459;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Oligonucleotide array related rat oligonucleotide probe No 75.
XX
KW   oligonucleotide array; orthologue; homology; expression distribution;
KW   change; gene-expression; rat; probe; ss.
XX
OS   Rattus norvegicus.
XX
PN   JP2004016070-A.
XX
PD   22-JAN-2004.
XX
PF   14-JUN-2002; 2002JP-00174208.
XX
PR   14-JUN-2002; 2002JP-00174208.
XX
PA   (HITA ) HITACHI LTD.
XX
DR   WPI; 2004-113862/12.
XX
PT   Oligonucleotide array, useful for measuring ortholog gene-expression
PT   distribution, comprising number of oligonucleotides derived from ortholog
PT   gene of different organism immobilized on support.
XX
PS   Disclosure; Page 16; 56pp; Japanese.
XX
CC   The invention relates to a novel oligonucleotide array comprising a
CC   number of oligonucleotides derived from an orthologue gene of a different
CC   organism or species immobilised on a support body. The oligonucleotide
CC   array has two sides comprising a gene derived from two different
CC   organisms, in which one side comprises a human gene. In the
CC   oligonucleotide array a base sequence differs in a different position on
CC   the support body. Each of the oligonucleotides is a partial sequence of
CC   the orthologue gene of the organism A and organism B. The sequence match
CC   degree of the organism species A and the organism species B is less than
CC   70%. The sequence homology of the genes other than the orthologue gene of
CC   the organism species A and the organism species B is the level-of-
CC   statistical-significance value, calculated using the homology searching
CC   algorithm; basic local alignment search tool (BLAST) and the value is 0.1
CC   or more. The found value or the calculated value of the melting-
CC   temperature of the variant genes other than the orthologue gene of the
CC   organism species A and the organism species B is 20 degrees C or more.
CC   The oligonucleotide array is useful for measuring expression distribution
CC   of the orthologue gene in different organisms. The method is useful for
CC   comparing expression change of the orthologue gene with respect to
CC   medical-agent administration and for comparing change of the function of
CC   the orthologue gene in different organisms. The oligonucleotide array has
CC   the ability to perform a measurement of gene-expression distribution of
CC   two or more types of organism simultaneously. The oligonucleotide array
CC   improves reliability of measurement. This polynucleotide sequence
CC   represents a probe of a rat gene for comparison against a human gene used
CC   in the oligonucleotide array of the invention.
XX
SQ   Sequence 80 BP; 19 A; 21 C; 19 G; 21 T; 0 U; 0 Other;

Query Match             1.1%;  Score 44;  DB 12;  Length 80;
Best Local Similarity   100.0%;  Pred. No. 3.9e-07;
Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2974 GACTACATTGACTGGAAGCCTTTCTTTGATGTCTGGCAGCTCCG 3017
           ||||||||||||||||||||||||||||||||||||||||||||
Db      1 GACTACATTGACTGGAAGCCTTTCTTTGATGTCTGGCAGCTCCG 44

RESULT 10
AAI29993
ID   AAI29993 standard; DNA; 31 BP.
XX
AC   AAI29993;
XX
DT   04-NOV-2004  (revised)
DT   18-OCT-2001  (first entry)
XX
DB   Human single nucleotide polymorphism (SNP) MTR 9.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       16
FT                   /tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO20016800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US007268.
XX
PR   07-MAR-2000; 2000US-0187510P.
PR   22-MAY-2000; 2000US-0206129P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M, Ireland JS, Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or severity
PT   of a particular phenotype or disorder (e.g. diabetes) associated with a
PT   particular genotype.
XX
PS   Claim 1; Page 62; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing
XX
CC   Revised record issued on 04-NOV-2004 : Correction to Feature Table Key
XX
SQ   Sequence 31 BP; 4 A; 4 C; 11 G; 12 T; 0 U; 0 Other;

Query Match            0.8%;  Score 31;  DB 4;  Length 31;
Best Local Similarity  100.0%;  Pred. No. 0.068;
Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1533 GTATGGAGCTGCTATGGTGGTCATGGCTTTT 1563
           |||||||||||||||||||||||||||||||
Db      1 GTATGGAGCTGCTATGGTGGTCATGGCTTTT 31

RESULT 11
AAI29989
ID   AAI29989 standard; DNA; 31 BP.
XX
AC   AAI29989;
XX
DT   04-NOV-2004  (revised)
DT   18-OCT-2001  (first entry)
XX
```

```
DE   Human single nucleotide polymorphism (SNP) MTR 5.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   variation        16
FT                    /*tag= a
FT                    /standard_name= "single nucleotide polymorphism"
XX
PN   WO20016800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US007268.
XX
PR   07-MAR-2000; 2000US-0187510P.
PR   22-MAY-2000; 2000US-0206129P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M, Ireland JS, Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or severity
PT   of a particular phenotype or disorder (e.g. diabetes) associated with a
PT   particular genotype.
XX
PS   Claim 1; Page 61; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI13314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing
CC   Revised record issued on 04-NOV-2004 : Correction to Feature Table Key
XX
SQ   Sequence 31 BP; 8 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match             0.8%;  Score 31;  DB 4;  Length 31;
Best Local Similarity  100.0%;  Pred. No. 0.068;
Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    359 GCAGCACTAGTATTGCCCAAGCTGACTATGG 389
          |||||||||||||||||||||||||||||||
Db      1 GCAGCACTAGTATTGCCCAAGCTGACTATGG 31

RESULT 12
AAI29985
ID   AAI29985 standard; DNA; 31 BP.
XX
AC   AAI29985;
XX
DT   04-NOV-2004  (revised)
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) MTR 1.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   variation        16
FT                    /*tag= a
FT                    /standard_name= "single nucleotide polymorphism"
XX
PN   WO20016800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US007268.
XX
PR   07-MAR-2000; 2000US-0187510P.
PR   22-MAY-2000; 2000US-0206129P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M, Ireland JS, Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or severity
PT   of a particular phenotype or disorder (e.g. diabetes) associated with a
PT   particular genotype.
XX
PS   Claim 1; Page 61; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI13314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing
CC   Revised record issued on 04-NOV-2004 : Correction to Feature Table Key
XX
SQ   Sequence 31 BP; 5 A; 11 C; 8 G; 7 T; 0 U; 0 Other;

Query Match             0.8%;  Score 31;  DB 4;  Length 31;
Best Local Similarity  100.0%;  Pred. No. 0.068;
Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3192 CATTCACCTGTACGCAGAGGCTGCTGTGCCC 3222
          |||||||||||||||||||||||||||||||
Db      1 CATTCACCTGTACGCAGAGGCTGCTGTGCCC 31

RESULT 13
AAI29988
ID   AAI29988 standard; DNA; 31 BP.
XX
AC   AAI29988;
XX
DT   04-NOV-2004  (revised)
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) MTR 4.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   variation        16
FT                    /*tag= a
FT                    /standard_name= "single nucleotide polymorphism"
XX
PN   WO20016800-A2.
XX
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```
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US007268.
XX
PR   07-MAR-2000; 2000US-0187510P.
PR   22-MAY-2000; 2000US-0206129P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M, Ireland JS, Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or severity
PT   of a particular phenotype or disorder (e.g. diabetes) associated with a
PT   particular genotype.
XX
PS   Claim 1; Page 61; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing
CC   Revised record issued on 04-NOV-2004 : Correction to Feature Table Key
XX
SQ   Sequence 31 BP; 11 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match     0.8%;  Score 31;  DB 4;  Length 31;
Best Local Similarity   100.0%;  Pred. No. 0.068;
Matches  31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   348 AAATACTTTAGCAGCACTAGTATTGCCCAA 378
         ||||||||||||||||||||||||||||||
Db     1 AAATACTTTAGCAGCACTAGTATTGCCCAA 31

RESULT 14
AAI29986
ID   AAI29986 standard; DNA; 31 BP.
XX
AC   AAI29986;
XX
DT   04-NOV-2004  (revised)
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) MTR 2.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   variation      16
FT                  /*tag= a
FT                  /standard_name= "single nucleotide polymorphism"
XX
PN   WO200166800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US007268.
XX
PR   07-MAR-2000; 2000US-0187510P.
PR   22-MAY-2000; 2000US-0206129P.
XX
```

```
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M, Ireland JS, Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or severity
PT   of a particular phenotype or disorder (e.g. diabetes) associated with a
PT   particular genotype.
XX
PS   Claim 1; Page 61; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing
CC   Revised record issued on 04-NOV-2004 : Correction to Feature Table Key
XX
SQ   Sequence 31 BP; 8 A; 5 C; 10 G; 8 T; 0 U; 0 Other;

Query Match     0.8%;  Score 31;  DB 4;  Length 31;
Best Local Similarity   100.0%;  Pred. No. 0.068;
Matches  31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   311 AGGAATACTTGCTGGCTGGGGCAGATATCAT 341
         |||||||||||||||||||||||||||||||
Db     1 AGGAATACTTGCTGGCTGGGGCAGATATCAT 31

RESULT 15
AAI29992
ID   AAI29992 standard; DNA; 31 BP.
XX
AC   AAI29992;
XX
DT   04-NOV-2004  (revised)
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) MTR 8.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   variation      16
FT                  /*tag= a
FT                  /standard_name= "single nucleotide polymorphism"
XX
PN   WO200166800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US007268.
XX
PR   07-MAR-2000; 2000US-0187510P.
PR   22-MAY-2000; 2000US-0206129P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M, Ireland JS, Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
```

Left column

```
PT   sites, useful in methods for predicting the presence, absence or severity
PT   of a particular phenotype or disorder (e.g. diabetes) associated with a
PT   particular genotype.
XX
PS   Claim 1; Page 61; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing
XX
CC   Revised record issued on 04-NOV-2004 : Correction to Feature Table Key
XX
SQ   Sequence 31 BP; 7 A; 8 C; 11 G; 5 T; 0 U; 0 Other;

Query Match             0.8%;  Score 31;  DB 4;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches  31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       3540 CGTCGCAGACCTGCGAAGGTTGCGGTACAAG 3570
              |||||||||||||||||||||||||||||||
Db          1 CGTCGCAGACCTGCGAAGGTTGCGGTACAAG 31

RESULT 16
AAI29987
ID   AAI29987 standard; DNA; 31 BP.
XX
AC   AAI29987;
XX
DT   04-NOV-2004  (revised)
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) MTR 3.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   variation      16
FT                  /*tag= a
FT                  /standard_name= "single nucleotide polymorphism"
XX
PN   WO20016800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US007268.
XX
PR   07-MAR-2000; 2000US-0187510P.
PR   22-MAY-2000; 2000US-0206129P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M, Ireland JS, Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or severity
PT   of a particular phenotype or disorder (e.g. diabetes) associated with a
PT   particular genotype.
XX
PS   Claim 1; Page 61; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
```

Right column

```
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing
XX
CC   Revised record issued on 04-NOV-2004 : Correction to Feature Table Key
XX
SQ   Sequence 31 BP; 11 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match             0.8%;  Score 31;  DB 4;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches  31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        324 GGCTGGGCAGATATCATTGAAACAAATACT 354
              ||||||||||||||||||||||||||||||
Db          1 GGCTGGGCAGATATCATTGAAACAAATACT 31

RESULT 17
AAI29990
ID   AAI29990 standard; DNA; 31 BP.
XX
AC   AAI29990;
XX
DT   04-NOV-2004  (revised)
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) MTR 6.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   variation      16
FT                  /*tag= a
FT                  /standard_name= "single nucleotide polymorphism"
XX
PN   WO20016800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US007268.
XX
PR   07-MAR-2000; 2000US-0187510P.
PR   22-MAY-2000; 2000US-0206129P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M, Ireland JS, Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or severity
PT   of a particular phenotype or disorder (e.g. diabetes) associated with a
PT   particular genotype.
XX
PS   Claim 1; Page 61; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
```

```
CC  testing
CC
XX  Revised record issued on 04-NOV-2004 : Correction to Feature Table Key
XX
SQ  Sequence 31 BP; 8 A; 3 C; 9 G; 11 T; 0 U; 0 Other;

Query Match        0.8%; Score 31; DB 4; Length 31;
Best Local Similarity   100.0%; Pred. No. 0.068;
Matches  31; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy     988 AAGGATTTTGCTATGGATGGCTTGGTCAATA 1018
           ||||||||||||||||||||||||||||||
Db       1 AAGGATTTTGCTATGGATGGCTTGGTCAATA 31


RESULT 18
AAI29991
ID  AAI29991 standard; DNA; 31 BP.
XX
AC  AAI29991;
XX
DT  04-NOV-2004 (revised)
DT  18-OCT-2001 (first entry)
XX
DE  Human single nucleotide polymorphism (SNP) MTR 7.
XX
KW  Human; resequence; genotype; disease; forensic; paternity testing;
KW  single nucleotide polymorphism; SNP; ss.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  variation       16
FT                  /*tag= a
FT                  /standard_name= "single nucleotide polymorphism"
XX
PN  WO20016800-A2.
XX
PD  13-SEP-2001.
XX
PF  07-MAR-2001; 2001WO-US007268.
XX
PR  07-MAR-2000; 2000US-0187510P.
PR  22-MAY-2000; 2000US-0206129P.
XX
PA  (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI  Cargill M, Ireland JS, Lander ES;
XX
DR  WPI; 2001-522952/57.
XX
PT  Nucleic acid molecules from the human genome which include polymorphic
PT  sites, useful in methods for predicting the presence, absence or severity
PT  of a particular phenotype or disorder (e.g. diabetes) associated with a
PT  particular genotype.
XX
PS  Claim 1; Page 61; 145pp; English.
XX
CC  The invention relates to the identification of nucleic acid molecules
CC  (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC  which can predispose individuals to disease. Various genes from a number
CC  of individuals were resequenced and single nucleotide polymorphisms
CC  (SNPs) in these genes discovered. The method is useful for predicting the
CC  presence, absence or severity of a particular phenotype or disorder (e.g.
CC  diabetes) associated with a particular genotype. The nucleic acids
CC  containing the polymorphic sites may be useful in forensics and paternity
CC  testing
CC
XX  Revised record issued on 04-NOV-2004 : Correction to Feature Table Key
XX
SQ  Sequence 31 BP; 7 A; 9 C; 11 G; 4 T; 0 U; 0 Other;

Query Match        0.8%; Score 31; DB 4; Length 31;
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```
Best Local Similarity   100.0%; Pred. No. 0.068;
Matches  31; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy    3525 CAGTGAGCAGTGGAGTCGCAGACCTGCGA 3555
           |||||||||||||||||||||||||||||
Db       1 CAGTGAGCAGTGGACGTCGCAGACCTGCGA 31


RESULT 19
AAV34083/c
ID  AAV34083 standard; DNA; 28 BP.
XX
AC  AAV34083;
XX
DT  01-MAR-1999 (first entry)
XX
DE  Methionine synthase primer 1758.
XX
KW  Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW  cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW  ss.
XX
OS  Synthetic.
XX
PN  CA2217153-A.
XX
PD  27-MAY-1998.
XX
PF  27-NOV-1997;    97CA-02217153.
XX
PR  27-NOV-1996;    96US-0031964P.
PR  20-JUN-1997;    97US-0050310P.
XX
PA  (MART-) MARTINEX R & D INC.
XX
PI  Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR  WPI; 1998-569373/49.
XX
PT  DNA encoding methionine synthase polypeptide - and corresponding
PT  polypeptide, cells, antibody and therapeutic methods.
XX
PS  Claim 49; Page 52; 64pp; English.
XX
CC  This is the nucleotide sequence of oligonucleotide 1758, a primer based
CC  on a highly conserved region found in the methionine synthases of
CC  different organisms. It corresponds to nucleotides 2432-2405 of the human
CC  methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC  (see AAV34064-104) based on such conserved regions are provided. These
CC  have been used for human and mouse methionine synthase cDNA cloning,
CC  chromosome mapping and in a claimed method for mutation detection.
CC  Mutations in the human methionine synthase gene are associated with
CC  hyperhomocysteinaemia. The invention relates to the diagnosis and
CC  treatment of patients at risk for methionine synthase deficiency, and
CC  associated altered risk for neural tube defects, cardiovascular disease
CC  and colon cancer. Claimed methods for detecting sequence variants involve
CC  SSCP or RFLP polymorphism analysis
XX
SQ  Sequence 28 BP; 10 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match        0.7%; Score 28; DB 2; Length 28;
Best Local Similarity   100.0%; Pred. No. 1.1;
Matches  28; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy    2468 GAGTTATTGATTTAGGAGTCATGACTCC 2495
           ||||||||||||||||||||||||||||
Db      28 GAGTTATTGATTTAGGAGTCATGACTCC 1


RESULT 20
ADO57182/c
ID  ADO57182 standard; DNA; 27 BP.
XX
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AC   AD057182;
XX
DT   15-JUL-2004   (first entry)
XX
DE   Human MTR gene PCR primer #30.
XX
KW   ss; PCR; primer; human; thrombosis; MTR.
XX
OS   Homo sapiens.
XX
PN   DE10237073-A1.
XX
PD   19-FEB-2004.
XX
PF   09-AUG-2002; 2002DE-01037073.
XX
PR   09-AUG-2002; 2002DE-01037073.
XX
PA   (OGHA-) OGHAM GMBH.
PI   Cullen P, Seedorf U;
XX
DR   WPI; 2004-215770/21.
XX
PT   Determining genetic disposition to thrombosis, by testing for presence of
PT   at least two allelic polymorphisms associated with increased risk,
PT   followed by multifactorial analysis of the results.
XX
PS   Example 1; SEQ ID NO 129; 59pp; German.
XX
CC   The invention relates to a method of determining the genetic
CC   predisposition of a subject for development of thrombosis which comprises
CC   examining at least 2 nucleic acid segments from the genome, followed by
CC   multifactorial analysis of the results. The nucleic acid segments can
CC   contain allelic polymorphisms whose presence is correlated with an
CC   increased risk of thrombosis. The method is used to detect polymorphisms,
CC   or combinations of them, associated with increased inherited risk of
CC   developing thrombosis. The method can detect the synergistic effects of
CC   allelic variants when present together, and requires only a single test
CC   kit (reducing time and costs). The present sequence represents a
CC   thrombosis predisposition PCR primer.
XX
SQ   Sequence 27 BP; 7 A; 6 C; 2 G; 12 T; 0 U; 0 Other;

Query Match             0.7%;  Score 27;  DB 12;  Length 27;
Best Local Similarity 100.0%;  Pred. No. 2.7;
Matches   27;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        2759 AAAATCTAAAGGATGAATACTTTGAGG 2785
               |||||||||||||||||||||||||||
Db          27 AAAATCTAAAGGATGAATACTTTGAGG 1

RESULT 21
AAV34086
ID   AAV34086 standard; DNA; 26 BP.
XX
AC   AAV34086;
XX
DT   01-MAR-1999   (first entry)
XX
DE   Methionine synthase primer 1772.
XX
KW   Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW   cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW   ss.
XX
OS   Synthetic.
XX
PN   CA2217153-A.
XX
PD   27-MAY-1998.
XX
PF   27-NOV-1997; 97CA-02217153.
XX
PR   27-NOV-1996; 96US-0031964P.
PR   20-JUN-1997; 97US-0050310P.
XX
PA   (MART-) MARTINEX R & D INC.
XX
PI   Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR   WPI; 1998-569373/49.
XX
PT   DNA encoding methionine synthase polypeptide - and corresponding
PT   polypeptide, cells, antibody and therapeutic methods.
XX
PS   Claim 49; Page 52; 64pp; English.
XX
CC   This is the nucleotide sequence of oligonucleotide 1772, a primer based
CC   on a highly conserved region found in the methionine synthases of
CC   different organisms. It corresponds to nucleotides 2359-2384 of the human
CC   methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC   (see AAV34064-104) based on such conserved regions are provided. These
CC   have been used for human and mouse methionine synthase cDNA cloning,
CC   chromosome mapping and in a claimed method for mutation detection.
CC   Mutations in the human methionine synthase gene are associated with
CC   hyperhomocysteinaemia. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease
CC   and colon cancer. Claimed methods for detecting sequence variants involve
CC   SSCP or RFLP polymorphism analysis
XX
SQ   Sequence 26 BP; 10 A; 2 C; 8 G; 6 T; 0 U; 0 Other;

Query Match             0.7%;  Score 26;  DB 2;  Length 26;
Best Local Similarity 100.0%;  Pred. No. 6.9;
Matches   26;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        2422 ATAGGCAAGAACATAGTTGGAGTAGT 2447
               ||||||||||||||||||||||||||
Db           1 ATAGGCAAGAACATAGTTGGAGTAGT 26

RESULT 22
AAV34073
ID   AAV34073 standard; DNA; 26 BP.
XX
AC   AAV34073;
XX
DT   01-MAR-1999   (first entry)
XX
DE   Methionine synthase primer 407A.
XX
KW   Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW   cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW   ss.
XX
OS   Synthetic.
XX
PN   CA2217153-A.
XX
PD   27-MAY-1998.
XX
PF   27-NOV-1997; 97CA-02217153.
XX
PR   27-NOV-1996; 96US-0031964P.
PR   20-JUN-1997; 97US-0050310P.
XX
PA   (MART-) MARTINEX R & D INC.
XX
PI   Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR   WPI; 1998-569373/49.
XX
PT   DNA encoding methionine synthase polypeptide - and corresponding
```

PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 51; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 407A, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 151-176 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,
CC chromosome mapping and in a claimed method for mutation detection.
CC Mutations in the human methionine synthase gene are associated with
CC hyperhomocysteinaemia. The invention relates to the diagnosis and
CC treatment of patients at risk for methionine synthase deficiency, and
CC associated altered risk for neural tube defects, cardiovascular disease
CC and colon cancer. Claimed methods for detecting sequence variants involve
CC SSCP or RFLP polymorphism analysis
XX
SQ Sequence 26 BP; 9 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match   0.7%;   Score 26; DB 2; Length 26;
Best Local Similarity   100.0%; Pred. No. 6.9;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 214 TTCCGAGGTCAGGAATTAAAGATCA 239
        |||||||||||||||||||||||||
Db   1 TTCCGAGGTCAGGAATTAAAGATCA 26

RESULT 23
AAV34091
ID AAV34091 standard; DNA; 26 BP.
XX
AC AAV34091;
XX
DT 01-MAR-1999 (first entry)
XX
DE Methionine synthase primer 1796.
XX
KW Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN CA2217153-A.
XX
PD 27-MAY-1998.
XX
PF 27-NOV-1997;   97CA-02217153.
XX
PR 27-NOV-1996;   96US-0031964P.
PR 20-JUN-1997;   97US-0050310P.
XX
PA (MART-) MARTINEX R & D INC.
XX
PI Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR WPI; 1998-569373/49.
XX
PT DNA encoding methionine synthase polypeptide - and corresponding
PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 52; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 1796, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 2727-2752 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,
CC chromosome mapping and in a claimed method for mutation detection.
CC Mutations in the human methionine synthase gene are associated with
CC hyperhomocysteinaemia. The invention relates to the diagnosis and
CC treatment of patients at risk for methionine synthase deficiency, and
CC associated altered risk for neural tube defects, cardiovascular disease
CC and colon cancer. Claimed methods for detecting sequence variants involve
CC SSCP or RFLP polymorphism analysis
XX
SQ Sequence 26 BP; 12 A; 2 C; 6 G; 6 T; 0 U; 0 Other;

Query Match   0.7%;   Score 26; DB 2; Length 26;
Best Local Similarity   100.0%; Pred. No. 6.9;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 2790 CATGGAAGAATATGAAGAGATATTAGAC 2815
         ||||||||||||||||||||||||||
Db   1 CATGGAAGAATATGAAGAGATATTAGAC 26

RESULT 24
AAV34095/c
ID AAV34095 standard; DNA; 26 BP.
XX
AC AAV34095;
XX
DT 01-MAR-1999 (first entry)
XX
DE Methionine synthase primer 1808.
XX
KW Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN CA2217153-A.
XX
PD 27-MAY-1998.
XX
PF 27-NOV-1997;   97CA-02217153.
XX
PR 27-NOV-1996;   96US-0031964P.
PR 20-JUN-1997;   97US-0050310P.
XX
PA (MART-) MARTINEX R & D INC.
XX
PI Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR WPI; 1998-569373/49.
XX
PT DNA encoding methionine synthase polypeptide - and corresponding
PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 52; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 1808, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 2458-2433 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,
CC chromosome mapping and in a claimed method for mutation detection.
CC Mutations in the human methionine synthase gene are associated with
CC hyperhomocysteinaemia. The invention relates to the diagnosis and
CC treatment of patients at risk for methionine synthase deficiency, and
CC associated altered risk for neural tube defects, cardiovascular disease
CC and colon cancer. Claimed methods for detecting sequence variants involve
CC SSCP or RFLP polymorphism analysis
XX
SQ Sequence 26 BP; 7 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

Query Match   0.7%;   Score 26; DB 2; Length 26;
Best Local Similarity   100.0%; Pred. No. 6.9;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2496 ATGTGATAAGATACTGAAAGCTGCTC 2521
           |||||||||||||||||||||||||||
Db   26 ATGTGATAAGATACTGAAAGCTGCTC 1

RESULT 25
AAV34101/c
ID AAV34101 standard; DNA; 26 BP.
XX
AC AAV34101;
XX
DT 01-MAR-1999 (first entry)
XX
DE Methionine synthase primer 2606B.
XX
KW Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN CA2217153-A.
XX
PD 27-MAY-1998.
XX
PF 27-NOV-1997; 97CA-02217153.
XX
PR 27-NOV-1996; 96US-0031964P.
PR 20-JUN-1997; 97US-0050310P.
XX
PA (MART-) MARTINEX R & D INC.
XX
PI Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR WPI; 1998-569373/49.
XX
PT DNA encoding methionine synthase polypeptide - and corresponding
PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 52; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 2606B, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 1139-1114 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,
CC chromosome mapping and in a claimed method for mutation detection.
CC Mutations in the human methionine synthase gene are associated with
CC hyperhomocysteinaemia. The invention relates to the diagnosis and
CC treatment of patients at risk for methionine synthase deficiency, and
CC associated altered risk for neural tube defects, cardiovascular disease
CC and colon cancer. Claimed methods for detecting sequence variants involve
CC SSCP or RFLP polymorphism analysis
XX
SQ Sequence 26 BP; 8 A; 8 C; 3 G; 7 T; 0 U; 0 Other;

Qy   1177 GTTAACATTGGAGAGCGCTGTAATGT 1202
           ||||||||||||||||||||||||||
Db   26 GTTAACATTGGAGAGCGCTGTAATGT 1

Query Match   0.7%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 26
ABZ36026
ID ABZ36026 standard; cDNA; 1008 BP.
XX
AC ABZ36026;
XX
DT 10-FBB-2003 (first entry)

XX
DE Human secretory polynucleotide SPTM SEQ ID NO 190.
XX
KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;
KW anti-inflammatory; immunosuppressive; neuroprotective; nootropic;
KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
KW antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
KW secretory polynucleotide; secretory protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200283876-A2.
XX
PD 24-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-US009921.
XX
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-075543/07.
DR P-PSDB; ABP75581.
XX
PT New human secretory proteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
PT cancers.
XX
PS Claim 1; SEQ ID NO 190; 458pp + Sequence Listing; English.
XX
CC The invention relates to a secretory polynucleotide (designated sptm)
CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a
CC naturally occurring polynucleotide sequence at least 90 % identical to
CC the polynucleotide sequence, or cancers including adenocarcinoma,
CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
CC treating, preventing or diagnosing a disease or condition associated with
CC the expression of functional SPTM. These are particularly useful for
CC diagnosing, treating or preventing autoimmune/inflammatory disorders
CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
CC breast, cervix or prostate). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1008 BP; 282 A; 229 C; 234 G; 263 T; 0 U; 0 Other;

Query Match   0.7%; Score 26; DB 8; Length 1008;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3862 CTTTTTTTTTTTTTTTTTGCCTTTTTT 3887

Db   211 |||||||||||||||||||||||||| 236
          CTTTTTTTTTTTTTTTTGCCTTTTTT

RESULT 27
AAV34097
ID AAV34097 standard; DNA; 25 BP.
XX
AC AAV34097;
XX
DT 01-MAR-1999 (first entry)
XX
DE Methionine synthase primer 1828.
XX
KW Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN CA2217153-A.
XX
PD 27-MAY-1998.
XX
PF 27-NOV-1997; 97CA-02217153.
XX
PR 27-NOV-1996; 96US-0031964P.
PR 20-JUN-1997; 97US-0050310P.
XX
PA (MART-) MARTINEX R & D INC.
XX
PI Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR WPI; 1998-569373/49.
XX
PT DNA encoding methionine synthase polypeptide - and corresponding
PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 52; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 1828, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 1125-1149 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,
CC chromosome mapping and in a claimed method for mutation detection.
CC Mutations in the human methionine synthase gene are associated with
CC hyperhomocysteinaemia. The invention relates to the diagnosis and
CC treatment of patients at risk for methionine synthase deficiency, and
CC associated altered risk for neural tube defects, cardiovascular disease
CC and colon cancer. Claimed methods for detecting sequence variants involve
CC SSCP or RFLP polymorphism analysis
XX
SQ Sequence 25 BP; 7 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match   0.6%; Score 25; DB 2; Length 25;
Best Local Similarity   100.0%; Pred. No. 17;
Matches   25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1188 AGAGCGCTGTAATGTTGCAGGATCA 1212
          |||||||||||||||||||||||||
Db   1 AGAGCGCTGTAATGTTGCAGGATCA 25

RESULT 28
AAV34099/c
ID AAV34099 standard; DNA; 25 BP.
XX
AC AAV34099;
XX
DT 01-MAR-1999 (first entry)
XX

DE Methionine synthase primer 1907C.
XX
KW Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN CA2217153-A.
XX
PD 27-MAY-1998.
XX
PF 27-NOV-1997; 97CA-02217153.
XX
PR 27-NOV-1996; 96US-0031964P.
PR 20-JUN-1997; 97US-0050310P.
XX
PA (MART-) MARTINEX R & D INC.
XX
PI Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR WPI; 1998-569373/49.
XX
PT DNA encoding methionine synthase polypeptide - and corresponding
PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 52; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 1907C, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 1464-1488 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,
CC chromosome mapping and in a claimed method for mutation detection.
CC Mutations in the human methionine synthase gene are associated with
CC hyperhomocysteinaemia. The invention relates to the diagnosis and
CC treatment of patients at risk for methionine synthase deficiency, and
CC associated altered risk for neural tube defects, cardiovascular disease
CC and colon cancer. Claimed methods for detecting sequence variants involve
CC SSCP or RFLP polymorphism analysis
XX
SQ Sequence 25 BP; 8 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match   0.6%; Score 25; DB 2; Length 25;
Best Local Similarity   100.0%; Pred. No. 17;
Matches   25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1117 GAAGGACATATGTTACTGTCTGGTC 1141
          |||||||||||||||||||||||||
Db   25 GAAGGACATATGTTACTGTCTGGTC 1

RESULT 29
AAV34098/c
ID AAV34098 standard; DNA; 25 BP.
XX
AC AAV34098;
XX
DT 01-MAR-1999 (first entry)
XX
DE Methionine synthase primer 1907B.
XX
KW Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN CA2217153-A.
XX
PD 27-MAY-1998.
XX

PF 27-NOV-1997; 97CA-02217153.
XX
PR 27-NOV-1996; 96US-0031964P.
PR 20-JUN-1997; 97US-0050310P.
XX
PA (MART-) MARTINEX R & D INC.
XX
PI Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR WPI; 1998-569373/49.
XX
PT DNA encoding methionine synthase polypeptide - and corresponding
PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 52; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 1907B, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 2057-2033 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,
CC chromosome mapping and in a claimed method for mutation detection.
CC Mutations in the human methionine synthase gene are associated with
CC hyperhomocysteinaemia. The invention relates to the diagnosis and
CC treatment of patients at risk for methionine synthase deficiency, and
CC associated altered risk for neural tube defects, cardiovascular disease
CC and colon cancer. Claimed methods for detecting sequence variants involve
CC SSCP or RFLP polymorphism analysis
XX
SQ Sequence 25 BP; 5 A; 6 C; 5 G; 9 T; 0 U; 0 Other;

Query Match   0.6%;   Score 25;   DB 2;   Length 25;
Best Local Similarity   100.0%;   Pred. No. 17;
Matches   25;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 2096 CCCTTGTGAAGGGCATTGAAAAACA 2120
         |||||||||||||||||||||||||
Db   25 CCCTTGTGAAGGGCATTGAAAAACA 1

RESULT 30
AAV34100/c
ID AAV34100 standard; DNA; 25 BP.
XX
AC AAV34100;
XX
DT 01-MAR-1999 (first entry)
XX
DE Methionine synthase primer 2606A.
XX
KW Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN CA2217153-A.
XX
PD 27-MAY-1998.
XX
PF 27-NOV-1997; 97CA-02217153.
XX
PR 27-NOV-1996; 96US-0031964P.
PR 20-JUN-1997; 97US-0050310P.
XX
PA (MART-) MARTINEX R & D INC.
XX
PI Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR WPI; 1998-569373/49.
XX
PT DNA encoding methionine synthase polypeptide - and corresponding
PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 52; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 2606A, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 1078-1054 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,
CC chromosome mapping and in a claimed method for mutation detection.
CC Mutations in the human methionine synthase gene are associated with
CC hyperhomocysteinaemia. The invention relates to the diagnosis and
CC treatment of patients at risk for methionine synthase deficiency, and
CC associated altered risk for neural tube defects, cardiovascular disease
CC and colon cancer. Claimed methods for detecting sequence variants involve
CC SSCP or RFLP polymorphism analysis
XX
SQ Sequence 25 BP; 8 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match   0.6%;   Score 25;   DB 2;   Length 25;
Best Local Similarity   100.0%;   Pred. No. 17;
Matches   25;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 1117 GAAGGACATATGTTACTGTCTGGTC 1141
         |||||||||||||||||||||||||
Db   25 GAAGGACATATGTTACTGTCTGGTC 1

RESULT 31
AAV34096/c
ID AAV34096 standard; DNA; 25 BP.
XX
AC AAV34096;
XX
DT 01-MAR-1999 (first entry)
XX
DE Methionine synthase primer 1827.
XX
KW Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN CA2217153-A.
XX
PD 27-MAY-1998.
XX
PF 27-NOV-1997; 97CA-02217153.
XX
PR 27-NOV-1996; 96US-0031964P.
PR 20-JUN-1997; 97US-0050310P.
XX
PA (MART-) MARTINEX R & D INC.
XX
PI Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR WPI; 1998-569373/49.
XX
PT DNA encoding methionine synthase polypeptide - and corresponding
PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 52; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 1827, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 1657-1633 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,
CC chromosome mapping and in a claimed method for mutation detection.
CC Mutations in the human methionine synthase gene are associated with

CC   hyperhomocysteinaemia. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease
CC   and colon cancer. Claimed methods for detecting sequence variants involve
CC   SSCP or RFLP polymorphism analysis
XX
SQ   Sequence 25 BP; 5 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match   0.6%; Score 25; DB 2; Length 25;
Best Local Similarity   100.0%; Pred. No. 17;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1696 ACTGGAATGAGGAGGAACACAACTTGT 1720
             |||||||||||||||||||||||||||
Db   25 ACTGGAATGAGGAGGAACACAACTTGT 1

RESULT 32
AAV34103/c
ID   AAV34103 standard; DNA; 25 BP.
XX
AC   AAV34103;
XX
DT   01-MAR-1999 (first entry)
XX
DE   Methionine synthase primer 2706B.
XX
KW   Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW   cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW   ss.
XX
OS   Synthetic.
XX
PN   CA2217153-A.
XX
PD   27-MAY-1998.
XX
PF   27-NOV-1997;   97CA-02217153.
XX
PR   27-NOV-1996;   96US-0031964P.
PR   20-JUN-1997;   97US-0050310P.
XX
PA   (MART-) MARTINEX R & D INC.
XX
PI   Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR   WPI; 1998-569373/49.
XX
PT   DNA encoding methionine synthase polypeptide - and corresponding
PT   polypeptide, cells, antibody and therapeutic methods.
XX
PS   Claim 49; Page 52; 64pp; English.
XX
CC   This is the nucleotide sequence of oligonucleotide 2706B, a primer based
CC   on a highly conserved region found in the methionine synthases of
CC   different organisms. It corresponds to nucleotides 3749-3725 of the human
CC   methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC   (see AAV34064-104) based on such conserved regions are provided. These
CC   have been used for human and mouse methionine synthase cDNA cloning,
CC   chromosome mapping and in a claimed method for mutation detection.
CC   Mutations in the human methionine synthase gene are associated with
CC   hyperhomocysteinaemia. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease
CC   and colon cancer. Claimed methods for detecting sequence variants involve
CC   SSCP or RFLP polymorphism analysis
XX
SQ   Sequence 25 BP; 6 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match   0.6%; Score 25; DB 2; Length 25;
Best Local Similarity   100.0%; Pred. No. 17;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3788 CATTGAGGAAGAACATATCTGTGGC 3812
             |||||||||||||||||||||||||
Db   25 CATTGAGGAAGAACATATCTGTGGC 1

RESULT 33
AAV34087/c
ID   AAV34087 standard; DNA; 25 BP.
XX
AC   AAV34087;
XX
DT   01-MAR-1999 (first entry)
XX
DE   Methionine synthase primer 1773.
XX
KW   Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW   cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW   ss.
XX
OS   Synthetic.
XX
PN   CA2217153-A.
XX
PD   27-MAY-1998.
XX
PF   27-NOV-1997;   97CA-02217153.
XX
PR   27-NOV-1996;   96US-0031964P.
PR   20-JUN-1997;   97US-0050310P.
XX
PA   (MART-) MARTINEX R & D INC.
XX
PI   Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR   WPI; 1998-569373/49.
XX
PT   DNA encoding methionine synthase polypeptide - and corresponding
PT   polypeptide, cells, antibody and therapeutic methods.
XX
PS   Claim 49; Page 52; 64pp; English.
XX
CC   This is the nucleotide sequence of oligonucleotide 1773, a primer based
CC   on a highly conserved region found in the methionine synthases of
CC   different organisms. It corresponds to nucleotides 2698-2674 of the human
CC   methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC   (see AAV34064-104) based on such conserved regions are provided. These
CC   have been used for human and mouse methionine synthase cDNA cloning,
CC   chromosome mapping and in a claimed method for mutation detection.
CC   Mutations in the human methionine synthase gene are associated with
CC   hyperhomocysteinaemia. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease
CC   and colon cancer. Claimed methods for detecting sequence variants involve
CC   SSCP or RFLP polymorphism analysis
XX
SQ   Sequence 25 BP; 8 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match   0.6%; Score 25; DB 2; Length 25;
Best Local Similarity   100.0%; Pred. No. 17;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2737 GTGTGTTCCCAGCTGTTAGATGAAA 2761
             |||||||||||||||||||||||||
Db   25 GTGTGTTCCCAGCTGTTAGATGAAA 1

RESULT 34
AAV34077
ID   AAV34077 standard; DNA; 25 BP.
XX
AC   AAV34077;
XX
DT   01-MAR-1999 (first entry)

```
DE   Methionine synthase primer 1406D.
XX
KW   Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW   cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW   ss.
XX
OS   Synthetic.
XX
PN   CA2217153-A.
XX
PD   27-MAY-1998.
XX
PF   27-NOV-1997;   97CA-02217153.
XX
PR   27-NOV-1996;   96US-0031964P.
PR   20-JUN-1997;   97US-0050310P.
XX
PA   (MART-) MARTINEX R & D INC.
XX
PI   Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR   WPI; 1998-569373/49.
XX
PT   DNA encoding methionine synthase polypeptide - and corresponding
PT   polypeptide, cells, antibody and therapeutic methods.
XX
PS   Claim 49; Page 51; 64pp; English.
XX
CC   This is the nucleotide sequence of oligonucleotide 1406D, a primer based
CC   on a highly conserved region found in the methionine synthases of
CC   different organisms. It corresponds to nucleotides 2170-2194 of the human
CC   methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC   (see AAV34064-104) based on such conserved regions are provided. These
CC   have been used for human and mouse methionine synthase cDNA cloning,
CC   chromosome mapping and in a claimed method for mutation detection.
CC   Mutations in the human methionine synthase gene are associated with
CC   hyperhomocysteinaemia. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease
CC   and colon cancer. Claimed methods for detecting sequence variants involve
CC   SSCP or RFLP polymorphism analysis
XX
SQ   Sequence 25 BP; 7 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match             0.6%;  Score 25;  DB 2;  Length 25;
Best Local Similarity  100.0%;            Pred. No. 17;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   2233 GGAGCTGGAAAAATGTTTCTACCTC 2257
          |||||||||||||||||||||||||
Db      1 GGAGCTGGAAAAATGTTTCTACCTC 25

RESULT 35
AAV34079/c
ID   AAV34079 standard; DNA; 25 BP.
XX
AC   AAV34079;
XX
DT   01-MAR-1999  (first entry)
XX
DE   Methionine synthase primer 1707A.
XX
KW   Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW   cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW   ss.
XX
OS   Synthetic.
XX
PN   CA2217153-A.
XX
PD   27-MAY-1998.
XX
PF   27-NOV-1997;   97CA-02217153.
XX
PR   27-NOV-1996;   96US-0031964P.
PR   20-JUN-1997;   97US-0050310P.
XX
PA   (MART-) MARTINEX R & D INC.
XX
PI   Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR   WPI; 1998-569373/49.
XX
PT   DNA encoding methionine synthase polypeptide - and corresponding
PT   polypeptide, cells, antibody and therapeutic methods.
XX
PS   Claim 49; Page 51; 64pp; English.
XX
CC   This is the nucleotide sequence of oligonucleotide 1707A, a primer based
CC   on a highly conserved region found in the methionine synthases of
CC   different organisms. It corresponds to nucleotides 2129-2105 of the human
CC   methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC   (see AAV34064-104) based on such conserved regions are provided. These
CC   have been used for human and mouse methionine synthase cDNA cloning,
CC   chromosome mapping and in a claimed method for mutation detection.
CC   Mutations in the human methionine synthase gene are associated with
CC   hyperhomocysteinaemia. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease
CC   and colon cancer. Claimed methods for detecting sequence variants involve
CC   SSCP or RFLP polymorphism analysis
XX
SQ   Sequence 25 BP; 6 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match             0.6%;  Score 25;  DB 2;  Length 25;
Best Local Similarity  100.0%;            Pred. No. 17;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   2168 CCCGACCTCTCAATATAATTGAAGG 2192
          |||||||||||||||||||||||||
Db     25 CCCGACCTCTCAATATAATTGAAGG 1

RESULT 36
ABV61053
ID   ABV61053 standard; cDNA; 237 BP.
XX
AC   ABV61053;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 61044.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005171.
XX
PR   17-FEB-2000; 2000US-0183319P.
PR   16-MAR-2000; 2000US-0189862P.
PR   25-MAY-2000; 2000US-0207454P.
PR   09-JUN-2000; 2000US-0211314P.
PR   18-JUL-2000; 2000US-0219007P.
PR   13-DEC-2000; 2000US-0255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R, Endege WO, Monahan JE;
```

```
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS   Claim 1; Page 11601; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for: (a) assessing whether
CC   a patient is afflicted with prostate cancer; (b) monitoring the
CC   progression of prostate cancer in a patient; (c) assessing the efficacy
CC   of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC   the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC   determining whether prostate cancer has metastasized in a patient; (h)
CC   assessing the aggressiveness or indolence of prostate cancer in a patient
CC   ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
XX
SQ   Sequence 237 BP; 49 A; 45 C; 43 G; 100 T; 0 U; 0 Other;

Query Match        0.6%;  Score 25; DB 5; Length 237;
Best Local Similarity 100.0%;  Pred. No. 14;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   3863  TTTTTTTTTTTTTTTGCCTTTTTT  3887
           ||||||||||||||||||||||||
Db     10  TTTTTTTTTTTTTTTGCCTTTTTT  34

RESULT 37
ABL86554/c
ID   ABL86554 standard; cDNA; 296 BP.
XX
AC   ABL86554;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human ovarian cancer related cDNA clone SEQ ID NO:9532.
XX
KW   Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192581-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US017756.
XX
PR   26-MAY-2000; 2000US-0207484P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Algate PA, Harlocker SL, Jones R;
XX
DR   WPI; 2002-122075/16.
XX
PT   Composition for therapy and diagnosis of ovarian cancer comprising
PT   polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT   polypeptide, antibody specific to polypeptide or T cell expressing
PT   polypeptide.
XX
PS   Claim 1; SEQ ID NO 9532; 489pp; English.
XX
CC   The present invention describes a composition (I) comprising: carriers
CC   and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC   polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
CC   from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
CC   (III) encoding (II) having a sequence (S2), a T cell population of (III),


CC   or antigen presenting cells that express (II). (I) has cytostatic
CC   activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
CC   detecting ovarian cancer in a patient's biological sample preferably
CC   serum or ovarian tissue. The method comprises contacting a biological
CC   sample from a patient with (IV), detecting the amount of polynucleotide
CC   hybridising to (IV) and comparing the amount to a predetermined cutoff
CC   value and thereby detecting ovarian cancer in the patient, where the
CC   amount of polynucleotide hybridising to (IV) is detected preferably by
CC   polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
CC   useful for stimulating and/or expanding T cells specific for an ovarian
CC   tumour protein comprising contacting T cells with (III) or (II). (III) is
CC   useful in design and preparation of ribozyme molecules for inhibiting
CC   expression of the tumour polypeptides and proteins in tumour cells; and
CC   to isolate a full length gene from a suitable library e.g., a tumour cDNA
CC   library using well known techniques
XX
SQ   Sequence 296 BP; 132 A; 65 C; 53 G; 46 T; 0 U; 0 Other;

Query Match        0.6%;  Score 25; DB 6; Length 296;
Best Local Similarity 100.0%;  Pred. No. 13;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   3863  TTTTTTTTTTTTTTTGCCTTTTTT  3887
           ||||||||||||||||||||||||
Db    288  TTTTTTTTTTTTTTTGCCTTTTTT  264

RESULT 38
ACN52851/c
ID   ACN52851 standard; cDNA; 433 BP.
XX
AC   ACN52851;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-F10, SEQ:7632.
XX
KW   Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium;
KW   variety Nucotton33B; library LIB3828; molecular tag; molecular marker;
KW   genetic mapping; molecular mapping; seed germination; plant growth;
KW   plant quality; plant yield; plant breeding; tissue printing; ss.
XX
OS   Gossypium hirsutum.
XX
XX   US2004123340-A1.
PN
XX
PD   24-JUN-2004.
XX
PF   12-DEC-2001; 2001US-00021323.
PR   14-DEC-2000; 2000US-0255619P.
XX
PA   (DEIK/)  DEIKMAN J.
PA   (FENG/)  FENG P C C.
PA   (FINC/)  FINCHER K L.
PA   (ZIEG/)  ZIEGLER T E.
XX
PI   Deikman J, Feng PCC, Fincher KL, Ziegler TE;
XX
DR   WPI; 2004-479808/45.
XX
PT   New isolated nucleic acid molecule that encodes a plant protein or its
PT   fragment, useful for isolating a variety of agronomically significant
PT   genes associated with plant growth, quality or yield, and as molecular
PT   tags to map genes.
XX
PS   Claim 1; SEQ ID NO 7632; 34pp; English.
XX
CC   The invention relates to 17880 cotton expressed sequence tags (ESTs)
CC   ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
CC   from primed or non-primed seeds from variety DP50B, mature seeds from
CC   variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
CC   tissue, developing fibres, carpel walls and septa from variety
```

CC   Nucotton33B. The invention also relates to substantially purified
CC   proteins or their fragments encoded by nucleic acid molecules of the
CC   invention, and to transformed plants having a nucleic acid construct
CC   comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC   molecular tags to isolate genetic regions, to isolate genes, to map
CC   genes, to determine gene function and to determining whether genes are
CC   members of a particular gene family. The nucleic acid molecules may be
CC   used for isolating a variety of agronomically significant genes
CC   associated with plant growth, quality, yield, and could also serve as
CC   links in metabolic and catabolic pathways. The nucleic acid molecules are
CC   also useful for identifying genes important in initiating and maintaining
CC   seed germination or that may be used to mitigate stresses encountered
CC   during seed germination. The ESTs additionally enable the acquisition of
CC   promoters and cis-regulatory elements which will be useful to express
CC   agronomically significant genes in these tissues and/or other tissues,
CC   and also permits the acquisition of molecular markers useful in breeding
CC   schemes, genetic and molecular mapping, and in cloning of agronomically
CC   significant genes. The nucleic acid molecules are further useful for
CC   detecting the expression level or pattern of a protein or mRNA and for
CC   detecting the presence or quantity of a protein by tissue printing. The
CC   present sequence represents a specifically claimed EST isolated from a
CC   cotton variety Nucotton33B androecium tissue cDNA library (LIB3828). The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from the US
CC   patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
XX
SQ   Sequence 433 BP; 254 A; 58 C; 101 G; 20 T; 0 U; 0 Other;

Query Match   0.6%;   Score 25;   DB 13;   Length 433;
Best Local Similarity   100.0%;   Pred. No. 13;
Matches   25;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3863   TTTTTTTTTTTTTTTTTTGCCTTTTT   3887
            ||||||||||||||||||||||||||
Db   188   TTTTTTTTTTTTTTTTTTGCCTTTTT   164

RESULT 39
ACN52668/c
ID   ACN52668 standard; cDNA; 475 BP.
XX
AC   ACN52668;
XX
DT   02-DEC-2004 (first entry)
XX
DE   Cotton androecium tissue EST Clone ID: LIB3828-017-Q1-N6-A10, SEQ:7449.
XX
KW   Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium;
KW   variety Nucotton33B; library LIB3828; molecular marker;
KW   genetic mapping; molecular mapping; seed germination; plant growth;
KW   plant quality; plant yield; plant breeding; tissue printing; ss.
XX
OS   Gossypium hirsutum.
XX
PN   US2004123340-A1.
XX
PD   24-JUN-2004.
XX
PF   12-DEC-2001; 2001US-00021323.
XX
PR   14-DEC-2000; 2000US-0255619P.
XX
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
XX
PI   Deikman J, Feng PCC, Fincher KL, Ziegler TE;
XX
DR   WPI; 2004-479808/45.
XX
PT   New isolated nucleic acid molecule that encodes a plant protein or its
PT   fragment, useful for isolating a variety of agronomically significant

---

PT   genes associated with plant growth, quality or yield, and as molecular
PT   tags to map genes.
XX
PS   Claim 1; SEQ ID NO 7449; 34pp; English.
XX
CC   The invention relates to 17880 cotton expressed sequence tags (ESTs;
CC   ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
CC   from primed or non-primed seeds from variety DP50B, mature seeds from
CC   variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
CC   tissue, developing fibres, carpel walls and septa from variety
CC   Nucotton33B. The invention also relates to substantially purified
CC   proteins or their fragments encoded by nucleic acid molecules of the
CC   invention, and to transformed plants having a nucleic acid construct
CC   comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC   molecular tags to isolate genetic regions, to isolate genes, to map
CC   genes, to determine gene function and to determining whether genes are
CC   members of a particular gene family. The nucleic acid molecules may be
CC   used for isolating a variety of agronomically significant genes
CC   associated with plant growth, quality, yield, and could also serve as
CC   links in metabolic and catabolic pathways. The nucleic acid molecules are
CC   also useful for identifying genes important in initiating and maintaining
CC   seed germination or that may be used to mitigate stresses encountered
CC   during seed germination. The ESTs additionally enable the acquisition of
CC   promoters and cis-regulatory elements which will be useful to express
CC   agronomically significant genes in these tissues and/or other tissues,
CC   and also permits the acquisition of molecular markers useful in breeding
CC   schemes, genetic and molecular mapping, and in cloning of agronomically
CC   significant genes. The nucleic acid molecules are further useful for
CC   detecting the expression level or pattern of a protein or mRNA and for
CC   detecting the presence or quantity of a protein by tissue printing. The
CC   present sequence represents a specifically claimed EST isolated from a
CC   cotton variety Nucotton33B androecium tissue cDNA library (LIB3828). The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from the US
CC   patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
XX
SQ   Sequence 475 BP; 217 A; 38 C; 201 G; 19 T; 0 U; 0 Other;

Query Match   0.6%;   Score 25;   DB 13;   Length 475;
Best Local Similarity   100.0%;   Pred. No. 13;
Matches   25;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3863   TTTTTTTTTTTTTTTTTTGCCTTTTT   3887
            ||||||||||||||||||||||||||
Db   235   TTTTTTTTTTTTTTTTTTGCCTTTTT   211

RESULT 40
AAH03248
ID   AAH03248 standard; cDNA; 789 BP.
XX
AC   AAH03248;
XX
DT   26-JUN-2001 (first entry)
XX
DE   Human cDNA clone (5'-primer) SEQ ID NO:83.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-00116126.
XX
PR   29-JUL-1999;   99JP-00248036.
PR   27-AUG-1999;   99JP-00300253.
PR   11-JAN-2000;   2000JP-00118776.
PR   02-MAY-2000;   2000JP-00183767.
PR   09-JUN-2000;   2000JP-0241899.
XX

PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 1; SEQ ID NO 83; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 789 BP; 237 A; 145 C; 145 G; 258 T; 0 U; 4 Other;
XX

Query Match   0.6%; Score 25; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 12;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 3862 CTTTTTTTTTTTTTTTGCCTTTTT 3886
         |||||||||||||||||||||||||
Db 757 CTTTTTTTTTTTTTTTTGCCTTTTT 781

RESULT 41
AAA61270/c
ID AAA61270 standard; DNA; 1180 BP.
XX
AC AAA61270;
XX
DT 18-OCT-2000 (first entry)
XX
DE Human secreted protein gene 11 clone HFPBY77.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; AIDS; autoimmune disorder; allergy;
KW cardiovascular; viral; bacterial; fungal infection; immunosuppressive;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200029422-A1.
XX
PD 25-MAY-2000.
XX
PF 09-NOV-1999; 99WO-US026409.
XX
PR 12-NOV-1998; 98US-0108207P.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Ruben SM, Rosen CA, Ebner R, Florence KA, Young PE;
PI Birse CE, Carter KC, Komatsoulis G;
XX
DR WPI; 2000-387729/33.
XX
PT Novel human secreted proteins useful for diagnosing, preventing, treating
PT and ameliorating a medical condition e.g. cardiovascular disease.
XX
PS Claim 1; Page 234-235; 295pp; English.
XX
CC The present sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number and the clone it was derived from
CC are given in the descriptor line. The invention relates to 31 novel genes
CC and their fragments (nucleic acid sequences: AAA61260-A61293; amino acid
CC sequences AAB12301-B12371) which are useful for preventing, treating or
CC ameliorating medical conditions e.g. by protein or gene therapy. Also
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 31 polynucleotides, based on which tissues they are most highly expressed
CC in and include products for the diagnosis or treatment of cancer,
CC tumours, AIDS, autoimmune disorders, allergy, cardiovascular disorders,
CC viral, bacterial and fungal infection. The genes are used to generate
CC fusion proteins by linking to the gene a human immunoglobulin portion
CC (AAA61251) for increasing stability of the fused protein as compared to
CC the secreted protein only
XX
SQ Sequence 1180 BP; 308 A; 290 C; 335 G; 247 T; 0 U; 0 Other;
XX

Query Match   0.6%; Score 25; DB 3; Length 1180;
Best Local Similarity 100.0%; Pred. No. 12;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 3863 TTTTTTTTTTTTTTTTGCCTTTTT 3887
         ||||||||||||||||||||||||
Db 1167 TTTTTTTTTTTTTTTTGCCTTTTT 1143

RESULT 42
ABX10897/c
ID ABX10897 standard; DNA; 2050 BP.
XX
AC ABX10897;
XX
DT 24-APR-2003 (first entry)
XX
DE DNA encoding human orphan chemokine receptor RDC1.
XX
KW Human; neokine family; NEOKINE-1; non-NEOKINE chemokine; chemokine;
KW proliferative disease; cancer; epithelia cancer; liver cancer;
KW secretory gland cancer; bladder cancer; reproductive tract cancer;
KW central nervous system cancer; connective tissue cancer; inflammation;
KW psoriasis; immune rejection; skin graft; kidney transplant; stroke;
KW ischaemia; viral infection; orphan chemokine receptor; RDC1; gene; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   91..1179
FT   /tag= a
FT   /product= "RDC-1"
FT   /note= "Orphan chemokine receptor"
XX
PN US2002166133-A1.
XX
PD 07-NOV-2002.
XX
PF 27-AUG-2001; 2001US-00940240.
XX
PR 10-FEB-1998; 98US-00023664.
PR 10-FEB-1999; 99US-00248239.
XX

```
XX
PA  (MILL-) MILLENNIUM PHARM INC.
XX
PI  Barnes TM, Mackay C;
XX
DR  WPI; 2003-255230/25.
DR  P-PSDB; ABG74459.
XX
PT  New NEOKINE polypeptides and nucleic acids, useful as modulating agents
PT  in regulating a variety of cellular processes, in chromosome mapping,
PT  tissue typing, and in forensic biology.
XX
PS  Claim 20; Fig 7; 64pp; English.
XX
CC  The invention describes an isolated NEOKINE nucleic acid molecule (I)
CC  comprising a sequence of 1656, 300, 1372, 237, 1458 or 285 bp given in
CC  the specification (designated S1-S6, respectively) or their complements.
CC  The NEOKINE molecules are useful as modulating agents in regulating a
CC  variety of cellular processes, as primers or hybridisation probes for the
CC  detection of NEOKINE-encoding nucleic acids, in screening assays, in
CC  predictive medicine (e.g. diagnostic assays, prognostic assays,
CC  monitoring clinical trials, and pharmacogenetics), and in a method of
CC  treatment (therapeutic or prophylactic). The nucleic acids are useful in
CC  chromosome mapping, tissue typing, and in forensic biology. The proteins
CC  can be used to treat disorders characterised by insufficient or excessive
CC  production of non-NEOKINE chemokine or chemokine forms which have
CC  decreased or aberrant activity compared to wild type chemokines, and to
CC  screen drugs or compounds which modulate NEOKINE activity. NEOKINE
CC  modulators are useful for treating and/or preventing proliferative
CC  diseases such as cancers of the epithelia, liver, secretory glands,
CC  bladder, reproductive tract, central nervous system, or connective
CC  tissues, inflammation, psoriasis, or immune rejection following skin
CC  graft or kidney transplant, and brain inflammation following stroke,
CC  ischaemia or viral infection. This sequence encodes the human orphan
CC  chemokine receptor RDC1 that functions as a receptor for NEOKINEs
XX
SQ  Sequence 2050 BP; 435 A; 578 C; 507 G; 530 T; 0 U; 0 Other;

Query Match       0.6%;  Score 25;  DB 8;  Length 2050;
Best Local Similarity  100.0%;  Pred. No. 11;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   3864 TTTTTTTTTTTTTTTGCCTTTTTA 3888
          |||||||||||||||||||||||
Db   2050 TTTTTTTTTTTTTTTGCCTTTTTA 2026


RESULT 43
ADK66235/c
ID  ADK66235 standard; DNA; 2050 BP.
XX
AC  ADK66235;
XX
DT  06-MAY-2004  (first entry)
XX
DE  Human NEOKINE-1 receptor RDC1 DNA.
XX
KW  NEOKINE; NEOKINE-associated disorder; genetic disorder; aminoaciduria;
KW  cystinosis; CNS disorder; Alzheimer's disease; epilepsy;
KW  Parkinson's disease; liver disease; skeletal muscle disorder;
KW  cellular proliferative disorder; cellular differentiative disorder;
KW  cancer; hormonal disorder; diabetes; thyroid disorder; immune disorder;
KW  inflammatory disorder; rheumatoid arthritis; osteoarthritis; ulcer;
KW  cardiovascular disorder; blood vessel disorder; neutrophil disorder;
KW  neutropaenia; lupus; testicular disorder; mumps; platelet disorder;
KW  tissue typing; gene therapy; human; gene; ds.
XX
OS  Homo sapiens.
XX
FH          Location/Qualifiers
FT  CDS       91..1179
FT            /*tag= a
FT            /product= "NEOKINE-1 receptor RDC1 protein"
```

```
XX
PN  US2004019917-A1.
XX
PD  29-JAN-2004.
XX
PF  14-APR-2003; 2003US-00413899.
XX
PR  10-FEB-1998;   98US-00023664.
PR  10-FEB-1999;   99US-00248239.
PR  27-AUG-2001; 2001US-00940240.
XX
PA  (MILL-) MILLENNIUM PHARM INC.
XX
PI  Barnes TM, Mackay C;
XX
DR  WPI; 2004-132242/13.
DR  P-PSDB; ADK66236.
XX
PT  New isolated nucleic acid molecules encoding NEOKINE proteins, useful for
PT  diagnosing and treating kinase-associated disorders, such as diabetes,
PT  Alzheimer's disease, aminoacidurias.
XX
PS  Claim 20; SEQ ID NO 15; 65pp; English.
XX
CC  The invention relates to NEOKINE proteins and their corresponding nucleic
CC  acid sequences. The nucleic acid molecules, polypeptides and antibodies
CC  of the invention are useful for diagnosing and treating NEOKINE-
CC  associated disorders, such as genetic disorders of the membrane transport
CC  (aminoacidurias, cystinosis), CNS disorders (Alzheimer's disease,
CC  epilepsy, Parkinson's disease), liver disorders, skeletal muscle
CC  disorders, cellular proliferative and/or differentiative disorders
CC  (cancer), hormonal disorders (diabetes, thyroid disorders), immune and
CC  inflammatory disorders (rheumatoid arthritis, osteoarthritis, ulcer),
CC  cardiovascular disorders, blood vessel disorders, neutrophil disorders
CC  (neutropaenia, lupus), testicular disorder (mumps) and platelet
CC  disorders. They are also useful in tissue typing, detection assays, and
CC  predictive medicine. The nucleic acids are useful as surrogate markers
CC  and also useful in gene therapy. The present sequence is human NEOKINE-1
CC  receptor RDC1 DNA.
XX
SQ  Sequence 2050 BP; 435 A; 578 C; 507 G; 530 T; 0 U; 0 Other;

Query Match       0.6%;  Score 25;  DB 12;  Length 2050;
Best Local Similarity  100.0%;  Pred. No. 11;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   3864 TTTTTTTTTTTTTTTGCCTTTTTA 3888
          |||||||||||||||||||||||
Db   2050 TTTTTTTTTTTTTTTGCCTTTTTA 2026


RESULT 44
ABA19751/c
ID  ABA19751 standard; DNA; 14231 BP.
XX
AC  ABA19751;
XX
DT  23-JAN-2002  (first entry)
XX
DE  Human nervous system related polynucleotide SEQ ID NO 12082.
XX
KW  Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW  immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW  antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW  antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW  antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW  antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW  neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS  Homo sapiens.
XX
PN  WO200159063-A2.
XX
```

```
PD   16-AUG-2001.
XX
PF   17-JAN-2001;  2001WO-US001334.
XX
PR   31-JAN-2000;  2000US-0179065P.
PR   04-FEB-2000;  2000US-0180628P.
PR   24-FEB-2000;  2000US-0184664P.
PR   02-MAR-2000;  2000US-0186350P.
PR   16-MAR-2000;  2000US-0189874P.
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PR   05-JAN-2001;  2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-541565/60.
```

Left column

```
XX
PT   Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating nervous system cancers
PT   and metastases.
XX
PS   Disclosure; SEQ ID NO 12082; 1701pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC   (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC   the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC   ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC   breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC   disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC   multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC   cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC   ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC   infectious diseases such as viral, bacterial, fungal and parasitic
CC   infections. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 14231 BP; 3443 A; 3744 C; 3440 G; 3604 T; 0 U; 0 Other;

Query Match             0.6%;  Score 25;  DB 5;  Length 14231;
Best Local Similarity 100.0%;  Pred. No. 8.9;
  Matches 25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db       8582 TTTTTTTTTTTTTTTTGCCTTTTTT 8558

RESULT 45
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ID   ABD32612 standard; DNA; 142976 BP.
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AC   ABD32612;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human cancer-associated genomic DNA HD12-017.
XX
KW   Human; ds; cancer-associated protein; gene; cytostatic; cancer;
KW   leukaemia; lymphoma; CAP.
XX
OS   Homo sapiens.
XX
PN   WO200407320-A2.
XX
PD   02-SEP-2004.
XX
PF   17-FEB-2004; 2004WO-US004730.
XX
PR   14-FEB-2003; 2003US-00367094.
PR   14-MAR-2003; 2003US-00388838.
PR   15-APR-2003; 2003US-00417375.
PR   13-JUN-2003; 2003US-00461862.
PR   15-SEP-2003; 2003US-00663431.
PR   15-DEC-2003; 2003US-00733318.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW, Morris DW, Malandro MS;
XX
DR   WPI; 2004-652914/63.
XX
PT   New isolated cancer-associated polynucleotides and polypeptides useful
PT   for diagnosing, preventing or treating cancers, especially lymphoma and
PT   leukaemia, or in screening for agents that modulate cancer.
```

Right column

```
XX
PS   claim 16; seqid 125; 310pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising at least 10
CC   contiguous nucleotides of any of the 233 polynucleotide sequences given
CC   in the specification, or its complement. The nucleic acids encode cancer-
CC   associated proteins. Also included are an expression vector comprising
CC   the isolated nucleic acid cited above, a host cell comprising the above
CC   recombinant nucleic acid or expression vector, a microarray for detecting
CC   a cancer-associated (CA) nucleic acid comprising at least one probe
CC   comprising at least 10 contiguous nucleotides of any of the above-
CC   mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC   an open reading frame of a CA sequence selected from any of the 95
CC   polynucleotide sequences as mentioned in the specification, or its
CC   complement), an isolated antibody, (or its antigen binding fragment) that
CC   binds to the above polypeptide, a hybridoma that produces the above
CC   monoclonal antibody, a pharmaceutical composition comprising the above
CC   antibody and a pharmaceutical excipient, a kit for detecting cancer
CC   cells(comprising the antibody cited above, methods for diagnosing cancer
CC   or for detecting the presence or absence of cancer cells in an
CC   individual, a method for inhibiting growth of cancer cells in an
CC   individual, a method for delivering a therapeutic agent to cancer cells
CC   in an individual, an electronic library comprising the above
CC   polynucleotide or polypeptide (or their fragments), methods of screening
CC   for anticancer activity or for a bioactive agent capable of modulating
CC   the activity of a CA protein (CAP), methods for detecting cancer
CC   associated with expression of a polypeptide in a test cell sample, a
CC   method for treating cancers and a method for inhibiting the expression of
CC   CA gene in a cell. The composition and methods are useful for detecting,
CC   diagnosing, preventing and treating cancers, especially lymphoma and
CC   leukaemia. These may also be used in screening for agents that modulate
CC   cancer. The present sequence is a human CAP genomic sequence. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification. but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
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SQ   Sequence 142976 BP; 35484 A; 31242 C; 34145 G; 42085 T; 0 U; 20 Other;

Query Match             0.6%;  Score 25;  DB 13;  Length 142976;
Best Local Similarity 100.0%;  Pred. No. 6.9;
  Matches 25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db       7785 TTTTTTTTTTTTTTTTGCCTTTTTT 7809

RESULT 46
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ID   AEB96535 standard; DNA; 151909 BP.
XX
AC   AEB96535;
XX
DT   06-OCT-2005  (first entry)
XX
DE   Human CABIN1 gene, SEQ ID 19.
XX
KW   hepatitis C virus infection; antiinflammatory; hepatotropic; virucide;
KW   liver cirrhosis; fibrosis; hepatoma; SNP detection; CABIN1; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT            /standard_name= "Single nucleotide polymorphism"
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Best Local Similarity 100.0%;
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Db 54162 CTTTTTTTTTTTTTTTTTTGCCTTTTT 54138

RESULT 47
ADL13693/c
ID ADL13693 standard; DNA; 231222 BP.
XX
AC ADL13693;
XX
DT 06-MAY-2004 (first entry)
XX
DE Osteoarthritis-associated polymorphic nucleotide #225.
XX
KW ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW joint space narrowing; osteophyte development; joint pain;
KW osteoarthritis; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200305416-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041225.
XX
PR 20-DEC-2001; 2001US-0342603P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jones KA, Schafer A;
XX
DR WPI; 2003-559141/52.
XX
PT Determining susceptibility of an individual to joint space narrowing,
PT osteophyte development and/or joint pain comprises identifying whether
PT the individual has at least one polymorphism in a polynucleotide encoding

PT a protein.
XX
PS Disclosure; SEQ ID NO.225; 297pp; English.
XX
CC The invention relates to a method of determining susceptibility of an
CC individual to joint space narrowing and/or osteophyte development and/or
CC joint pain comprising identifying whether the individual has at least one
CC polymorphism in a polynucleotide encoding a protein. The methods,
CC listed in the specification. The methods, composition and agent are
CC useful for modulating the susceptibility of an individual to joint space
CC narrowing and/or osteophyte development and/or joint pain that is
CC associated with a disease, preferably osteoarthritis. The cell line and
CC the non-human animal are useful for screening for an agent for diagnosing
CC an individual having susceptibility to joint space narrowing and/or
CC osteophyte development and/or joint pain. This sequence corresponds to
CC the polynucleotide encoding a protein listed in the specification. (Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 231222 BP; 64006 A; 52087 C; 53478 G; 61650 T; 0 U; 1 Other;

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RESULT 48
AAV34076/c
ID AAV34076 standard; DNA; 24 BP.
XX
AC AAV34076;
XX
DT 01-MAR-1999 (first entry)
XX
DE Methionine synthase primer 1107A.
XX
KW Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN CA2217153-A.
PD 27-MAY-1998.
XX
PF 27-NOV-1997; 97CA-02217153.
XX
PR 27-NOV-1996; 96US-0031964P.
PR 20-JUN-1997; 97US-0050310P.
XX
PA (MART-) MARTINEX R & D INC.
XX
PI Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR WPI; 1998-569373/49.
XX
PT DNA encoding methionine synthase polypeptide - and corresponding
PT polypeptide, cells, antibody and therapeutic methods.
XX
PS Claim 49; Page 51; 64pp; English.
XX
CC This is the nucleotide sequence of oligonucleotide 1107A, a primer based
CC on a highly conserved region found in the methionine synthases of
CC different organisms. It corresponds to nucleotides 3856-3833 of the human
CC methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC (see AAV34064-104) based on such conserved regions are provided. These
CC have been used for human and mouse methionine synthase cDNA cloning,

CC   chromosome mapping and in a claimed method for mutation detection.
CC   Mutations in the human methionine synthase gene are associated with
CC   hyperhomocysteinaemia. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease
CC   and colon cancer. Claimed methods for detecting sequence variants involve
CC   SSCP or RFLP polymorphism analysis
XX
SQ   Sequence 24 BP; 4 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred. No. 44;
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RESULT 49
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XX
AC   AAV34078;
XX
DT   01-MAR-1999 (first entry)
XX
DE   Methionine synthase primer 1706A.
XX
KW   Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW   cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW   SS.
XX
OS   Synthetic.
XX
PN   CA2217153-A.
XX
PD   27-MAY-1998.
XX
PF   27-NOV-1997;   97CA-02217153.
XX
PR   27-NOV-1996;   96US-0031964P.
PR   20-JUN-1997;   97US-0050310P.
XX
PA   (MART-) MARTINEX R & D INC.
XX
PI   Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR   WPI; 1998-569373/49.
XX
PT   DNA encoding methionine synthase polypeptide - and corresponding
PT   polypeptide, cells, antibody and therapeutic methods.
XX
PS   Claim 49; Page 51; 64pp; English.
XX
CC   This is the nucleotide sequence of oligonucleotide 1706A, a primer based
CC   on a highly conserved region found in the methionine synthases of
CC   different organisms. It corresponds to nucleotides 1963-1986 of the human
CC   methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC   (see AAV34064-104) based on such conserved regions are provided. These
CC   have been used for human and mouse methionine synthase cDNA cloning,
CC   chromosome mapping and in a claimed method for mutation detection.
CC   Mutations in the human methionine synthase gene are associated with
CC   hyperhomocysteinaemia. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease
CC   and colon cancer. Claimed methods for detecting sequence variants involve
CC   SSCP or RFLP polymorphism analysis
XX
SQ   Sequence 24 BP; 10 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match   0.6%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 44;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 50
AAV34088
ID   AAV34088 standard; DNA; 24 BP.
XX
AC   AAV34088;
XX
DT   01-MAR-1999 (first entry)
XX
DE   Methionine synthase primer 1774.
XX
KW   Methionine synthase; human; hyperhomocysteinaemia; neural tube defect;
KW   cardiovascular disease; colon cancer; diagnosis; therapy; PCR; primer;
KW   SS.
XX
OS   Synthetic.
XX
PN   CA2217153-A.
XX
PD   27-MAY-1998.
XX
PF   27-NOV-1997;   97CA-02217153.
XX
PR   27-NOV-1996;   96US-0031964P.
PR   20-JUN-1997;   97US-0050310P.
XX
PA   (MART-) MARTINEX R & D INC.
XX
PI   Rozen R, Leclerc D, Campeau E, Goyette P, Gravel RA;
XX
DR   WPI; 1998-569373/49.
XX
PT   DNA encoding methionine synthase polypeptide - and corresponding
PT   polypeptide, cells, antibody and therapeutic methods.
XX
PS   Claim 49; Page 52; 64pp; English.
XX
CC   This is the nucleotide sequence of oligonucleotide 1774, a primer based
CC   on a highly conserved region found in the methionine synthases of
CC   different organisms. It corresponds to nucleotides 3241-3264 of the human
CC   methionine synthase cDNA open reading frame (see AAV34063). 41 Primers
CC   (see AAV34064-104) based on such conserved regions are provided. These
CC   have been used for human and mouse methionine synthase cDNA cloning,
CC   chromosome mapping and in a claimed method for mutation detection.
CC   Mutations in the human methionine synthase gene are associated with
CC   hyperhomocysteinaemia. The invention relates to the diagnosis and
CC   treatment of patients at risk for methionine synthase deficiency, and
CC   associated altered risk for neural tube defects, cardiovascular disease
CC   and colon cancer. Claimed methods for detecting sequence variants involve
CC   SSCP or RFLP polymorphism analysis
XX
SQ   Sequence 24 BP; 3 A; 11 C; 3 G; 7 T; 0 U; 0 Other;

Query Match   0.6%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1 TGCCTCTCGAGACTTCATCGCTCCC 24

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Job time : 2110 secs

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       Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    March 7, 2006, 02:09:54 ; Search time 653 Seconds
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Scoring table:  OLIGO_NUC
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Searched:  1303057 seqs, 888780828 residues

Word size :  18

Total number of hits satisfying chosen parameters:     10958

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	4	3517	89.7	7122	3	US-09-347-878-4	Sequence 4, Appli
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Wed Mar 8 09:49:11 2006

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102	c	601	0.6	22	US-09-949-016-77832	Sequence 77832, A
103	c	601	0.6	22	US-09-949-016-80323	Sequence 80323, A
104		601	0.6	22	US-09-949-016-89245	Sequence 89245, A
105		601	0.6	22	US-09-949-016-89246	Sequence 89246, A
106		601	0.6	22	US-09-949-016-90121	Sequence 90121, A
107		601	0.6	22	US-09-949-016-135415	Sequence 135415,
108		601	0.6	22	US-09-949-016-135416	Sequence 135416,
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110	c	601	0.6	22	US-09-949-016-141857	Sequence 141857,
111		601	0.6	22	US-09-949-016-141858	Sequence 141858,
112		601	0.6	22	US-09-949-016-141860	Sequence 141860,
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114		601	0.6	22	US-09-949-016-153315	Sequence 153315,
115		601	0.6	22	US-09-949-016-153316	Sequence 153316,
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118		601	0.6	22	US-09-949-016-198107	Sequence 198107,
119		601	0.6	22	US-09-949-016-198108	Sequence 198108,
120	c	601	0.6	22	US-09-949-016-200373	Sequence 200373,
121	c	601	0.6	22	US-09-949-016-200374	Sequence 200374,
122		601	0.6	22	US-09-949-016-200641	Sequence 200641,
123		601	0.6	22	US-09-949-016-200787	Sequence 200787,
124		776	0.6	22	US-09-372-422A-43	Sequence 43, Appl
125		1113	0.6	22	US-09-857-498A-1	Sequence 1, Appli
126		1352	0.6	22	US-09-010-147B-9	Sequence 9, Appli
127		5001	0.6	22	US-09-949-016-1495	Sequence 1495, Ap
128		5286	0.6	22	US-09-949-016-14866	Sequence 14866, A
129	c	6450	0.6	22	US-09-041-886-34	Sequence 34, Appl
130		6450	0.6	22	US-08-453-998-1	Sequence 1, Appl
131		6450	0.6	22	US-09-949-016-18	Sequence 18, Appl
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133	c	6450	0.6	22	US-10-052-092-7	Sequence 7, Appli
134	c	6450	0.6	22	US-10-052-092-1	Sequence 1, Appli
135	c	6450	0.6	22	US-10-081-563-1	Sequence 1, Appli
136		9950	0.6	22	US-09-949-016-12075	Sequence 12075, A
137		9950	0.6	22	US-09-949-016-14226	Sequence 14226, A
138		13182	0.6	22	US-09-817-199-3	Sequence 3, Appli
139		15975	0.6	22	US-09-949-016-17469	Sequence 17469, A
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141		24150	0.6	22	US-09-949-016-12438	Sequence 12438, A
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143		24707	0.6	22	US-10-274-968-3	Sequence 3, Appli
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146		26334	0.6	22	US-09-949-016-17354	Sequence 17354, A
147		28556	0.6	22	US-09-949-016-13064	Sequence 13064, A
148		32881	0.6	22	US-09-949-016-16048	Sequence 16048, A
149		34408	0.6	22	US-09-949-016-14010	Sequence 14010, A
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154		40037	0.6	22	US-09-949-016-12715	Sequence 12715, A
155	c	40408	0.6	22	US-09-949-016-16206	Sequence 16206, A
156		40505	0.6	22	US-09-949-016-12574	Sequence 12574, A
157		44377	0.6	22	US-09-949-016-11840	Sequence 11840, A
158		44378	0.6	22	US-09-949-016-15969	Sequence 15969, A
159	c	44971	0.6	22	US-09-949-016-17049	Sequence 17049, A
160		54246	0.6	22	US-09-949-016-16331	Sequence 16331, A
161		72843	0.6	22	US-09-949-016-12574	Sequence 12574, A
162		84296	0.6	22	US-09-949-016-17375	Sequence 17375, A
163		90150	0.6	22	US-09-949-016-17383	Sequence 17383, A
164		93320	0.6	22	US-09-949-016-12461	Sequence 12461, A
165		93920	0.6	22	US-09-949-016-16853	Sequence 16853, A
166	c	95621	0.6	22	US-09-949-016-13237	Sequence 13237, A
167	c	102304	0.6	22	US-09-949-016-12589	Sequence 12589, A
168		105413	0.6	22	US-10-427-923-3	Sequence 3, Appli
169		107937	0.6	22	US-09-949-016-17192	Sequence 17192, A
170	c	112219	0.6	22	US-09-949-016-12453	Sequence 12453, A

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172		22	0.6	113186	3	US-09-949-016-17572	Sequence 17572, A
173		22	0.6	113332	3	US-09-949-016-15535	Sequence 15535, A
174	c	22	0.6	131978	3	US-09-949-016-13117	Sequence 13117, A
175		22	0.6	152582	3	US-09-949-016-12086	Sequence 12086, A
176		22	0.6	152583	3	US-09-949-016-17390	Sequence 17390, A
177		22	0.6	152583	3	US-09-949-016-17391	Sequence 17391, A
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180		22	0.6	164061	3	US-09-949-016-17422	Sequence 17422, A
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183		22	0.6	202111	3	US-09-949-016-13877	Sequence 13877, A
184		22	0.6	237510	3	US-09-949-016-14273	Sequence 14273, A
185		22	0.6	264358	3	US-09-949-016-15725	Sequence 15725, A
186		22	0.6	301828	3	US-09-949-016-13969	Sequence 13969, A
187		22	0.6	363032	3	US-09-949-016-12415	Sequence 12415, A
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192	c	21	0.5	53	3	US-09-091-332A-50	Sequence 50, Appl
193	c	21	0.5	302	3	US-09-621-976-16091	Sequence 16091, App
194	c	21	0.5	353	3	US-09-621-976-644	Sequence 644, App
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196		21	0.5	601	3	US-09-949-016-18787	Sequence 18787, A
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198		21	0.5	601	3	US-09-949-016-23642	Sequence 23642, A
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233		21	0.5	601	3	US-09-949-016-86671	Sequence 86671, A
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236		21	0.5	601	3	US-09-949-016-93771	Sequence 93771, A
237		21	0.5	601	3	US-09-949-016-94154	Sequence 94154, A
238		21	0.5	601	3	US-09-949-016-107611	Sequence 107611,
239		21	0.5	601	3	US-09-949-016-110729	Sequence 110729,
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241		21	0.5	601	3	US-09-949-016-111051	Sequence 111051,
242		21	0.5	601	3	US-09-949-016-111212	Sequence 111212,
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252	21	0.5	601	3	US-09-949-016-142510	3	Sequence 142510,
253	21	0.5	601	3	US-09-949-016-144581	3	Sequence 144581,
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262	21	0.5	601	3	US-09-949-016-158671	3	Sequence 158671,
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269	21	0.5	601	3	US-09-949-016-177021	3	Sequence 177021,
270	21	0.5	601	3	US-09-949-016-177022	3	Sequence 177022,
271	21	0.5	601	3	US-09-949-016-177023	3	Sequence 177023,
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273	21	0.5	601	3	US-09-949-016-182220	3	Sequence 182220,
274	21	0.5	601	3	US-09-949-016-185193	3	Sequence 185193,
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284	21	0.5	601	3	US-09-949-001-108	3	Sequence 108, App
285	21	0.5	601	3	US-09-949-001-562	3	Sequence 562, App
286	21	0.5	601	3	US-09-949-001-563	3	Sequence 563, App
287	21	0.5	601	3	US-09-949-001-564	3	Sequence 564, App
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289	21	0.5	601	3	US-09-949-002-2663	3	Sequence 2663, Ap
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291	21	0.5	601	3	US-09-949-002-2665	3	Sequence 2665, Ap
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293	21	0.5	601	3	US-09-949-002-5301	3	Sequence 5301, Ap
294	21	0.5	601	3	US-09-949-002-5302	3	Sequence 5302, Ap
295	21	0.5	601	3	US-09-949-002-10416	3	Sequence 10416, A
296	21	0.5	645	3	US-09-522-217-108	3	Sequence 108, App
297	21	0.5	645	3	US-09-923-246-108	3	Sequence 108, App
298	21	0.5	645	3	US-10-076-522-108	3	Sequence 108, App
299	21	0.5	674	3	US-09-620-405B-465	3	Sequence 465, App
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303	21	0.5	674	3	US-09-590-751A-465	3	Sequence 465, App
304	21	0.5	674	3	US-09-551-621-465	3	Sequence 465, App
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306	21	0.5	674	3	US-10-295-723-108	3	Sequence 108, App
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308	21	0.5	772	3	US-09-533-559-7581	3	Sequence 7581, Ap
309	21	0.5	1239	3	US-09-614-912-67	3	Sequence 67, Appl
310	21	0.5	1356	3	US-09-252-991A-13894	3	Sequence 13894, A
311	21	0.5	1559	3	US-09-489-847-42	3	Sequence 42, Appl
312	21	0.5	2465	3	US-10-104-047-1278	3	Sequence 1278, Ap
313	21	0.5	2731	3	US-10-104-047-284	3	Sequence 284, Appl
314	21	0.5	2766	3	US-09-117-447-5	3	Sequence 5, Appli
315	21	0.5	2846	3	US-08-915-795-1	3	Sequence 1, Appli
c 316	21	0.5	2846	3	US-09-296-275-1	3	Sequence 1, Appli

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318	Sequence 1148, Ap	US-09-949-016-1148	3	3473	0.5	21
c 319	Sequence 13448, A	US-09-252-991A-13448	3	3762	0.5	21
320	Sequence 13693, A	US-09-252-991A-13693	3	3795	0.5	21
321	Sequence 49, Appl	US-08-832-883-49	2	4576	0.5	21
322	Sequence 49, Appli	US-08-832-877-49	2	4576	0.5	21
323	Sequence 3, Appli	US-08-612-521-3	3	6143	0.5	21
324	Sequence 2149, Ap	US-09-949-016-2149	3	6479	0.5	21
325	Sequence 1063, Ap	US-09-949-016-1063	3	6930	0.5	21
326	Sequence 16350, A	US-09-949-016-16350	3	7008	0.5	21
327	Sequence 15445, A	US-09-949-016-15445	3	8230	0.5	21
328	Sequence 13815, A	US-09-949-016-13815	3	11378	0.5	21
329	Sequence 16178, A	US-09-949-016-16178	3	12437	0.5	21
330	Sequence 13081, A	US-09-949-016-13081	3	12779	0.5	21
c 331	Sequence 16894, A	US-09-949-016-16894	3	14160	0.5	21
332	Sequence 15001, A	US-09-949-016-15001	3	15133	0.5	21
333	Sequence 12356, A	US-09-949-016-12356	3	15273	0.5	21
334	Sequence 13341, A	US-09-949-016-13341	3	15853	0.5	21
335	Sequence 12121, A	US-09-949-016-12121	3	16051	0.5	21
336	Sequence 16051, A	US-09-949-016-16051	3	16835	0.5	21
337	Sequence 17309, A	US-09-949-016-17309	3	17415	0.5	21
338	Sequence 13513, A	US-09-949-016-13513	3	17644	0.5	21
339	Sequence 16342, A	US-09-949-016-16342	3	17645	0.5	21
340	Sequence 11805, A	US-09-949-016-11805	3	18200	0.5	21
341	Sequence 14188, A	US-09-949-016-14188	3	18591	0.5	21
342	Sequence 15660, A	US-09-949-016-15660	3	19719	0.5	21
343	Sequence 15661, A	US-09-949-016-15661	3	19719	0.5	21
344	Sequence 14719, A	US-09-949-016-14719	3	20354	0.5	21
345	Sequence 15662, A	US-09-949-016-15662	3	20677	0.5	21
346	Sequence 15663, A	US-09-949-016-15663	3	20901	0.5	21
347	Sequence 13219, A	US-09-949-016-13219	3	21723	0.5	21
c 348	Sequence 724, App	US-09-949-002-724	3	23932	0.5	21
349	Sequence 11866, A	US-09-949-016-11866	3	23953	0.5	21
350	Sequence 16383, A	US-09-949-016-16383	3	24593	0.5	21
351	Sequence 16099, A	US-09-949-016-16099	3	24971	0.5	21
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378	Sequence 842, App	US-09-949-002-842	3	51101	0.5	21
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381	Sequence 13563, A	US-09-949-016-13563	3	54950	0.5	21
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No.	c					Reference	Sequence
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No.	c					Reference	Sequence
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469		21	0.5	203093	3	US-09-949-016-14445	Sequence 14445, A
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479	c	21	0.5	246240	2	US-08-724-394A-22	Sequence 22, Appl
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	600	20	0.5	601	3	US-09-949-016-90348	Sequence 90348, A
	601	20	0.5	601	3	US-09-949-016-92430	Sequence 92430, A
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c	604	20	0.5	601	3	US-09-949-016-96831	Sequence 96831, A
	605	20	0.5	601	3	US-09-949-016-97097	Sequence 97097, A
c	606	20	0.5	601	3	US-09-949-016-97363	Sequence 97363, A
	607	20	0.5	601	3	US-09-949-016-97629	Sequence 97629, A
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	611	20	0.5	601	3	US-09-949-016-98693	Sequence 98693, A
	612	20	0.5	601	3	US-09-949-016-98959	Sequence 98959, A
	613	20	0.5	601	3	US-09-949-016-99225	Sequence 99225, A
	614	20	0.5	601	3	US-09-949-016-99491	Sequence 99491, A
	615	20	0.5	601	3	US-09-949-016-99757	Sequence 99757, A
	616	20	0.5	601	3	US-09-949-016-100023	Sequence 100023
	617	20	0.5	601	3	US-09-949-016-100289	Sequence 100289
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	624	20	0.5	601	3	US-09-949-016-102343	Sequence 102343
	625	20	0.5	601	3	US-09-949-016-102483	Sequence 102483
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733	20	0.5	601	3	US-09-820-003C-31	Sequence 31, Appl
734	20	0.5	636	3	US-09-991-181-411	Sequence 411, Appl
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736	20	0.5	636	3	US-09-997-333-411	Sequence 411, App
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738	20	0.5	700	3	US-09-735-271-287	Sequence 287, App
739	20	0.5	751	3	US-09-621-976-3052	Sequence 3052, Ap
c 740	20	0.5	817	3	US-09-270-767-12401	Sequence 12401, A
741	20	0.5	924	3	US-09-118-554-62	Sequence 62, Appl
742	20	0.5	924	3	US-09-118-627-62	Sequence 62, Appl
c 743	20	0.5	924	3	US-09-602-877A-62	Sequence 62, Appl
744	20	0.5	1134	3	US-09-248-335-29	Sequence 29, Appl
745	20	0.5	1198	3	US-09-270-767-13061	Sequence 13061, A
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747	20	0.5	1235	3	US-09-565-177A-5	Sequence 5, Appli
748	20	0.5	1336	3	US-09-257-179-13	Sequence 13, Appl
749	20	0.5	1346	3	US-09-589-733C-9	Sequence 9, Appli
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758	20	0.5	2280	3	US-09-546-553-1	Sequence 1, Appli
759	20	0.5	2280	3	US-10-349-806-1	Sequence 1, Appli
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762	20	0.5	2878	3	US-10-104-047-568	Sequence 568, App
763	20	0.5	3701	3	US-09-023-655-309	Sequence 309, App
764	20	0.5	3967	3	US-09-672-749-14	Sequence 14, Appl
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772	20	0.5	9931	3	US-09-949-016-14377	Sequence 14377, A
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774	20	0.5	10010	3	US-09-949-002-840	Sequence 840, App
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780	20	0.5	12587	3	US-09-949-016-15712	Sequence 15712, A
781	20	0.5	13248	3	US-09-949-016-12024	Sequence 12024, A
782	20	0.5	13248	3	US-09-949-016-14230	Sequence 14230, A
783	20	0.5	13451	3	US-09-949-016-16779	Sequence 16779, A
784	20	0.5	13554	3	US-09-949-016-16130	Sequence 16130, A
785	20	0.5	14189	3	US-09-949-016-15783	Sequence 15783, A
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798	20	0.5	18650	3	US-09-949-016-13440	Sequence 13440, A
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803	20	0.5	21885	3	US-09-949-016-12600	Sequence 12600, A
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806	20	0.5	22205	3	US-09-949-016-16199	Sequence 16199, A
807	20	0.5	22303	3	US-09-949-016-12616	Sequence 12616, A
808	20	0.5	22303	3	US-09-949-016-12964	Sequence 12964, A
809	20	0.5	22686	3	US-09-949-016-12279	Sequence 12279, A
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814	20	0.5	24056	3	US-09-949-016-14320	Sequence 14320, A
815	20	0.5	24204	3	US-09-949-016-16232	Sequence 16232, A
816	20	0.5	24345	3	US-09-949-016-17549	Sequence 17549, A
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822	20	0.5	27783	3	US-09-949-016-16736	Sequence 16736, A
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825	20	0.5	29671	3	US-09-949-016-12229	Sequence 12229, A
826	20	0.5	29671	3	US-09-949-016-17105	Sequence 17105, A
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Left block (rows 828–900):

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833		20	0.5	32798	3	US-09-949-016-17366	Sequence 17366, A
834		20	0.5	33821	3	US-09-949-002-613	Sequence 613, App
835		20	0.5	33822	3	US-09-949-002-737	Sequence 737, App
836		20	0.5	33827	3	US-09-949-002-760	Sequence 760, App
837		20	0.5	34047	3	US-09-949-016-17555	Sequence 17555, A
838		20	0.5	34310	3	US-09-949-016-12518	Sequence 12518, A
839		20	0.5	34315	3	US-09-949-016-15469	Sequence 15469, A
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841	c	20	0.5	35059	3	US-09-949-016-13831	Sequence 13831, A
842		20	0.5	35060	3	US-08-814-095-7	Sequence 7, Appli
843		20	0.5	35355	3	US-09-949-016-14197	Sequence 14197, A
844	c	20	0.5	35916	3	US-09-949-016-15957	Sequence 15957, A
845		20	0.5	36171	3	US-09-949-016-13876	Sequence 13876, A
846		20	0.5	36274	3	US-09-949-016-12389	Sequence 12389, A
847	c	20	0.5	36538	3	US-09-949-016-11752	Sequence 11752, A
848		20	0.5	36907	3	US-09-813-133A-3	Sequence 3, Appli
849		20	0.5	36913	3	US-09-949-016-12633	Sequence 12633, A
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ALIGNMENTS

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RESULT 1
US-08-980-326-1
; Sequence 1, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
;   APPLICANT: Gravel, Roy A.
;   APPLICANT: Rozen, Rima
;   APPLICANT: LeClerc, Daniel
;   APPLICANT: Goyette, Philippe
;   APPLICANT: Campeau, Eric
;   TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
;   TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
;   TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
;   FILE REFERENCE: 50004/002003
;   CURRENT APPLICATION NUMBER: US/08/980,326
;   CURRENT FILING DATE: 1997-11-26
;   EARLIER APPLICATION NUMBER: 60/050,310
;   EARLIER FILING DATE: 1997-06-20
;   EARLIER APPLICATION NUMBER: 60/031,964
;   EARLIER FILING DATE: 1996-11-27
;   NUMBER OF SEQ ID NOS: 75
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 3919
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;     NAME/KEY: Other
;     LOCATION: (1)..(3919)
;     OTHER INFORMATION: Entire cloned cDNA encoding wild type methionine
;     OTHER INFORMATION: synthase.
US-08-980-326-1

  Query Match             100.0%;  Score 3919;  DB 3;  Length 3919;
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Db  2461  AATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGTGCT  2520

Qy  2521  CTTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAA  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CTTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAA  2580

Qy  2581  ATGATTTTGTTGCCAAGGAAATGAGCAGAGATTAGCTATAAGGATTCCGAGATACAGTGGACCT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  ATGATTTTGTTGCCAAGGAAATGAGCAGAGATTAGCTATAAGGATTCCGAGATACAGTGGACCT  2640

Qy  2641  GGAGCAACCACTTCAAAAACCCACACAGTTAAAATAGTCCGAGATACAGTGGATGAA  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GGAGCAACCACTTCAAAAACCCACACAGTTAAAATAGTCCGAGATACAGTGGATGAA  2700

Qy  2701  GTAATCCATGTCCTGACGCGGTCCAAGAGTGTGGTGGTCTTCCCAGCTGTTAGATGAA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  GTAATCCATGTCCTGACGCGGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTAGATGAA  2760

Qy  2761  AATCTAAAGGATGAATACTTTGAGGAGATGATACTTACCCTTAAGTCAAGCCAGTTTATTGGACCCCAG  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  AATCTAAAGGATGAATACTTTGAGGAGATGATACTTACCCTTAAGTCAAGCCCAGTTTATTGGACCCCAG  2820

Qy  2821  CATTATGAGTCTCAAGGAGATGAATCATGGGAAATAATCATGAGTCAAGCCCAGTTGACTGGAAGCCTTTCTT  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  CATTATGAGTCTCAAGGAGATGAATCATGGGAAATAATCATGAGTCAAGCCCAGTTGACTGGAAGCCTTTCTT  2880

Qy  2881  TTCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAACCTCACCCAGTTGACTGGACCCAG  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TTCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAACCTCACCCAGTTGACTGGACCCAG  2940

Qy  2941  GTCTTTGAAGACTATGACCTGCAGAAGCTGCGGAGAGCTGCTGGACTACATTGACTGGAAGCCTTTCTT  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  GTCTTTGAAGACTATGACCTGCAGAAGCTGCGGAGAGCTGCTGGACTACATTGACTGGAAGCCTTTCTT  3000

Qy  3001  GATGTCTGGCAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAACGAC  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  GATGTCTGGCAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAACGAC  3060

Qy  3061  AAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACACA  3120
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  AAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACACA  3120

Qy  3121  CTGATTAGTCAAAAGAAACTCCGGGGCCCCGGCGGTGTTGGGGTTCGGCCCAGCACAGAGT  3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  CTGATTAGTCAAAAGAAACTCCGGGGCCCCGGCGGTGTTGGGGTTCGGCCCAGCACAGAGT  3180

Qy  3181  ATCCAAGACGACATTCACCTGTACGGCCTTAAGGATACTGAGAGGCTGCGTGCCCAGAGCCCATA  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  ATCCAAGACGACATTCACCTGTACGGCCTTAAGGATACTGAGAGGCTGCGTGCCCAGAGCCCATA  3240

Qy  3241  GCCACTTTCTATGGGTTAAGGCAACAGGCTCTGCCAGCAGGACTCTGAGAAGGACACCGAGCCATAC  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  GCCACTTTCTATGGGTTAAGGCAACAGGCTCTGCCAGCAGGACTCTGAGAAGGACACCGAGCCATAC  3300

Qy  3301  TACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCGGCCATCGTCCGTCGACTACCTGGGCCTG  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  TACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCGGCCATCGTCCGTCGACTACCTGGGCCTG  3360
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;  OTHER INFORMATION: G;2758 can be C or G.
;
US-08-980-326-75

       Query Match         91.9%;  Score 3601;  DB 3;  Length 3856;
       Best Local Similarity  99.9%;  Pred. No. 0;
       Matches 3851;  Conservative  0;  Mismatches  0;  Indels  5;  Gaps  0;

Qy      64 ATGTCACCCGCGCTCCAAGACCTGTCGCAACCGGAAGGTCTGAAGAAAACCCTGCGCGGAT 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGTCACCCGCGCTCCAAGACCTGTCCCAACCGGAAGGTCTGAAGAAAACCCTGCGCGGAT 60

Qy     124 GAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGAGGGATGGGGACCATG 183
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGAGGGATGGGGACCATG 120

Qy     184 ATCCAGCGGGAGAAGTAAACGAAGAACACTTCCGAGTCAGGAGTTCAAAGATCATGCC 243
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ATCCAGCGGGAGAAGTAAACGAAGAACACTTCCGAGTCAGGAGTTCAAAGATCATGCC 180

Qy     244 AGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTACCAA 303
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTACCAA 240

Qy     304 ATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAACACTTGGCCTACCGGAACATGTGC 363
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAACACTTGGCCTACCGGAACATGTGC 300

Qy     364 ACTAGTAGTTGCCCAAGCTGACTATGGCCTGCGAGGAGGTAACTCTCCAGACAGGAGTAAGAGG 423
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACTAGTAGTTGCCCAAGCTGACTATGGCCTGCGAGGAGGTAACTCTCCAGACAGGAGTAAGAGG 360

Qy     424 TCTGCAGGAGTGGCCAGAAAAGCTGCCGGAGGAGGTAACTCTCCAGACAGGAGTAAGAGG 483
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TCTGCAGGAGTGGCCAGAAAAGCTGCCGGAGGAGGTAACTCTCCAGACAGGAGTAAGAGG 420

Qy     484 TTTGTGGCAGGGGCTCTGGGTCCCCATCTGTCCCCATCTGTGTCA 543
           ||||||||||||||||||||||||||||||||||||||||||||
Db     421 TTTGTGGCAGGGGCTCTGGGTCCCCATCTGTCCCCATCTGTGAA 480

Qy     544 AGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCC 603
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGGCC 540

Qy     604 AAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTGCC 663
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTGCC 600

Qy     664 AATGCCAAGGCAGCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAAATATGTCTCCCGG 723
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AATGCCAAGGCAGCTTGTTTGCACTCCAAAATCTTTTGAGGAGAAAATATGTCTCCCGG 660

Qy     724 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGGCGGACTCTTTCCGGACAGACA 783
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGGCGGACTCTTTCCGGACAGACA 720

Qy     784 GGAGAGGGATTTGTCATCAGCGCTGTCTCATGAGAACCACTCTGCATTGGATTAAATTGT 843
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGAGAGGGATTTGTCATCAGCGCTGTCTCATGAGAACCACTCTGCATTGGATTAAATTGT 780

Qy     844 GCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAAATGTACAACAGCC 903
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAAATGTACAACAGCC 840

Qy     904 TATGTCCTCGTTATCCCAATGCAGGTCTTCCAACACCTTTGGTGACTATGGATGAAACG 963
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TATGTCCTCGTTATCCCAATGCAGGTCTTCCAACACCTTTGGTGACTATGGATGAAACG 900

Qy     964 CCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAGTT 1023
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CCTTCTATGATGGCCAAGCACCTAAAGGATTTTTGCTATGGATGGCTTGGTCAATATAGTT 960

Qy    1024 CGAGGAGGATGCGTGTGGGTCAACACCAGATCATATCGAGGAAATTGCTCAGACAGTGT... 1083
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3361 TTTGCCGTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGTGAC 3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TTTGCCGTTGCCTGCTTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGTGAC 3420

Qy   3421 GACTACAGCAGCAGCATCATGGTCAAGGCGCTGCGGGGGACCGGCTGGCAGAGGGCCTTTGCAGAA 3480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 GACTACAGCAGCAGCATCATGGTCAAGGCGCTGCGGGGGACCGGCTGGCAGAGGGCCTTTGCAGAA 3480

Qy   3481 GAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGTGAGCAGCTGGAC 3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAGCTCCATGAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGTGAGCAGCTGGAC 3540

Qy   3541 GTCGCAGACCTGCGAAGGTTGCGGTTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGC 3600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 GTCGCAGACCTGCGAAGGTTGCGGTTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGC 3600

Qy   3601 CAGCCCGACCACACCGAGAAGCTCACCATGTGAGACTGGAGACTGCAGACATCGCAGAGCAGTCTACA 3660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CAGCCCGACCACACCGAGAAGCTCACCATGTGAGACTGGAGACTGCAGACATCGCAGAGCAGTCTACA 3660

Qy   3661 GGCATTAGGTTAACAGAATCATTAGCAATGCAATGCACCTGCTTCAGCCAGTCTCAGCCCTCTAC 3720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GGCATTAGGTTAACAGAATCATTAGCAATGCAATGCACCTGCTTCAGCCAGTCTCAGCCCTCTAC 3720

Qy   3721 TTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTCCAAGGATCAGGTTGAG 3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTCCAAGGATCAGGTTGAG 3780

Qy   3781 GATTATGCATTGAGGAAGAACACATATCGTGGCTGGTTGAGAAATGGCTTGGAGACCCATT 3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GATTATGCATTGAGGAAGAACACATATCGTGGCTGGTTGAGAAATGGCTTGGAGACCCATT 3840

Qy   3841 TTGGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCC 3900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TTGGGGATATGATACAGACTAACTTTTTTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCC 3900

Qy   3901 TCAAGGAAATACAACCTAG 3919
           |||||||||||||||||||
Db   3901 TCAAGGAAATACAACCTAG 3919

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RESULT 2
US-08-980-326-75
;   Sequence 75, Application US/08980326
;   Patent No. 6703197
;   GENERAL INFORMATION:
;   APPLICANT: Gravel, Roy A.
;   APPLICANT: Rozen, Rima
;   APPLICANT: LeClerc, Daniel
;   APPLICANT: Goyette, Philippe
;   APPLICANT: Campeau, Eric
;   TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
;   TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
;   TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
;   FILE REFERENCE: 50004/002003
;   CURRENT APPLICATION NUMBER: US/08/980,326
;   CURRENT FILING DATE: 1997-11-26
;   EARLIER APPLICATION NUMBER: 60/050,310
;   EARLIER FILING DATE: 1997-06-20
;   EARLIER APPLICATION NUMBER: 60/031,964
;   EARLIER FILING DATE: 1996-11-27
;   NUMBER OF SEQ ID NOS: 75
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 75
;   LENGTH: 3856
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: (1)...(1265)
;   OTHER INFORMATION: Coding sequence for mutant methionine synthases:
;   OTHER INFORMATION: 2640-2642 can be AAT or deleted;2756 can be A or
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Db    961 GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAGAAT 1020

Qy   1084 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGTCTA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGTCTA 1080

Qy   1144 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATGTT 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATGTT 1140

Qy   1204 GCAGGATCAAGGAAGTTGCTAAACTCATCATCATGCAGGAAACTATGAAGAAGCCTTGTGT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCAGGATCAAGGAAGTTGCTAAACTCATCATCATGCAGGAAACTATGAAGAAGCCTTGTGT 1200

Qy   1264 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATGGC 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTTGGATGTCAACATGGATGATGGC 1260

Qy   1324 ATGCTAGATGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGAC 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ATGCTAGATGTGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAGAC 1320

Qy   1384 ATCGCAAAGTGTACCTTGTGCATCGATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTTA 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATCGCAAAGTGTACCTTGTGCATCGATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGTTA 1380

Qy   1444 AGTGCTGCCAAGGAAGTGCCAGGAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTTTT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGTGCTGCCAAGGAAGTGCCAGGAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTTTT 1440

Qy   1504 TTCTTGGAGAAGGGCCAGGAGACAACGAAACAGAGAAAACAGACAACAGCAACAGAAATCAGAGTGTGCACCCGGCCTAC 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTCTTGGAGAAGGGCCAGGAGACAACGAAACAGAGAAAACAGACAACAGCAACAGAAATCAGAGTGTGCACCCGGCCTAC 1500

Qy   1564 GATGAAGAAGGACAGGCAACAGACAACAGAAACAGACAGAAAAATCAGAGTGTCTAAATAGCTCCGAGATACAGTGCACCTGTA 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GATGAAGAAGGACAGGCAACAGACAACAGAAACAGACAGAAAAATCAGAGTGTCTAAATAGCTCCGAGATACAGTGCACCTGTA 1560

Qy   1624 CATCTGCTTGTGAAAAAACTGGGCTTAATCAAATGACATTATTTGACCCTAATATC 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CATCTGCTTGTGAAAAAACTGGGCTTAATCAAATGACATTATTTGACCCTAATATC 1620

Qy   1684 CTAACCATTGGGACTGGATGGAGGAACACAACTTGTATGCCATTTATTTTTATCCATGCA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CTAACCATTGGGACTGGATGGAGGAACACAACTTGTATGCCATTTATTTTATCCATGCA 1680

Qy   1744 ACAAAAGTCATTAAAGAAACATTACCTGGAGCCCAGAATAAGTGGAGTGGAGGTCTTCAACTTG 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACAAAAGTCATTAAAGAAACATTACCTGGAGCCCAGAATAAGTGGAGTGGAGGTCTTCAACTTG 1740

Qy   1804 TCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAGACTCAAGGCACATGGGGTTTTCCTTTAC 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 TCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAGACTCAAGGCACATGGGGTTTTCCTTTAC 1800

Qy   1864 CATGCAATCAAGTCTCTGGACTGGCATGGACGATGAGTGAATGCTCGAAAACCTCCCTGTGTAT 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATGCAATCAAGTCTCTGGACTGGCATGGACGATGAGTGAATGCTCGAAAACCTCCCTGTGTAT 1860

Qy   1924 GATGATATCATCGAGGAACTTCTGTCGAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCT 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GATGATATCATCGAGGAACTTCTGTCGAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCT 1920

Qy   1984 GAGGCCACTGAGAGCTCTTACGTTACGTTATGCCCGTGTCAAGGACACAGAGGGAAGAAGTC 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GAGGCCACTGAGAGCTCTTACGTTACGTTATGCCCGTGTCAAGGACACAGAGGGAAGAAGTC 1980

Qy   2044 ATTCAGAGACTGATGAGTGGAGAAAACATATATTATTTGAGGATACTGAGGAAGC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ATTCAGAGACTGATGAGTGGAGAAAACATATATTATTTGAGGATACTGAGGAAGC 2040

Qy   2104 AAGGGCATTGAAAAAACATATATTATTTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAAAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AAGGGCATTGAAAAAACATATATTATTTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAAAA 2100


Qy   2164 TATCCCGACCTTCTCAATATAATTGAAGACACCCCTGATGGATGAATGAAAATTGTTGGT 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TATCCCGACCTTCTCAATATAATTGAAGACACCCCTGATGGATGAATGAAAATTGTTGGT 2160

Qy   2224 GATCTTTTGGAGCTGGAAAAATGTTCTACCTCAGTTATAAAGTCAGCCCGGGTTATG 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GATCTTTTGGAGCTGGAAAAATGTTCTACCTCAGTTATAAAGTCAGCCCGGGTTATG 2220

Qy   2284 AAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAGAAGAGAAGAAACCAGAGTG 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AAGAAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAAGAAGAGAAGAAACCAGAGTG 2280

Qy   2344 CTTAACGGCACAGTAGAAGAGAGAGGACCCTTACCAGGGCCACCATCGTGCTGCCCACTGTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CTTAACGGCACAGTAGAAGAGAGAGGACCCTTACCAGGGCCACCATCGTGCTGCCCACTGTT 2340

Qy   2404 AAAGGGCACGTGCACGACATAGGCAAGAACATAGTTGGAGTGCTGCAATAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AAAGGGCACGTGCACGACATAGGCAAGAACATAGTTGGAGTGCTGCAATAAT 2400

Qy   2464 TTCCGAGTTATTGATTTAGGAGTCATGAGCTCCATGTGATAGAGATACTGAAAGCTGCTCTT 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TTCCGAGTTATTGATTTAGGAGTCATGAGCTCCATGTGATAGAGATACTGAAAGCTGCTCTT 2460

Qy   2524 GACCACAAAGCAGATATAATTGGCTGTCAGGACTCATCACTCCTTCCCTGGATGAATG 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GACCACAAAGCAGATATAATTGGCTGTCAGGACTCATCACTCCTTCCCTGGATGAATG 2520

Qy   2584 ATTTTTGTTGCCAAGAAATGGAGAGATTAGTAGTTATAAGGATTCCATTGTTGATTGGAGGA 2643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ATTTTTGTTGCCAAGAAATGGAGAGATTAGTAGTTATAAGGATTCCATTGTTGATTGGAGGA 2580

Qy   2644 GCAACCACTTCAAAAACCCACACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTA 2703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCAACCACTTCAAAAACCCACACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTGTN 2640

Qy   2704 ATCCATGTCCTGACGCGTCCAAGAGTGTGGTGTGGTTCCCAGCTGTGTTAGATGAGATGAAAAT 2763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 NNCCATGTCCTGACGCGTCCAAGAGTGTGGTGTGGTTGTTCCCAGCTGTTTTAGATGAGATGAAAAT 2700

Qy   2764 CTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAAGATATTAGACACAGGACCAT 2823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTAAAGGATGAATACTTTGAGGAAATCATGAAGAATATGAAGATATTAGACACAGGNCNAT 2760

Qy   2824 TATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGTTTTC 2883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAGTGGTTTC 2820

Qy   2884 CAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTC 2943
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGGTC 2880

Qy   2944 TTTGAAGACTATGACCTGCAGAAGCTGGTGTGACTACATTGACTGGAAGCCTTTCTTTGAT 3003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TTTGAAGACTATGACCTGCAGAAGCTGGTGTGACTACATTGACTGGAAGCCTTTCTTTGAT 2940

Qy   3004 GTCTTGGCAGCTCCCGGGGCAAGTACCCCGAGGCTTCCCCAAGATATTTAACGACAAA 3063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GTCTTGGCAGCTCCCGGGGCAAGTACCCCGAGGCTTCCCCAAGATATTTAACGACAAA 3000

Qy   3064 ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACACTGCTGAAGAACACTG 3123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACACTGCTGAAGAACACTG 3060

Qy   3124 ATTAGTCAAAAGAAACTCCGGCACCGCAGTATC 3183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 ATTAGTCAAAAGAAACTCCGGCACCGCAGTATC 3120

Qy   3184 CAAGACGACATTCACCTGTACGCGAGAGGCTGCTGCGCCCAGGCTGCAGAGCCCATAGCC 3243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 CAAGACGACATTCACCTGTACGCGAGAGGCTGCTGCGCCCAGGCTGCAGAGCCCATAGCC 3180
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Qy      2 GTCACCTGTGGAGAGCACGTCTTCTTCTGCCGCGCGCCCTCTGCGCAAGGAGGAGGAGACTCGACA    61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 GTCACCTGTGGAGAGCACGTCTTCTTCTGCCGCGCGCCCTCTGCGCAAGGAGGAGGAGACTCGACA   284

Qy     62 ACATGTCACCCGCGTCCAAGACCTGTCGCAACCTGTCGCAAGGTCTGAAGAAACCCTGCGGG    121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 ACATGTCACCCGCGTCCAAGACCTGTCGCATCCGACTCCGTGACATCCGACTCGAAGAAACCCTGCGGG   344

Qy    122 ATGAGATCAATGCCATTCTGCAGAAGAGGATTATGTGCTGATGGAGGGGGACCA    181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 ATGAGATCAATGCCATTCTGCAGAGAGGATTATGTGCTGATGGAGGGGGACCA   404

Qy    182 TGATCCAGCGGGAGAAGCTAAACGAGAACACTTCCGAGGTCAGGAATTAAAGATCATG    241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 TGATCCAGCGGGAGAAGCTAAACGAGAACACTTCCGAGGTCAGGAATTAAAGATCATG   464

Qy    242 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTACC    301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTACC   524

Qy    302 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCAGACACTTGGCCTACCCGATGAACATGT    361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCAGACACTTGGCCTACCCGATGAACATGT   584

Qy    362 GCACTAGTATTGCCCAAGCTGACTATGGCCTGGCACTCGAGACATCGACAGCAGTCTACAGGC    421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 GCACTAGTATTGCCCAAGCTGACTATGGCCTGGCACTCGAGACATCGACAGCAGTCTACAGGC   644

Qy    422 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA    481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA   704

Qy    482 GGTTGTTGGCAGGGGCTCTGGGCTCCGGGCTCCGGGCTCCGACTAATAAGACACTCTCTGTGTCCCATCGTGG    541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 GGTTGTTGGCAGGGGCTCTGGGCTCCGGGCTCCGACTAATAAGACACTCTCTGTGTCCCATCGTGG   764

Qy    542 AAAGGCCGGATTATAGGAACATATCGTGGCTTGAGGTTGAGAAATGGCTTGACCCCATTTTG    601
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 AAAGGCCGGATTATAGGAACATATCGTGGCTTGAGGTTGAGAAATGGCTTGACCCCATTTTG   824

Qy    602 CCAAAGGACTTCTGGATGGCCGGGGTTGATATCTTACTCATTGAAACTATTTTTGTATCTG    661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 CCAAAGGACTTCTGGATGGCCGGGGTTGATATCTTACTCATTGAAACTATTTTTGTATCTG   884

Qy    662 CCAATGCCAAGGCAGCCTTGTTGCACTCGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC    721
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 CCAATGCCAAGGCAGCCTTGTTGCACTCGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC   944

Qy    722 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGCGGACTCTTTCCGGACAGA    781
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGCGGACTCTTTCCGGACAGA   1004

Qy    782 CAGGAGGGGATTTGTCATCAGCGTGTCTCATGGAAACCACTCTGCATTGATTAAATT    841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 CAGGAGGGGATTTGTCATCAGCGTGTCTCATGGAGAAACCACTCTACATTGATTAAATT   1064

Qy    842 GTGCTTTGGGTGCCTGAGATGAGACCTTTATTGAAAATGTACAACAG    901
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 GTGCTTTGGGTGCCTGAGATGAGACCTTTATTGAAAATGTACAACAG   1124

Qy    902 CCTATGTCCCTGTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAA    961
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 CCTATGTCCCTGTATCCCAATGCAGTCTTCCCAACACCTTTGGTGACTATGATGAAA   1184

Qy    962 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG    1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185 CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG   1244

Qy   1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA    1081
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Db   1245 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA   1304

Qy   1082 ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTC   1141
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Qy   3244 ACTTTCTATGGGTTAAGGCAACAGGCTGAGAGGACTCTGCCAGACGGAGCCATACTAC   3303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 ACTTTCTATGGGTTAAGGCAACAGGCTGAGAGGACTCTGCCAGACGGAGCCATACTAC   3240

Qy   3304 TGCCCTCCAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGCCTGTTT   3363
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Db   3241 TGCCCTCCAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTT   3300

Qy   3364 GCCGTTGCCTGCTTTGGGTGAAGAGTCTGAGCGAAGGCCTATGAGGATGATGACGAC   3423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GCCGTTGCCTGCTTTGGGTGAGAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGAC   3360

Qy   3424 TACAGCAGCATCATGTGTCAAGGCGCTGGGGAGACCGGCGCTGGCAGAGGCCTTTGCAGAAGAG   3483
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TACAGCAGCATCATGTGTCAAGGCGCTGGGGAGACCGGCTGGCAGAGGCCTTTGCAGAAGAG   3420

Qy   3484 CTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGCTGAGCGACGTC   3543
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 CTCCATGAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGCTGAGCGACGTC   3480

Qy   3544 GCAGACCTGCGGAAGGTTGCCGTACAAGGGACATCGCACGAGACTCGAGCAGTCTACAGGC   3603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCAGACCTGCGGAAGGTTGCCGTACAAGGGGCATCGCACGAGACTCGAGCAGTCTACAGGC   3540

Qy   3604 CCCGACCACACCGAGAAGCTCACCATGTGGACTGGACATCATGCAGTCTTCAGCCTCTACTTC   3663
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Db   3541 CCCGACCACACCGAGAAGCTCACCATGTGGACTGGACATCATGCAGTCTTCAGCCTCTACTTC   3600

Qy   3664 ATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTTCAGGCCTTCAGCCCTCTACTTC   3723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 ATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTTCAGGCCTTCAGCCCTCTACTTC   3660

Qy   3724 TCCAATTGAAGTCCAAATATTTTGCTGTGTGGGAAGATTTCCAAGGATCAGGTTGAGGAT   3783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TCCAATTGAAGTCCAAATATTTTGCTGTGTGGGAAGATTTCCAAGGATCAGGTTGAGGAT   3720

Qy   3784 TATGCATTGAAGGAAGAAACATATCGTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTTG   3843
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Db   3721 TATGCATTGAAGGAAGAAACATATCGTGTGGCTGAGGTTGAGAAATGGCTTGGACCCCATTTG   3780

Qy   3844 GGATATGATACAGACTAACTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCCTCA   3903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGATATGATACAGACTAACTTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCCTCA   3840

Qy   3904 AGGAAATACAACCTAG   3919
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Db   3841 AGGAAATACAACCTAG   3856
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RESULT 3
US-09-318-448-2
; Sequence 2, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 2
; LENGTH: 7122
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-2

Query Match   89.7%; Score 3517; DB 3; Length 7122;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 3867; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

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Db          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1305  ATTGTAAGGCCTAGAGTTCCACCTGCCACTGCTTTTGAGAGACATATGTTACTGTCTGGTC  1364

Db          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1142  TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGCGCGCTGTAATG   1201
Db    1365  TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGCGCGCTGTAATG   1424

Qy    1202  TTGCAGGATCAAGGAAGTTGCTAAACTCATCATCGTCAGGAAACTATGAAGAAGCCTTGT   1261
Db    1425  TTGCAGGATCAAGGAAGTTGCTAAACTCATCATCGTCAGGAAACTATGAAGAAGCCTTGT   1484

Qy    1262  GTGTTGCCAAAGTCGAGTCAGTGCGAAATGGGAACCCCAGGTGTTGCAACTTAATTGCTTC  1321
Db    1485  GTGTTGCCAAAGTCGAGTCAGTGGGAAATGGGAACCCCAGGTGTTGCAACTTAATTGCTTC  1544

Qy    1322  GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTGCTTCCGAGCCAG        1381
Db    1545  GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTGCTTCCGAGCCAG        1604

Qy    1382  ACATCGCAAAGGTACCTTTGTGCATCAATAGCATTGTCAATAGTCGATTAGTCTGAGGAGG  1441
Db    1605  ACATCGCAAAGGTACCTTTGTGCATCAATAGCATTGTCAATAGTCGATTAGTCTGAGGAGG  1664

Qy    1442  TAAAGTGCTGCCAAGGAAGTCATTGTCAATAGCATTATTGTGGAGCTGCTATGGAGCTGCT  1501
Db    1665  TAAAGTGCTGCCAAGGAAGTCATTGTCAATAGCATTATTGTGGAGCTGCTATGGAGCTGCT  1724

Qy    1502  ACTTCTTGGAGAAGGCCAGGAAGAGATTAAAAAGTATGGGACTGCTATGGTGGTCATGGCTT  1561
Db    1725  ACTTCTTGGAGAAGGCCAGGAAGAGATTAAAAAGTATGGGACTGCTATGGTGGTCATGGCTT  1784

Qy    1562  TTGATGAAGAAGGAGGCAACGACAGCAGCAAACAGAAAAATCAGAGTGTGCACCGGGGCCT  1621
Db    1785  TTGATGAAGAAGGAGGCAACGACAGCAGCAAACAGAAAAATCAGAGTGTGCACCGGGGCCT  1844

Qy    1622  ACCATCTGCTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA    1681
Db    1845  ACCATCTGCTTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA    1904

Qy    1682  TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTATCCATG      1741
Db    1905  TCCTAACCATTGGGACTGGAATGGAGGAACAACTTGTATGCCATTAATTTATCCATG      1964

Qy    1742  CAACAAAGTCATTAAAGAGAAACATTACCTTGGAGCCAGGAGCCATTCGAGGAGATAAGTCA  1801
Db    1965  CAACAAAGTCATTAAAGAGAAACATTACCTTGGAGCCAGGAGCCATTCGAGGAGATAAGTCA  2024

Qy    1802  TGTCCTTCTTCTCCTTCCGAGGAAGTCTGGCATGCAATGAGCAATGCTGAGAAGGTTTCTTT  1861
Db    2025  TGTCCTTCTTCTCCTTCCGAGGAAGTCTGGCATGCAATGAGCAATGCTGAGAAGGTTTCTTT  2084

Qy    1862  ACCATGCAATCAAGTCTGGCACTGGACCATGCAATGGGACATCTGAGAAGCATGCATCGAGT  1921
Db    2085  ACCATGCAATCAAGTCTGGCACTGGACCATGCAATGGGACATCTGAGAAGCATGCATCGAGT  2144

Qy    1922  TCATTCAGACTGATCAGTGGAGAAATGCCCTGTCGAAGAACGCCCTTGAGTATGCCCTTG   1981
Db    2145  TCATTCAGACTGATCAGTGGAGAAATGCCCTGTCGAAGAACGCCCTTGAGTATGCCCTTG   2204

Qy    1982  CTGAGGGCCACCACTGAGGAGAAGCTCTTGACGGTTATGCCCAAGGCACAGGAGGGAAGAAAG  2041
Db    2205  CTGAGGGCCACCACTGAGGAGAAGCTCTTGACGGTTATGCCCAAGGCACAGGAGGGAAGAAAG  2264

Qy    2042  TCAATTCAGACTGATGAGTGGAGAAATGCCGGGGCCCCGTGTCGAAGAACCTGGAATAAAGACC  2101
Db    2265  TCAATTCAGACTGATGAGTGGAGAAATGCCGGGGCCCCGTGTCGAAGAACCTGGAATAAAGACC  2324

Qy    2102  TGAAGGGCATTGAAAAACTATATTATTGAGGATACTGAGGAGTTAAACCAAAAAA        2161
Db    2325  TGAAGGGCATTGAAAAACTATATTATTGAGGATACTGAGGAGTTAAACCAAAAAA        2384

Qy    2162  AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAAATTGTTG          2221
Db          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAAAATTGTTG          2444
Qy    2385  GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTATAAAGTCAGCCCGGGTTA      2281
Db    2222  GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTATAAAGTCAGCCCGGGTTA      2504

Qy    2282  TGAAGAAGGCTGTTGGCCACTTATCCCTTTCATGGAAAGAAAGAGAAGAAAACCAGAG      2341
Db    2505  TGAAGAGGGCTGTTGGCCACTTATCCCTTTCATGGAAAGAAAGAGAAGAAAACCAGAG      2564

Qy    2342  TGCTTAACGGCACAGTAGAAGAGAAGAGGACCCTTACCCAGGGCACCATCGTCTGCTGGCCACTG  2401
Db    2565  TGCTTAACGGCACAGTAGAAGAGAAGAGGACCCTTACCCAGGGCACCATCGTCTGCTGGCCACTG  2624

Qy    2402  TTAAAGGCGACGTGCACGACGTAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA   2461
Db    2625  TTAAAGGCGACGTGCACGACGTAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA   2684

Qy    2462  ATTTCCGAGTTATTGATTTAGGAGTCATGATCCATGTGATAAGATACTGAAAGCTGCTC    2521
Db    2685  ATTTCCGAGTTATTGATTTAGGAGTCATGATCCATGTGATAAGATACTGAAAGCTGCTC    2744

Qy    2522  TTGACCACAAAGCAGCAGATATAATTGGCCTGTCAGGACTCATCATCCCTCCTTCCCTGATGAAA  2581
Db    2745  TTGACCACAAAGCAGCAGATATAATTGGCCTGTCAGGACTCATCATCCCTCCTTCCCTGATGAAA  2804

Qy    2582  TGATTTTTGTTGCCAAGGAAATGAGAGATTAGCTATAGGAGATTCCATTGTGTTGATTGGAG   2641
Db    2805  TGATTTTTGTTGCCAAGGAAATGAGAGATTAGCTATAGGAGATTCCATTGTGTTGATTGGAG   2864

Qy    2642  GAGCAACCACTTCAAAAACCCACAGCAGTAAAATAGCTCCAGATACAGTGCACCTG        2701
Db    2865  GAGCAACCACTTCAAAAACCCACAGCAGTAAAATAGCTCCAGATACAGTGCACCTG        2924

Qy    2702  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTCCCAGCTGTTAGATGAAA          2761
Db    2925  TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTCCCAGCTGTTAGATGAAA          2984

Qy    2762  ATCTAAAGGATGAATACTTTGAGGAGAAATCATGGAGAAATCATGAAGATAATTAGACAGGACC  2821
Db    2985  ATCTAAAGGATGAATACTTTGAGGAGAAATCATGGAGAAATCATGAAGATAATTAGACAGGACC  3044

Qy    2822  ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCCTTAAGTCAAGCCAGAAAAAGTGGTT    2881
Db    3045  ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCCTTAAGTCAAGCCAGAAAAAGTGGTT    3104

Qy    2882  TCCAAATGATTGGCTGTCTGAAGAGCTGGTGTGACTACCTGCAGCTCGTGGACTCGAGTACATTGGGACCCAGG  2941
Db    3105  TCCAAATGATTGGCTGTCTGAAGAGCTGGTGTGACTACCTGCAGCTCGTGGACTCGAGTACATTGGGACCCAGG  3164

Qy    2942  TCTTTGAAGACTATGACCTGCAGAGCTGTGGACTACATTGACTGGAAGCCTTTCTTTG     3001
Db    3165  TCTTTGAAGACTATGACCTGCAGAGCTGTGGACTACATTGACTGGAAGCCTTTCTTTG     3224

Qy    3002  ATGTCTGGCAGCTCCGGGGCAAGTACCCCGGGGTGTGGTCTTCGGCCACGAGTA         3061
Db    3225  ATGTCTGGCAGCTCCGGGGCAAGTACCCCGGGGTGTGGTCTTCGGCCACAGAGTA        3284

Qy    3062  AAACAGTAGGTGGAGAGGCGGAAGGTCTACGAGGCTGATGATGCCCACACAC           3121
Db    3285  AAACAGTAGGTGGAGAGGCGGAAGGTCTACGAGGCTGATGATGCCCACACAC           3344

Qy    3122  TGATTAGTCAAAAGAAACTCCGGGGCAATCTTCGGCGTTCGGCCACAGAGTA           3181
Db    3345  TGATTAGTCAAAAGAAACTCCGGGGCAATCTTCGGCGTTCGGCCACAGAGTA           3404

Qy    3182  TCCAAGGACCATTCACCTGTACGCACAGGAAGCTGTGTGCCCCAGGCTCGAGAGCCCATAG   3241
Db    3405  TCCAAGGACCATTCACCTGTACGCACAGGAAGCTGTGTGCCCCAGGCTCGAGAGCCCATAG   3464

Qy    3242  CCACTTTCTATGGGTTAAGGCAACAGCGGCTGCGAAGGACTCTGCCAGCACGGAGCCATACT  3301
Db    3465  CCACTTTCTATGGGTTAAGGCAACAGCGGCTGCGAAGGACTCTGCCAGCACGGAGCCATACT  3524
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Qy   62 ACATGTCACCGGCGCTCCAAGACCCTGTCGCAACCCGAAGTCTGAAGAAAAACCCTGCGGG 121
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Db   285 ACATGTCACCGGCGCTCCAAGACCCTGTCGCAACCCGAAGTCTGAAGAAAAACCCTGCGGG 344

Qy   122 ATGAGATCAATGCCATTCTGCAGAAGCAGGATTATCGTGTCTGGATGGATGGGGACCA   181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 ATGAGATCAATGCCATTCTGCAGAAGCAGGATTATCGTGTCTGGATGGATGGGGACCA   404

Qy   182 TGATCCAGCGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG   241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 TGATCCAGCGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG   464

Qy   242 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC   301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC   524

Qy   302 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA   361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA   584

Qy   362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT   421
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Db   585 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT   644

Qy   422 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA   481
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Db   645 GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA   704

Qy   482 GGTTTGTGGCAGGGGCTCTGGGTCCGGAAGTTCAAGGATCAGGTTGAGG   541
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 GGTTTGTGGCAGGGGCTCTGGGTCCGGAAGTTCAAGGATCAGGTTGAGG   764

Qy   542 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG   601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   765 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG   824

Qy   602 CCAAAGGACTTCTCGATGGGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG   661
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   825 CCAAAGGACTTCTCGATGGGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG   884

Qy   662 CCAATGCCAAGGCAGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC   721
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Db   885 CCAATGCCAAGGCAGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCC   944

Qy   722 GGCCTATCTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA   781
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Db   945 GGCCTATCTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGACTCTTTCCGGACAGA   1004

Qy   782 CAGGAGGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT   841
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Db   1005 CAGGAGGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTACATTGGATTAAATT   1064

Qy   842 GTGCTTTGGGTGCAGCTGAGATGAGAGACCTTTATTGAAATAATTGAAAATGTACAACAG   901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 GTGCTTTGGGTGCAGCTGAGATGAGAGACCTTTATTGAAATAATTGAAAATGTACAACAG   1124

Qy   902 CCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA   961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 CCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAA   1184

Qy   962 CGCCTTCTATGATGGCCAAGACCTAAAGGATTTTGCTATGAAGGCTTGGTCAATATAG   1021
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Db   1185 CGCCTTCTATGATGGCCAAGACCTAAAGGATTTTGCTATGAAGGCTTGGTCAATATAG   1244

Qy   1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA   1081
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Db   1245 TTGGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA   1304

Qy   1082 ATTGTAAGCCTAGAGTTCCACCTGCCACGTCTTTGAAGGACATATGTTACTGTCTGTC   1141
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Db   1305 ATTGTAAGCCTAGAGTTCCACCTGCCACGTCTTTGAAGGACATATGTTACTGTCTGTC   1364

Qy   3302 ACTGCCTCTCAGACTTCATCGTCCCCTTGCATTCTGGCATCCGTGACTACCTGGGCTGT   3361
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Db   3525 ACTGCCTCTCAGACTTCATCGTCCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT   3584

Qy   3362 TTGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGGATGGATGGTGACG   3421
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3585 TTGCCGTTGCCTGCTTTGGGGTAGAAGAGCTGAGCAAGGCCTATGGATGGATGGTGACG   3644

Qy   3422 ACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCGCAGAGGGCCTTTGCAGAAG   3481
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Db   3645 ACTACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCGCAGAGGGCCTTTGCAGAAG   3704

Qy   3482 AGCTCCATGAAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGACG   3541
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Db   3705 AGCTCCATGAAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGACG   3764

Qy   3542 TCGCAGACCTGCGAAGGTTGCGGGTACAAGGGCATCCGCGCCTCCTGGCTACCCCCAGCC   3601
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Db   3765 TCGCAGACCTGCGCGCAGGCTGCGGGTACAAGGGCATCCGCGCCGTCCTGGCTACCCCCAGCC   3824

Qy   3602 AGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATGCAGTCTACAG   3661
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Db   3825 AGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATGCAGTCTACAG   3884

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTTCTCAGGCCTCTACT   3721
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Db   3885 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTTCTCAGGCCCTCTACT   3944

Qy   3722 TCTCCAATTTGAAGTCAAATATTTTGCTGTGGGAAGATTTCCAAGGATCAGGTTGAGG   3781
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Db   3945 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGAAGATTTCCAAGGATCAGGTTGAGG   4004

Qy   3782 ATTATGCATTGAGGAGAGAACATATCTGTGGCTGAGGTTGAGAAAATGGCTTGGACCCATTT   3841
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Db   4005 ATTATGCATTGAGGAGAGAACATATCTGTGGCTGAGGTTGAGAAAATGGCTTGGACCCATTT   4064

Qy   3842 TGGGATATGATACAGACTAACTTTTTTTTTTTTT   3875
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Db   4065 TGGGATATGATACAGACTAACTTTTTTTTTTTTTTT   4098

RESULT 4
US-09-347-878-4

; Sequence 4, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 4
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 7122
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (287)..(4084)
; OTHER INFORMATION: Human methionine synthase cDNA
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: U75743/GenBank

US-09-347-878-4

  Query Match   89.7%; Score 3517; DB 3; Length 7122;
  Best Local Similarity 99.8%; Pred. No. 0;
  Matches 3867; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

Qy   2 GTCACCTGTGGAGAGCACGTCTTCTTCTGCGCGCCCTTCGCGCGGAGGAGGAGACTCGACA   61
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Db   225 GTCACCTGTGGAGAGCACGTCTTCTTCTGCGCGCCCTTCGCGCGGAGGAGGAGACTCGACA   284

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Db  2445  GTGATCTTTTGGAGCTGGAAAAATGTTTCTACCTCCAGGTTATAAAGTCAGCCCGGGTTA  2504
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Qy  2282  TGAAGAGGCGTGTTGGCCACCTGATTAATCCCTTCATGCAATGGAAAAGAAGAACCAGAG  2341

Db  2505  TGAAGAGGGCGTGTTGGCCACCTGATTAATCCCTTCATGCAATGGAAAAGAAAGAACCAGAG  2564
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Qy  2342  TGCTTAACGGCACAGTAGAGAAGAGAGACCCTACCAGGGACACCATCGTGTGGCCACTG  2401

Db  2565  TGCTTAACGGCACAGTAGAGAAGAGAGACCCTACCAGGGACACCATCGTGTGGCCACTG  2624
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Qy  2402  TTAAAGGCGACGTGCACGACGACATAGTTGGAGTAGTCCTTGGCTGCAATA  2461

Db  2625  TTAAAGGCGACGTGCACGACGACATAGTTGGAGTAGTCCTTGGCTGCAATA  2684
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Qy  2462  ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGTCTC  2521

Db  2685  ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTC  2744
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Qy  2522  TTGACCACAAAGCAGTATAATTGGCTGTGTCAGGACTCATCACTCCTTCCCTGGATGAAA  2581

Db  2745  TTGACCACAAAGCAGTATAATTGGCTGTGTCAGGACTCATCACTCCTTCCCTGGATGAAA  2804
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Qy  2582  TGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCATTGTTGATTGGAG  2641

Db  2805  TGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCATTGTTGATTGGAG  2864
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Qy  2642  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  2701

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Qy  2702  TAATCCATGTCCTGGACGCGTCCAAGAGTGGTGTGTTCCCAGCTGTTAGATGAAA  2761

Db  2925  TAATCCATGTCCTGGACGCGTCCAAGAGTGGTGTGTTCCCAGCTGTTAGATGAAA  2984
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Qy  2762  ATCTAAAGGATGAATCTTTGAGGAAATCATGAGAATATGAAGATATTAGACAGGACC  2821

Db  2985  ATCTAAAGGATGAATCTTTGAGGAAATCATGAGAATATGAAGATATTAGACAGGACC  3044
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Qy  2822  ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT  2881

Db  3045  ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT  3104
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Qy  2882  TCCAAATGATTGGCTGTCTGAACCTCACCCAGTGAAGCTTCACCGAGTTTATTGGGACCCAGG  2941

Db  3105  TCCAAATGATTGGCTGTCTGAACCTCACCCAGTGAAGCTTCACCGAGTTTATTGGGACCCAGG  3164
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Qy  2942  TCTTTGAAGACTATGACCTGCAGAGCTGGACTACATTGACTGGAAGCTTTCTTTTG  3001

Db  3165  TCTTTGAAGACTATGACCTGCAGAGCTGGACTACATTGACTGGAAGCTTTCTTTTG  3224
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Qy  3002  ATGTCTGGCAGCTCCGGGGCAAGTACGCCAGAGGCTTCCCAGAGCTATTTTCAACGACA  3061

Db  3225  ATGTCTGGCAGCTCCGGGGCAAGTACGCCAGAGGCTTCCCAGAGCTATTTTCAACGACA  3284
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Qy  3062  AAACAGTAGGTGGAGAGGCCAGGAAGGCTCTACGATGATGATGCTGAACACAC  3121

Db  3285  AAACAGTAGGTGGAGAGGCCAGGAAGGCTCACGATGATGATGCTGAACACAC  3344
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Qy  3122  TGATTAGTCAAAAGAAACTCCGGGCACGCCTTGAGTATGCCCCTTG  3181

Db  3345  TGATTAGTCAAAAGAAACTCCGGGCACGCCTTGAGTATGCCCCTTG  3404
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Qy  3182  TCCAAGACGACATTCACCTGTACGGGAAGCTTGTGCCCCAGAGGCTGCGAGAGCCCATAG  3241

Db  3405  TCCAAGACGACATTCACCTGTACGGGAAGCTTGTGCCCCAGAGGCTGCGAGAGCCCATAG  3464
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Qy  3242  CCACTTTCTATGGGTTAAGGCAACAGGCTGCGAGAAGGCTGCCAGCACCGAGCACCATACT  3301

Db  3465  CCACTTTCTATGGGTTAAGGCAACAGGCTGCGAGAAGGCTGCCAGCACCGAGCACCATACT  3524
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Qy  3302  ACTGCCTCTCCAGACTTCATCGCGTCATTCGGCATCCGTCGGACTACCTTGGGCCGGTTA  3361
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Qy  1142  TAGAGCCCTTCAGGATTGGACCGTACCACCAACTTGTTAACATTGGAGAGCGCTGTAATG  1201
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Db  1365  TAGAGCCCTTCAGGATTGGACCGTACCACCAACTTTGTTAACATTGGAGAGCGCTGTAATG  1424

Qy  1202  TTGCAGGATCAAGGAAGTTGTCTAAACTCATCATCATGGCAGGAAAACTATGAGAAGCCTTGT  1261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1425  ACATCGCAAAGGTACCTTGTGCCATCGACGACTCCTCCAATTTTGCTGTGTGATTGAAGCTGGGT  1484

Qy  1262  GTGTTGCCAAGTGCAGGTGGAGCCCAGTGTTGGATGTCAACATGGATGATG  1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1485  GTGTTGCCAAGTGCAGGTGGAGCCCAGTGTTGGATGTCAACATGGATGATG  1544

Qy  1322  GCATGCTAGATGGTCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCCGAGCCAG  1381
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Db  1545  GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCCGAGCCAG  1604

Qy  1382  ACATGCAAAGGTACCTTGTGCCATCGACGACTCCTCCAATTTGCTGTGTGATTGAAGCTGGGT  1441
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Db  1605  ACATCGCAAAGGTACCTTGTGCCATCGACGACTCCTCCAATTTTGCTGTGTGATTGAAGCTGCTC  1664

Qy  1442  TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGGACG  1501
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Db  1665  TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGGACG  1724

Qy  1502  ACTTCTTGGAGAAGGCCAGGAAGTATGGAGCTGCTATGGTGGTCATGGCTT  1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1725  ACTTCTTGGAGAAGGCCAGGAAGTATGGAGCTGCTATGGTGGTCATGGCTT  1784

Qy  1562  TTGATGAAGAGGAGGCAGGCAACAGAAACAGACAGAAAAATCAGAGTGTGTCACCCGGCCT  1621
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Db  1785  TTGATGAAGAGGAGGCAGGCAACAGAAACAGACAGAAAAATCAGAGTGTGTCACCCGGCCT  1844

Qy  1622  ACCATCTGCTTGTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA  1681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1845  ACCATCTGCTTGTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTGACCCTAATA  1904

Qy  1682  TCCTAACCATTGGGACTGGAATGGAAGTCATTCATTGGAACAACAACTGTATGCCATTAATTTATCCATG  1741
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Db  1905  TCCTAACCATTGGGACTGGAATGGAAGTCACAACTGTATGCCATTAATTTTATCCATG  1964

Qy  1742  CAACAAAGTCATTCATTATTACCTGGAGCCAGATGAACATGGGGATAGTTGAAGTCAACT  1801
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Db  1965  CAACAAAGTCATTCATTATTACCTGGAGCCAGATGAACATGGGGATAGTTGAAGTCAACT  2024

Qy  1802  TGTCCTTCTCCTTCCGAGGAAGCCATTCTGCAGCCAATGCATGGGGTTTCTTT  1861
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Db  2025  TGTCCTTCTCCTTCCGAGGAAGCCATTCGAGAAGCCATTGGGGTTTATTTCTTT  2084

Qy  1862  ACCATGCAATCAAGTCGGATGGACATGGACATGGGATAGTTGAATGCTGGAAAACCTCCGTGT  1921
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Db  2085  ACCATGCAATCAAGTCTGGATGCCATGGGATAGTTGAATGCTGGAAAACCTCCCTGTGT  2144

Qy  1922  ATGATGATATCCATAAAACTATATTGAAGAAGCTCAGGTTAAACCAAGACC  1981
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Db  2145  ATGATGATATCCATAAAACATATTATTGAGGATCTCATCTGGAATAAAGACC  2204

Qy  1982  CTGAGGCCACTGAGAAGCTCTTACGTATGCCCAGACTCAAGGCAACCAGGAGGAAGAAAG  2041
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Db  2205  CTGAGGCCACTGAGAAGCTCTTACGTATGCCCAGACTCAAGGCAACCAGGAGGAAGAAAG  2264

Qy  2042  TCATTCAGACTGATGAGTGAGAAATGGCCCGTGCCAAGAACGCCTTGAGTATGCCCCTTG  2101
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Db  2265  TCATTCAGACTGATGAGTGAGAAATGGCCCGTGCCAAGAACGCCTTGAGTATGCCCCTTG  2324

Qy  2102  TGAAGGGCATTGAAAAACATATTATTGAGGAAGCCAAGGTTAAACCAAAGACC  2161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2325  TGAAGGGCATTGAAAAACATATTATTGAGGATCTCATCTGGAATAAAGACC  2384

Qy  2162  AATATCCCGACCTCTCAATATAATAATTGAAGGACCCCTGATGAATGGAATTGTTTTG  2221
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Db  2385  AATATCCCGACCTCTCAATATAATAATTGAAGGACCCCTGATGAATGGAATTGTTTTG  2444

Qy  2222  GTGATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCCAGGTTATAAAGTCAGCCCGGGTTA  2281
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Db    3525  ACTGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3584
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Qy     122  ATGAGATCAATGCCATTCTGCGAGAGAGAGGATTATGTGCTTGGATGTGAGGGATGGGACCA  181

Qy    3362  TTGCCGTTGCCTGCTGTTTGGGGTAGAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG  3421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     345  ATGAGATCAATGCCATTCTGCGAGAGAGAGGATTATGTGCTTGGATGTGAGGGATGGGACCA  404

Db    3585  TTGCCGTTGCCTGCTGTTTGGGGTAGAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACG  3644
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Qy     182  TGATCCAGCGGGAGAAGCTAAACGAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG  241

Qy    3422  ACTACAGCAGCATCATGGTCAAGGCGTCAAGGCGTGGGGGACCGGCTGGGCAGGGCCTTTGCAGAAG  3481
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Db     405  TGATCCAGCGGGAGAAGCTAAACGAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG  464

Db    3645  ACTACAGCAGCATCATGGTCAAGGCGTCAAGGCGTGGGGGACCGGCTGGGCAGGGCCTTTGCAGAAG  3704
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Qy     242  CCAGGCCGCTGAAAGGCCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC  301

Qy    3482  AGTTCCATGAAAGAGTTCGCCGAGAACTGTGGGCTTGGGCCTACTGTGGCAGTGAGCAGCTGGACG  3541
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Db     465  CCAGGCCGCTGAAAGGCCAACAATGACATTTTAAGTATAACTCAGCCTGATGTCATTTACC  524

Db    3705  AGTTCCATGAAAGAGTTCGCCGAGAACTGTGGGCTTGGGCCTACTGTGGCAGTGAGCAGCTGGACG  3764
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Qy     302  AAATCATAAGGAATACTTGCCCAAGCTGACATTGCCCTGACACTTGCCTACCGATGAACATGT  361

Qy    3542  TCGCAGAACCTGCGAAGGTTGCGAAGGTCGCAGCCAGGCTGCGGGGTACAAGGCATCCGCCGGCTCCTGGCTACCCCAGCC  3601
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Db     525  AAATCATAAGGAATACTTGCCCAAGCTGACATTGCCCTGACACTTGCCTACCGATGAACATGT  584

Db    3765  TCGCAGAACCTGCGAAGGTTGCGAAGGTCGCAGCCAGGCTGCGGGGTACAAGGCATCCGCCGGCTCCTGGCTACCCCAGCC  3824
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Qy     362  GCACTAGTATTGCCCAAGCTGACTATGGCCTTGACACTTGACACTTGCCTACCGGATGAACATGT  421

Qy    3602  AGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCGAGTCTACAG  3661
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Db     585  GCACTAGTATTGCCCAAGCTGACTATGGCCTTGACACTTGCCTACCGGATGAACATGT  644

Db    3825  AGCCCGACCACCACCGAGAAGCTCACCATGTGAGACTCGCAGACATCGAGCGAGTCTACAG  3884
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Qy     422  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA  481

Qy    3662  GCATTAGGTTAACAGAATCATTAGCAATGCCACCTGCTTCAGCAGTCTCAGGCCTTCTACT  3721
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Db     645  GCTCTGCAGGAGTGGCCAGAAAAGCTGCCGAGGAGGTAACTCTCCAGACAGGAATTAAGA  704

Db    3885  GCATTAGGTTAACAGAATCATTAGCAATGCCACCTGCTTCAGCAGTCTCAGGCCTTCTACT  3944
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Qy     482  GGTTTGTTGGGCAGGGGGGCTCTGGGTCCCATCTGTGTCCCATCTGTGG  541

Qy    3722  TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTTTCCAAGGATCAGGTTGAGG  3781
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Db     705  GGTTTGTTGGGCAGGGGGGCTCTGGGTCCCATCTGTGTCCCATCTGTGG  764

Db    3945  TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTTTCCAAGGATCAGGTTGAGG  4004
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Qy     542  AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGTGAAGCATACCAAGAGCAGG  601

Qy    3782  ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCCATTT  3841
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Db     765  AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGTGAAGCATACCAAGAGCAGG  824

Db    4005  ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCCATTT  4064
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Qy     602  CCAAAGGACTTCTGGATGGCCGGGGTTGATATCTTACTCATTCATTGATACTG  661

Qy    3842  TGGGATATGATACAGACTAACTTTTTTTTTTTTT  3875
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Db     825  CCAAAGGACTTCTGGATGGCCGGGGTTGATATCTTACTCATTCATTGATACTG  884

Db    4065  TGGGATATGATACAGACTAACTTTTTTTTTTTTTTT  4098

Qy     662  CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC  721
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Db     885  CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC  944

Qy     722  GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGGACTCTTTCCGGACAGA  781
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Db     945  GGCCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGGGACTCTTTCCGGACAGA  1004

Qy     782  CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTGCATTGGATTAAATT  841
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1005  CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAACCACTCTACATTGGATTAAATT  1064

Qy     842  GTGCTTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACACACAG  901
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1065  GTGCTTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACACACAG  1124

Qy     902  CCTATGTCCTCGTTATCCCAATGCAAGCACCTAAAGGATTTTGCTTGGTGACTATGATGAAA  961
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1125  CCTATGTCCTCGTTATCCCAATGCAAGCACCTAAAGGATTTTGCTTGGTGACTATGATGAAA  1184

Qy     962  CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTTGGTGACTATGATGGTCAATATAG  1021
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1245  TTGGAGGATGCTGTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTGAAGCTGTGAAAA  1304

Qy    1082  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTC  1141
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1305  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTC  1364

Qy    1142  TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCTGTAATG  1201
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1365  TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGAGAGCGCTGTAATG  1424

Qy    1202  TTGCAGGATCAAGGAAGTTGCTAAACTCATCATCATGGCAGGAAACTATGAAGAAGCCTTGT  1261
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RESULT 5
US-09-577-266-2
; Sequence 2, Application US/09577266
; Patent No. 6912492
; GENERAL INFORMATION:
;   APPLICANT: Johnson, William G.
;   APPLICANT: Stenroos, Edward S.
;   TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
;   TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
;   FILE REFERENCE: 601-1-057N
;   CURRENT APPLICATION NUMBER: US/09/577,266
;   CURRENT FILING DATE: 2000-05-23
;   PRIOR APPLICATION NUMBER: 60/136,198
;   PRIOR FILING DATE: 1999-05-25
;   NUMBER OF SEQ ID NOS: 46
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 7122
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;US-09-577-266-2

Query Match   89.7%; Score 3517; DB 3; Length 7122;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3867; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

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Qy       2  GTCACCTGTGAGAGCACGTCTTCTCTGCCCGCGCCCTCGCCCAAGGAGGAGACTCGACA  61
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Db     225  GTCACCTGTGAGAGCACGTCTTCTCTGCCGCGCCCTCGCCCAAGGAGGAGACTCGACA  284

Qy      62  ACATGTCACCCGCCTCCCAAGACCTGTCGCACACCCGAAGGTCGAAGAAAACCCTGCGGG  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     285  ACATGTCACCCGCCTCCCAAGACCTGTCGCACCCGAAGGTCTGAAGAAAACCCTGCGGG  344
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Qy  2505  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAAGAAGAGAAGAAACCAGAG  2564
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1425  TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGCAGGAAACTATGAAGAAGCCTTGT  1484

Qy  2342  TGCTTAACGGCACAGTAGAGAGAGAGAACCCTTACCAGGTGCTGGCCACTG  2401
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2565  TGCTTAACGGCACAGTAGAGAGAGAGAACCCTTACCAGGTGCTGGCCACTG  2624

Qy  1262  GTGTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGTGTGTTGGATGTGTCAACATGATGATG  1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1485  GTGTTGCCAAAGTGGCAGGTGGAAATGGGAGCCCAGTGTGTTGGATGTGTCAACATGATGATG  1544

Qy  2402  TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA  2461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2625  TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA  2684

Qy  1322  GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAG  1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1545  GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTGCAACTTAATTGCTTCCGAGCCAG  1604

Qy  2462  ATTTCCGAGTTATTGATTTAGGAGTCATGAGTCCATGTGATAAGAACTGAAGCTGCTC  2521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2685  ATTTCCGAGTTATTGATTTAGGAGTCATGAGTCCATGTGATAAGAACTGAAGCTGCTC  2744

Qy  1382  ACATCGCCAAAGTACCTTTGTCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGT  1441
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Db  1605  ACATCGCCAAAGTACCTTTGTCATCGACTCCTCCAATTTGCTGTGATTGAAGCTGGGT  1664

Qy  2522  TTGACACCAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGGATGAAA  2581
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Db  2745  TTGACACCAAAGCAGATATAATTGGCCTGTCAGGACTCATCATCCTTCCCTGGATGAAA  2804

Qy  1442  TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGGACG  1501
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Db  1665  TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGGACG  1724

Qy  2582  TGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG  2641
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Db  2805  TGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG  2864

Qy  1502  ACTTCTTCTTGGAGAAGGCCAGGAAGTTAAAAAGTGTATGGGCTGCTATGGTCGTCATGGCTT  1561
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Db  1725  ACTTCTTCTTGGAGAAGGCCAGGAAGTTAAAAAGTGTATGGGCTGCTATGGTCGTCATGGCTT  1784

Qy  2642  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTACAGTGCCACCTG  2701
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Db  2865  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTACAGTGCCACCTG  2924

Qy  1562  TTGATGAAGAAGGACAGGCAACAGAGAACAGAGAAAAATCAGAGTTTTTATCCATGTGTGCACCCGGGCCT  1621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1785  TTGATGAAGAAGGACAGGCAACAGAGAACAGAGAAAAATCAGAGTTTTTATCCATGTGTGCACCCGGGCCT  1844

Qy  2702  TAATCCATGTCCTGGACGCGTCCAAGAGTGGTGGTGTTCCCAGCTGTTAGATGAAA  2761
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Db  2925  TAATCCATGTCCTGGACGCGTCCAAGAGTGGTGGTGTTCCCAGCTGTTAGATGAAA  2984

Qy  1622  ACCATCTGCTTGTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA  1681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1845  ACCATCTGCTTGTGTGAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA  1904

Qy  2762  ATCTAAAGGATGAATACTTTGAGGAATCATGGAAATCATGGAAGATATTAGACAGGACC  2821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2985  ATCTAAAGGATGAATACTTTGAGGAATCATGGAAATCATGGAAGATATTAGACAGGACC  3044

Qy  1682  TCCTTAACCATTGGAACTGGAGGAACACAACTTGTATGCCATTTATTTAATTTTATCCATG  1741
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1905  TCCTTAACCATTGGAACTGGAGGAACACAACTTGTATGCCATTTATTTAATTTTATCCATG  1964

Qy  2822  ATTATGAGTCTCTCAAGGAGGAGGAGAGACTTACCCTAAGTCAAGCCAGAGATATTAGACAGGACC  2881
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3045  ATTATGAGTCTCTCAAGGAGGAGGAGAGACTTACCCTAAGTCAAGCCAGAGATATTAGACAGGACC  3104

Qy  1742  CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGTCTTTCCAACT  1801
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Db  1965  CAACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGAGTCTTTCCAACT  2024

Qy  2882  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAGACCTCGAGCCCACGTTTATTGGACCCAGG  2941
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3105  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAGACCTCGAGCCCACGTTTATTGGGACCCAGG  3164

Qy  1802  TGTCCTTCCTTCCGAGGAATGGAAGCCATTCGAGAAGAAGCCATTCGAGAAGCAATGGGGTTTTCTTT  1861
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2025  TGTCCTTCCTTCCGAGGAATGGAAGCCATTCGAGAAGAAGCCATTCGAGAAGCAATGGGGTTTTCTTT  2084

Qy  2942  TCTTTGAAGACTATGACCTGCGAGAGCTGGTGGACTACATTGACTGAAGCCTTTCTTTG  3001
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Db  3165  TCTTTGAAGACTATGACCTGCGAGAGCTGGTGGACTACATTGACTGAAGCCTTTCTTTG  3224

Qy  1862  ACCATGCAATCAAGTCTGGCATGCATGGGACATGGGGAGAAATGCTGGAAGTCTGGAAGCTGGAA  1921
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Db  2085  ACCATGCAATCAAGTCTGGCATGCATGGGACATGGGGAGAAATGCTGGAAGTCTGGAAGCTGGAA  2144

Qy  3002  ATGTCTGGCCAGCTCCGGGGCCAAGTCTACGCAGAGGCTTCCCAAGATATTATTAACGACA  3061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3225  ATGTCTGGCCAGCTCCGGGGCCAAGTCTACGCAGAGGCTTCCCAAGATATTATTAACGACA  3284

Qy  1982  CTGAGGCCACTGAGAGTGTGAGTGTGTTACCTTCACCTGTATAAAGTCAGCCCGGGTTA  2041
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Db  2205  CTGAGGCCACTGAGAGTGTGAGTGTGTTACCTTCACCTGTATAAAGTCAGCCCGGGTTA  2264

Qy  3062  AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGAGAAGTCTACGAGTCCACAATATGCTGAAACAC  3121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3285  AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGAGAAGTCTACGAGTCCACAATATGCTGAAACAC  3344

Qy  2102  TCATTCAGACTGATGAGTGAGAAATGGGCCCTTGAGTGAGTATGCCCTTG  2161
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2325  TCATTCAGACTGATGAGTGAGAAATGGGCCCTTGAGTGAGTATGCCCTTG  2384

Qy  3122  TGATTAGTCAAAAGAAACTCCGGGCCTGTGGTTGTGGTTCTGGCCAGCACACAGAGTA  3181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3345  TGATTAGTCAAAAGAAACTCCGGGCCTGTGGTTGTGGTTCTGGCCAGCACACAGAGTA  3404

Qy  2162  AATATCCCCGACCTCTCAATTATTATTGAAGGACCCCTGATGAATGGAATGAAATTGTTG  2221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2385  AATATCCCCGACCTCTCAATTATTATTGAAGGACCCCTGATGAATGGAATGAAATTGTTG  2444

Qy  3182  TCCAAGACGCACATTCACCTGTTAAGGCAACAGCTCTGCCAGGCTGCTCGTGTCGCCAGCCCATAG  3241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3405  TCCAAGACGCACATTCACCTGTTAAGGCAACAGCTCTGCCAGGCTGCTCGTGTCGCCAGCCCATAG  3464

Qy  2222  GTGATCTTTTTGGGAGCTGGAAAAATGTTTCTACCTGGGTTATAAAGTCAGCCCGGGTTA  2281
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Db  2445  GTGATCTTTTTGGGAGCTGGAAAAATGTTTCTACCTGGGTTATAAAGTCAGCCCGGGTTA  2504

Qy  3242  CCACTTTCTATGGGTTAAGGCAACAGCTCTGCCGAGAAGACTCTGCGAGAAGCTGAGAAGACGCCATACT  3301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3465  CCACTTTCTATGGGTTAAGGCAACAGCTCTGCCGAGAAGACTCTGCGAGAAGCTGAGAAGACGCCATACT  3524

Qy  2282  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAGAAAGAAGAGAAGAAACCAGAG  2341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3585  TTGCCGTTGGCCTGCTTTTGGGGTTTGGGGTTAGAAGAGCTGAGAAGAGCTGAGCAAGGCCTATGAGATGGTGACG  3644
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RESULT 6
US-09-347-878-6
; Sequence 6, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin Ver. 2.0
US-09-347-878-6
;   SEQ ID NO 6
;   LENGTH: 7224
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (395)..(4192)
;   FEATURE:
;   OTHER INFORMATION: Human methionine synthase
;   PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: U73338/GenBank
US-09-347-878-6

Query Match   88.4%; Score 3466; DB 3; Length 7224;
Best Local Similarity   99.8%;
Matches 3866; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

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Qy 1262  GTGTTGCCAAAGTCAGGTCGAGGTGGAAATGGGAGCCCAGTGTGGATGTCAACATGATGATG  1321
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Db 1593  GTGTTGCCAAAGTCAGGTCGAGGTGGAAATGGGAGCCCAGTGTGGATGTCAACATGATGATG  1652

Qy 1322  GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCAG  1381
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1653  GCATGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCAG  1712

Qy 1382  ACATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCTTGTGATTGAAGCTGGGT  1441
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Db 1713  ACATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCTTGTGATTGAAGCTGGGT  1772

Qy 1442  TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACG  1501
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Db 1773  TAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGGAGGACG  1832

Qy 1502  ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT  1561
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Db 1833  ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT  1892

Qy 1562  TTGATGAAGAGGACAGGCCAACAGAAACAGACACAAAATCAGAGTGTGCACCCGGGCCT  1621
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1893  TTGATGAAGAGGACAGGCCAACAGAAACAGACACAAAATCAGAGTGTGCACCCGGGCCT  1952

Qy 1622  ACCATCTGCTTGTGAAAAAACTGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA  1681
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1953  ACCATCTGCTTGTGAAAAAACTGGCTTTAATCCAAATGACATTATTTTTGACCCTAATA  2012

Qy 1682  TCCTAACCATTGGGACTGGAATGGAGGGAACAACTGTTATGCCATTAATTTTATCCATG  1741
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2013  TCCTAACCATTGGGACTGGAATGGAGGGAACAACTGTTATGCCATTAATTTTATCCATG  2072

Qy 1742  CAACAAAAGTCATTAAGAACAACATTACCTGGAGCCAGAATAAGTTGGAGGTCTTTCCAACT  1801
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2073  CAACAAAAGTCATTAAGAACAACATTACCTGGAGCCAGAATAAGTTGGAGGTCTTTCCAACT  2132

Qy 1802  TGTCCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCAATGGGCATGGG  1861
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Db 2133  TGTCCCTTCTCCTTCCGAGGAATGGAAGCCATTCGAGAAGCAATGCAATGGGCATGGG  2192

Qy 1862  ACCATGCAATCAAGTCTCGGACATGGACGATAGTGAAGCTGTCGAAACCTCCCTGTGT  1921
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2193  ACCATGCAATCAAGTCTCGGACATGGACGATAGTGAAGCTGTCGAAACCTCCCTGTGT  2252

Qy 1922  ATGATGATATCCATAAGGAACTTCGCAGCTCTGAAGATCTCATCTGAAGATAAAGACC  1981
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2253  ATGATGATATCCATAAGGAACTTCGCAGCTCTGAAGATCTCATCTGAAGATAAAGACC  2312

Qy 1982  CTGAGGCCACTGAGAAGCTTCTTACGGTATGCCCAGACTCAAGGCACAGAGGAGGAAGAAG  2041
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Db 2313  CTGAGGCCACTGAGAAGCTTCTTACGGTATGCCCAGACTCAAGGCACAGAGGAGGAAGAAG  2372

Qy 2042  TCATTCAGACTGATGAGTGAGAAATGGCCCTGTGCGAAGACACGCCTTGAGTATGCCCTTG  2101
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Db 2373  TCATTCAGACTGATGAGTGAGAAATGGCCCTGTGCGAAGACACGCCTTGAGTATGCCCTTG  2432

Qy 2102  TGAAGGGCATTGAAAAACATTATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAA  2161
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Db 2433  TGAAGGGCATTGAAAAACATTATTATTGAGGATACTGAGGAAGCCAGGTTAAACCAAAAAA  2492

Qy 2162  AATATCCCCGACCTCTCAATAATTGAAGGACCCCCTGATGAATGGAATGAAATTGTTG  2221
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Db 2493  AATATCCCCGACCTCTCAATAATTGAAGGACCCCCTGATGAATGGAATGAAATTGTTG  2552

Qy 2222  GTGATCTTTTTGGGAGCTGAAAAATGTTTCTACCTCAGGTTATAAAAGTCAGCCCGGGTTA  2281
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Db 2553  GTGATCTTTTTGGGAGCTGAAAAATGTTTCTACCTCAGGTTATAAAAGTCAGCCCGGGTTA  2612

Qy 2282  TGAAGAAGGCTGTTGGCCACCTTGGCCACCTTATCCCTTTCATGGAAAAAGAGAAACCAGAG  2341
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Db 2613  TGAAGAAGGCTGTTGGCCACCTTGGCCACCTTATCCCTTTCATGGAAAAAGAGAAACCAGAG  2672


Qy 2342  TGCTTAACGGCACAGTAGAAGAAGAGGACCCTACCAGGGCACCATCGTGTCGGCCACTG  2401
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Db 2673  TGCTTAACGGCACAGTAGAAGAAGAGGACCCTACCAGGGCACCATCGTGTCGGCCACTG  2732

Qy 2402  TTAAAGGCGACGTGCGACGACATAGTGGAGTAGTCCTTGGCTGCAATA  2461
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 2733  TTAAAGGGCGACGTGCGACGACATAGTGGAGTAGTCCTTGGCTGCAATA  2792

Qy 2462  ATTTCCGAGTTATTGATTTAGGAGTCATGGAGTCCATGTGATGATAAGACTGAAAGCTGCTC  2521
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2793  ATTTCCGAGTTATTGATTTAGGAGTCATGGAGTCCATGTGATGATAAGACTGAAAGCTGCTC  2852

Qy 2522  TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA  2581
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2853  TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAAA  2912

Qy 2582  TGATTTTGTTGTCCAAGGAAATGGAGAGATTAGCTATAAGGATTCATAAGGATTCCATTGTTGATTGGAG  2641
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Db 2913  TGATTTTGTTGTCCAAGGAAATGGAGAGATTAGCTATAAGGATTCATAAGGATTCCATTGTTGATTGGAG  2972

Qy 2642  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  2701
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Db 2973  GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG  3032

Qy 2702  TAATCCATGTCCTGACGCGTCCAAGAGTGTGTCCCAGCTGTTAGATGAAA  2761
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Db 3033  TAATCCATGTCCTGACGCGTCCAAGAGTGTGTCCCAGCTGTTAGATGAAA  3092

Qy 2762  ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAAATATGAAGATATTAGACAGGACC  2821
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3093  ATCTAAAGGATGAATACTTTGAGGAAATCATGGAAAATATGAAGATATTAGACAGGACC  3152

Qy 2822  ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTTGTT  2881
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Db 3153  ATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTTGTT  3212

Qy 2882  TCCAAATGGATTGGCTGTGTCTGAACCTCACCCAGTGAAGCCCAGTTTATTGGGACCCAGG  2941
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Db 3213  TCCAAATGGATTGGCTGTGTCTGAACCTCACCCAGTGAAGCCCAGTTTATTGGGACCCAGG  3272

Qy 2942  TCTTTGAAGACTATGACCTGCAGAAGCTGTGGAGACTACATTGGAAGCCTTTCTTTG  3001
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3273  TCTTTGAAGACTATGACCTGCAGAAGCTGTGGAGACTACATTGGAAGCCTTTCTTTG  3332

Qy 3002  ATGTCTGCAGCTCCCGGGCAAGTACCCGAGATCGAGGCTTCCCAAGATATTTAACGACA  3061
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3333  ATGTCTGCAGCTCCCGGGCAAGTACCCGAGATCGAGGCTTCCCAAGATATTTAACGACA  3392

Qy 3062  AAACAGTAGGTGGAGAGGCCAGGAGGTCTACGATGATGCCCACAATATGCTGAACACAC  3121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3393  AAACAGTAGGTGGAGAGGCCAGGAGGTCTACGATGATGCCCACAATATGCTGAACACAC  3452

Qy 3122  TGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGTTGGGGTTGGGTTGGTTCTGGCCAGCAGTA  3181
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3453  TGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGTTGGGGTTGGGTTGGTTCTGGCCAGCAGTA  3512

Qy 3182  TCCAAGGACGACATTCACCTGTACGGCAGAGGCTGCTGCTGCGAGAGCCCATAG  3241
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3513  TCCAAGGACGACATTCACCTGTACGGCAGAGGCTGCTGCTGCGAGAGCCCATAG  3572

Qy 3242  CCACTTTCTATGGGTTAAGGCAACAGGCTGGAAGGACTCTGCCAGCACGGAGCCATACT  3301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3573  CCACTTTCTATGGGTTAAGGCAACAGGCTGGAAGGACTCTGCCAGCACGGAGCCATACT  3632

Qy 3302  ACTGCCTCTCAGATCTTCATCGCTCCTTGGCATCCGTGACTACCTGGGCCTGT  3361
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3633  ACTGCCTCTCAGATCTTCATCGCTCCTTGGCATCCGTGACTACCTGGGCCTGT  3692

Qy 3362  TTGCCGTTGCCTGCTTTGGGGTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGTGACG  3421
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3693  TTGCCGTTGCCTGCTTTGGGGTGGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGTGACG  3752

Qy 3422  ACTACAGCAGCATCATGGTCAAGGCGCTGCTCGGGGGACCCGGCTGCGAGAGGCCTTTGCAGAAG  3481
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;   NAME/KEY: misc_feature
;   LOCATION: 5444
;   OTHER INFORMATION: n = c or a
US-09-962-665-1

Query Match   79.3%; Score 3109; DB 3; Length 7224;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3859; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy   2 GTCACCTGTGGAGACAGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACA 61
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   333 GTCACCTGTGGAGACAGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACA 392

Qy   62 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCTGAGACTCGAGAAACCCTGCGGG 121
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   393 ACATGTCACCCGCGCTCCAAGACCTGTCGCAACCTGAGACTCGAGAAACCCTGCGGG 452

Qy   122 ATGAGATCAATGCCATTCTGCGAGAAGAGGATTATGTGCTCGATGGGATGGGGACCA 181
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   453 ATGAGATCAATGCCATTCTGCGAGAAGAGGATTATGTGCTCGATGGGATGGGGACCA 512

Qy   182 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAGTTAAAGATCATG 241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   513 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAGTTAAAGATCATG 572

Qy   242 CCAGGCCGCTGAAAGGCAACAATGACATCTTAAGTATAACTCAGCCTGATGTCATTTACC 301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   573 CCAGGCCGCTGAAAGGCAACAATGACATCTTAAGTATAACTCAGCCTGATGTCATTTACC 632

Qy   302 AAATCCATAAGGAATACTTGCTGGCTGGGTGGGCCAGATATCATTGAAACAAATACTTTTAGCA 361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   633 AAATCCATAAGGAATACTTGCTGGCTGGGTGGGCCAGATATCATTGAAACAAATACTTTTAGCA 692

Qy   362 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 421
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   693 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCCTACCGGATGAACATGT 752

Qy   422 GCTCTGCAGGAGTGGCCAGAAAGCTGCCGAGGAGGAGTAACTCTCCAGACACAGGAATTAAGA 481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   753 GCTCTGCAGGAGTGGCCAGAAAGCTGCCGAGGAGGAGTAACTCTCCAGACACAGGAATTAAGA 812

Qy   482 GGTTTGTTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG 541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   813 GGTTTGTTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGG 872

Qy   542 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 601
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   873 AAAGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 932

Qy   602 CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG 661
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   933 CCAAAGGACTTCTGGATGGCGGGGTTGATATCTTACTCATTGAAACTATTTTTGATACTG 992

Qy   662 CCAATGCCAAGGCAGCCTTGTTTGCACTCACTGATAAAAGTGGGCGGCCGACTCTTCCCGGACAGA 721
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   993 CCAATGCCAAGGCAGCCTTGTTTGCACTCACTGATAAAAGTGGGCGGCCGACTCTTCCCGGACAGA 1052

Qy   722 GGCCTATCTTTATTTCAGGGAGCGATCGTGTTGATAAAGTGGGGCCGGACCACTCTGCATTGATTAATT 781
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1053 GGCCTATCTTTATTTCAGGGAGCGATCGTGTTGATAAAGTGGGGCCGGACCACTCTGCATTGATTAAATT 1112

Qy   782 CAGGAGAGGGAATTGTCATCAGCGTGTCTCATCAGNTGTCATGGAGAACCACTCTGCGATTGGATTAAATT 841
            |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1113 CAGGAGAGGGAATTGTCATCAGCGTGTCTCATCAGNTGTCATGGAGAACCACTCTGCGATTGGATTAAATT 1172

Qy   842 GTGCTTTGGGTGGCAGCTGAGATGAGAACCTTTATTGAATAATTGGAAAATGTACAACAG 901
            |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1173 GTGCTTTGGGTGGCAGCTGAGATGAAATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAG 1232

Qy   902 CCTATGTCCTCTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGGATGAAA 961
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1233 CCTATGTCCTCTGTTATCCCNAATGCAGGTCTTCCCAACACCTTTGGTGACTATGGATGAAA 1292

Db   3753 ACTACAGCAGCATCATGGTCAAGGGCGTCGGGGGACCGGCTGGCGCAGCAGACGTCGGAGAAG 3812
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3482 AGCTCCATGAAAGAGAGTTCGCGGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGACG 3541
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3813 AGCTCCATGAAAGAGAGTTCGCGGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGACG 3872
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3542 TCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGCC 3601
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3873 TCGCAGACCTGCGCAGGCTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCCCAGCC 3932
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3602 AGCCCGACCACCACCGAGAAGCTCACCATGTGGAGACTCGGAGACTCGAGCAGTCTACAG 3661
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3933 AGCCCGACCACCACCGAGAAGCTCACCATGTGGAGACTTGCGAGACATGCAGCAGTCTACAG 3992
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCCAGCAGTCTCAGGCCTCTACT 3721
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3993 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCCAGCAGTCTCAGGCCTCTACT 4052
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3722 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 3781
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4053 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 4112
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3782 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT 3841
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4113 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT 4172
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3842 TGGGATATGATACAGACTAACTTTTTTTTTTTTT 3875
            |||||||||||||||||||||||||||||||
Db   4173 TGGGATATGATACAGACTAACTTTTTTTTTTTTT 4206

RESULT 7
US-09-962-665-1

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Qy   962  CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGGCTTGGTCAATATAG  1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1293  CGCCTTCTATGATGGCCAAGCACCTAAAGGATTTTGCTATGGATGNATGGCTTGGTCAATATAG  1352

Qy  1022  TTGGAGGATGCTGTGGGTCAACACCAGATCATATCATCAGGGGAAATTGCTGAAGCTGTGAAAA  1081
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1353  TTGGAGGATGCTGTGGGTCAACACCAGATCATATCATCAGGGGAAATTGCTGAAGCTGTGAAAA  1412

Qy  1082  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCCTTTGAAGGACATATGTTACTGTCTGGTC  1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1413  ATTGTAAGCCTAGAGTTCCACCTGCCACTGCCTTTGAAGGACATATGTTACTGTCTGGTC  1472

Qy  1142  TAGAGCCCTTCAGGATTGGACCGTACACCAGATACACCAACTTTGTAACATTGGAGAGCGCTGTAATG  1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1473  TAGAGCCCTTCAGGATTGGACCGTACACCAGATACACCAACTTTGTAACATTGGAGAGCGCCTGTAATG  1532

Qy  1202  TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGCAGGAAACATGAAGAAGCCTTGT  1261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1533  TTGCAGGATCAAGGAAGTTGCTAAACTCATCATGCAGGAAACATGAAGAAGCCTTGT  1592

Qy  1262  GTGTTGCCAAACTGCAGGTGGAAATGGGAGCCCAGTGTGTTGATGTCAACATGGATGATG  1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1593  GTGTTGCCAAACTGCAGGTGGAAATGGGAGCCCAGTGTGTTGATGTCAACATGGATGATG  1652

Qy  1322  GCATGTCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATTGCTTCCGAGCCAG  1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1653  GCATGTCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTTAATNGCTTCCGAGCCAG  1712

Qy  1382  ACATCGCCAAAGTACCTTGTGCATGCACTCCTCCAATTTGCTGTGATTGAAGCTGGGT  1441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1713  ACATCGCCAAAGTACCTTGTGCATGCACTCCTCCAATTTGCTGTGATTGAAGCTGGGT  1772

Qy  1442  TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTAGTCTGAAGGAAGGAGGACG  1501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1773  TAAAGTGCTGCCAAGGAAGTGCATTGTCAATAGCATTAGTAGTCTGAAGGAAGGAGGACG  1832

Qy  1502  ACTTCTTGGAGAAGGGCCAGGAAGATTAAAAGTATGGAGCTGCTATGGTGTGTCATGGCTT  1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1833  ACTTCTTGGAGAAGGGCCAGGAAGATTAAAAGTATGGAGCTGCTATGGTGTGTCATGGCTT  1892

Qy  1562  TTGAATGAAGAAGGACAGGCAACAGGCAACAGAACAGACAAAAATCAGAGTGTGCACCCGGCCT  1621
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1893  TTGAATGAAGAAGGACAGGCAACAGGCAACAGAACAGACAAAAATCAGAGTGTGCACCCGGCCT  1952

Qy  1622  ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTGACCCCTAATA  1681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1953  ACCATCTGCTTGTGAAAAAACTGGGCTTAATCCAAATGACATTATTTTTGACCCCTAATA  2012

Qy  1682  TCCTAACCATGGGAACTGGAATGGAGGAACAAACTTGTATGCCATTAATTTAATCCATG  1741
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2013  TCCTAACCATGGGAACTGGAATGGAGGAACAACTTGTATGCCATTAATTTAATCCATG  2072

Qy  1742  CAACAAAAGTCATTAAGAAGAAACATTACCTGGAGCCAGGAAGTGGAGGTCTTCCAACT  1801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2073  CAACAAAAGTCATTAAGAAGAAACATTACCTGGAGCCAGGAAGTGGAGGTCTTCCAACT  2132

Qy  1802  TGTCCTTCTCCTTCCGGAATGGAGAAGCCATTCGAGAGCAATGCATGGGGTTTCTTTG  1861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2133  TGTCCTTCTCCTTCCGGAATGGAGAAGCCATTCGAGAGCAATGCATGGGGTTTCCTTT  2192

Qy  1862  ACCATGCCAATCAAGCTCGGGACATGGACATGGGGAATGCTGGAAAACCTCCCTGTGT  1921
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2193  ACCATGCCAATCAAGCTCGGGACATGGACATGGGGAATGCTGGAAAACCTCCCTGTGT  2252

Qy  1922  ATGATGATATCATCAATAAGGAACTTCTGTGTGAGATCTGTGAAGATCTTGGAATAAAGACC  1981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2253  ATGATGATATCATCAATAAGGAACTTCTGTGTGAGATCTGTGAAGATCTTGGAATAAAGACC  2312

Qy  1982  CTGAGGCCACTGAGAGACTTCTTACGTTATGCCCAGACTCGAGGCACAGGAGGAAGAAAG  2041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2313  CTGAGGCCACTGAGAGACTTCTTACGTTATGCCCAGACTCGAGGCACAGGAGGAAGAAAG  2372

Qy  2042  TCATTCAGACTGATGAGTGAGTGGGAGAAATGGCCCCTGTCGAAGAAGACGCCCTTG  2101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2373  TCATTCAGACTGATGAGTGAGTGGGAGAAATGGCCCCTGTCGAAGAAGACGCCCTTG  2432
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Qy  2102  TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAA  2161
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2433  TGAAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAA  2492

Qy  2162  AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGGAATGAAAATTGTTG  2221
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2493  AATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGGAATGAAAATTGTTG  2552

Qy  2222  GTGAATCTTTTGGAGCTGGAAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA  2281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2553  GTGATCTTTTGGAGCTGGAAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA  2612

Qy  2282  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAGAAGGAAGAAACCAGAG  2341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2613  TGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAGAAGGAAGAAACCAGAG  2672

Qy  2342  TGCTTAACGGCACAGTAGAAGAGAGACCCTTACCAGGGCACCATGCTGTGCTGGCCACTG  2401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2673  TGCTTAACGGCACAGTAGAAGAGAGACCCTTACCAGGGCACCATGCTGTGCTGGCCACTG  2732

Qy  2402  TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA  2461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2733  TTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCCTTGGCTGCAATA  2792

Qy  2462  ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTC  2521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2793  ATTTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTC  2852

Qy  2522  TTGACCACAAAGCAGATATAATTGGCGCGTCCAGAGTGTGGTGGTGTCCCAGCTGTTAGACAGGACC  2581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2853  TTGACCACAAAGCAGATATAATTGGCGCGTCCAGAGTGTGGTGGTGTCCCAGCTGTTAGACAGGACC  2912

Qy  2582  TGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGTTGGAG  2641
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2913  TGATTTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGTTGGAG  2972

Qy  2642  GAGCAACCACTTCAAAAACCCACACACAGTAAAATAGCTCCGAGATACAGTGCACCTG  2701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2973  GAGCAACCACTTCAAAAACCCACACACAGTAAAATAGCTCCGAGATACAGTGCACCTG  3032

Qy  2702  TAATCCATGTCCTGGACGCGTCCCAAGAGTGTTGGTCGTTCCCAGCTGTGTTAGAGTGAAA  2761
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3033  TAATCCATGTCCTGGACGCGTCCCAAGAGTGTTGGTCGTTCCCAGCTGTGTTAGAGTGAAA  3092

Qy  2762  ATCTAAAGGATGAATCATTTGAGGAAATCATGAAGAATATGAAGATATTAGACAGGACC  2821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  3093  ATCTAAAGGATGAATCATTTGAGGAAATCATGAAGAATATGAAGATATTAGACAGGNCC  3152

Qy  2822  ATTATGAGTCTCTCAAGGAGGAGGAGACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT  2881
          |||||||||||||||||||||||||||||||||||||| ||||
Db  3153  ATTATGAGTCTCTCAAGGAGGAGGAGACTTACCCTTAAGTCAAGCCAGAAAAAANTNGTT  3212

Qy  2882  TCCAAATGGATTGGCTGTCTCGAACCTCGAACCTCACCCAGTGGACTACATTGGGACCCAGG  2941
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3213  TCCAAATGGATTGGCTGTCTCGAACCTCGAACCTCACCCAGTGGACTACATTGGGACCCAGG  3272

Qy  2942  TCTTTGAAGACTATGACCTGCGGAGCAAGTCGAAGCCTTTCTTTG  3001
          ||||||||||||||||||||||||||||||||||||||||||||
Db  3273  TCTTTGAAGACTATGACCTGCGGAGCAAGTCGAAGCCTTTCTTTG  3332

Qy  3002  ATGTCTGCAGCTCCGGGCAAGTCACCCGAATGCAAGCCTTCCCAAGATATTTAACGACA  3061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3333  ATGTCTGCAGCTCCGGGCAAGTCACCCGAATGCAAGCCTTTCCCAAGATATTTAACGACA  3392

Qy  3062  AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGACGATGCGGAAGAAAG  3121
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  3393  AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGACGATGCGGAAGAAAG  3452

Qy  3122  TGATTAGTCAAAAGAAACTCCGGGCCCGTGAGTGTGTGGGTTCTGCCACAGTA  3181
          |||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3453 TGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGTTGGGTTCTGCCAGCACAGAGTA 3512

Qy   3182 TCCAAGACGACATTCACCTGTACGCAGAGAGGCTGCTGCGCCAGCTGCAGAGAGCCCATAG 3241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3513 TCCAAGACGACATTCACCTGTACGCGGAGGCTGCTGCGCCAGCTGCAGAGAGCCCATAG 3572

Qy   3242 CCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACT 3301
              ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3573 CCACCTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACT 3632

Qy   3302 ACTGCCTCTCGACTTCATCGCTCCCTTGCATTCTGGCATCGTGACTACCTGGGCCTGT 3361
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Db   3633 ACTGCCTCTCGACTTCATCGCTCCCTTGCATTCTGGCATCGTGACTACCTGGGCCTGT 3692

Qy   3362 TTGCCGTTGCCTGCTGCTTTGGGTGGGTAGAAGAGCTGAGCAAGGCTGAGCAAGGCCA 3421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3693 TTGCCGTTGCCTGCTGCTTTGGGTGGGTAGAAGAGCTGAGCAAGGCTGAGCAAGGCCA 3752

Qy   3422 ACTACAGCAGCATCATGGTCAAGGCGCCTGGGGACCCGCTGCGCAGAGGCCTTTGCAGAAG 3481
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Db   3753 ACTACAGCAGCATCATGGTCAAGGCGCCTGGGGACCCGCTGCGCAGAGGCCTTTGCAGAAG 3812

Qy   3482 AGCTCCATGAAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGTCGGACG 3541
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Db   3813 AGCTCCATGAAAAGAGTTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGTCGGACG 3872

Gaps 3542 TCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCGCCGGCTCCTGGCTACCCCAGCC 3601
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Db   3873 TCGCAGACCTGCGCGCAGGCTGCGGTACAAGGGCATCCGCCGCCGGCTCCTGGCTACCCCAGCC 3932

Qy   3602 AGCCCGACCACACCGAGAAGCTCACCATGTGACGACTCGCAGACATCGAGCAGTTCACAG 3661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3933 AGCCCGACCACACCGAGAAGCTCACCATGTCAGACTTGCAGACATCGAGCAGTTCACAG 3992

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGTCTCAGGCCTCTACT 3721
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Db   3993 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGTCTCAGGCCTCTACT 4052

Qy   3722 TCTCCAATTTGAAGTCCAAATATTTGCTGTGTGGGGAAGATTCCAAGGATCAGGTTGAGG 3781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4053 TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 4112

Qy   3782 ATTATGCATTGAGGAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCCATTT 3841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4113 ATTATGCATTGAGGAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCCATTT 4172

Qy   3842 TGGGGATATGATACAGACTAACTTTTTTTTTTTTTT 3875
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Db   4173 TGGGGATATGATACAGACTAACTTTTTTTTTTTTTT 4206
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RESULT 8
US-09-963-333-1
; Sequence 1, Application US/09963333
; Patent No. 6664062
; GENERAL INFORMATION:
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: THYMIDINE SYNTHASE GENE SEQUENCE VARIANCES
; TITLE OF INVENTION: HAVING UTILITY IN DETERMINING THE TREATMENT
; TITLE OF INVENTION: OF DISEASE
; FILE REFERENCE: 11926-015002
; CURRENT APPLICATION NUMBER: US/09/963,333
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/658,659
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/596,033
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/357,743
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/357,024
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 60/093,484
; PRIOR FILING DATE: 1998-07-20

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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 194, 3209
; OTHER INFORMATION: n = c or g
; NAME/KEY: misc_feature
; LOCATION: 1136, 1334, 3150, 5551, 5934
; OTHER INFORMATION: n = a or g
; NAME/KEY: misc_feature
; LOCATION: 284, 1252, 1699, 5573, 5659, 5678, 5874
; OTHER INFORMATION: n = c or t
; NAME/KEY: misc_feature
; LOCATION: 3207
; OTHER INFORMATION: n = g or t
; NAME/KEY: misc_feature
; LOCATION: 5444
; OTHER INFORMATION: n = c or a
US-09-963-333-1

Query Match          79.3%;   Score 3109;   DB 3;   Length 7224;
Best Local Similarity 99.6%;   Pred. No. 0;
Matches 3859;  Conservative    0;  Mismatches 15;  Indels 0;  Gaps 0;
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Qy      2 GTCACCTGTGGAGAGCACGTCTTCTTCTGCCGCCGCCCTCTGCGCCAAGGAGGAGACTCGACA 61
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Db    333 GTCACCTGTGGAGAGCACGTCTTCTTCTGCCGCCGCCCTCTGCGCCAAGGAGGAGACTCGACA 392

Qy     62 ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCGCTGCGAACCCGAGAGGTCTGAAGAAAAACCCTGCGGG 121
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Db    393 ACATGTCACCCGGCGCTCCAAGACCTGTCGCAACCCGTGCGAACCCGAGAGGTCTGAAGAAAAACCCTGCGGG 452

Qy    122 ATGAGATCAATGCCATTCTGAGAGAGGATTATGGTGCTGGATGGAGGATGGGGACCA 181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 ATGAGATCAATGCCATTCTGAGAGAGGATTATGGTGCTGGATGGAGGATGGGGACCA 512

Qy    182 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 241
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513 TGATCCAGCGGGAGAAGCTAAACGAAGAACACTTCCGAGGTCAGGAATTTAAAGATCATG 572

Qy    242 CCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACCAGCCTGATGTCATTTACC 301
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Db    573 CCAGGCCGCTGAAAGGCAACAATGACATTTTAAGTATAACCAGCCTGATGTCATTTACC 632

Qy    302 AAATCCATAAGGAATACTTGCTGGCTGGCGGGCAGCAGATATCATTGAAACAAATACTTTTAGCA 361
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Qy    362 GCACTAGTATTGCCCCAAGCTGACTATGCCTTGAACACTTGGCCTACCGGATGAACATGT 421
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Db    693 GCACTAGTATTGCCCCAAGCTGACTATGCCTTGAACACTTGGCCTACCGGATGAACATGT 752

Qy    422 GCTCTGCAGGAGTGGCAGAAAAGCTGCCAGAAAAGCTGCCGACTAACTCTCCAGACAGGAATTAAGA 481
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Db    753 GCTCTGCAGGAGTGGCAGAAAAGCTGCCAGAAAAGCTGCCGACTAACTCTCCAGACAGGAATTAAGA 812

Qy    482 GGTTTGTGGCAGGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGG 541
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Db    813 GGTTTGTGGCAGGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGG 872

Qy    542 AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATACCAAGAGCAGCAG 601
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Db    873 AAAGGCCGATTATAGGAACATCACATTTGATGAGCTTGTTGAAGCATCACCAAGAGCAGCAG 932

Qy    602 CCAAAGGACTTCTGGATGCGGGGTTGAATATCTTGATATCTTGAAACTATTTTTGATACTG 661
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Db    933 CCAAAGGACTTCTGGATGCGGGGTTGAATATCTTGATATCTTGAAACTATTTTTGATACTG 992

Qy    662 CCAATGCCAAGGCAGCCTGTTTGCACTCCAAAATCTTTTTGACGGAGAAATATGCTCCCC 721
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Db   993 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1052
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Qy   722 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 781
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Db 1053 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1112
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Qy   782 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 841
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Db 1113 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1172
          CAGGAGAGGGATTTGTCATCAGCNTGTCTCATGGGAACCACTCTGCATTGGATTAAAATT

Qy   842 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 901
          GTGCTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAG

Db 1173 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1232
          GTGCTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAG

Qy   902 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 961
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Db 1233 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1292
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Qy   962 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1021
          CGCCTTCTATGTCTGTGGGTCAACACCAGATCATATACAGGGAAATTGCTGAAGCTGTGAAAA

Db 1293 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1352
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Qy 1022 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1081
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Db 1353 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1412
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Qy 1082 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1141
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Db 1413 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1472
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Qy 1142 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1201
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Qy 1202 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1261
          TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGCGCAGGTGTTGGATGTCAACATGATGATG

Db 1533 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1592
          TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGCGCAGGTGTTGGATGTCAACATGATGATG

Qy 1262 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1321
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Qy 1322 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1381
          GCATGCTAGATGGTGTCCAAGTGCAATGCAATGACCAGATTTTTGCAACTTAATTGCTTCCGAGCCAG

Db 1653 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1712
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Qy 1382 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1441
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Db 1713 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1772
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Db 1833 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1892
          ACTTCTTGGAGAAGGCTTTGTGCCAAGGAGATTAAAAGAATGGGCTTTAATGGAGCTGTCATGGCTT

Qy 1562 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1621
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Db 1893 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1952
          TTGATGAAGAAGGAGGCAACAGGCAACAGGCAACAGAAAAAATCAGAGTGTGCACCCGGGGCCT

Qy 1622 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1681
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Db 1953 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 2012
          ACCATCTGCTTGTGAAAAAACTGGGCTTTAATCCAAATGACATTATTTTTGACCCCTAATA

Qy 1682 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1741
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Db 2013 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 2072
          TCCTAACCATTGGGACTGGAATGGAGGAACACAACTTGTATGCCATTAATTTATCCATG

Qy 1742 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1801
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Db 2073 CAACAAAGTCATTAAAGAAACATTACCTGAGCCCAGAATAAGTGGAGGTCTTTCCAACT 2132
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Qy 1802 TGTCCTTCTCTCCTCCGAGGAATGGAAGCCATTGAGAAGCAATGCATGGGGTTTTCCTTT 1861
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Db 2133 TGTCCTTCTCTCCTCCGAGGAATGGAAGCCATTGAGAAGCAATGCATGGGGTTTTCCTTT 2192

Qy 1862 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGATGCTGATACTGAAAACCTCCCTGTGT 1921
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Db 2193 ACCATGCAATCAAGTCTGGCATGGACATGGAGATAGTGAATGCTGATACTGAAAACCTCCCTGTGT 2252

Qy 1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGTCGAAGATCTCATCTGAATAAAGACC 1981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2253 ATGATGATATCCATAAGGAACTTCTGCAGCTCTGTGTCGAAGATCTCATCTGAATAAAGACC 2312

Qy 1982 CTGAGGCCACTGAGAGCTCCTTACGTTATGCCCAGTATGCGGCCAGACTCAAGGACGCCTTGAGTATGCCCCTG 2041
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Db 2313 CTGAGGCCACTGAGAGCTCCTTACGTTATGCCCAGTATGCGGCCAGACTCAAGGACGCCTTGAGTATGCCCCTG 2372

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Db 2373 TCATTCAGACTGATGAGTGGAGAAAAACACATATTATTGAGGAATACTGAGGAGGAAGCCAGTTAAACCAAAAA 2432

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Db 2433 TGAAGGGCATTGAAAAATTGAAGCCACTTATTGAGGAATTAATGAAGGACACCCCTGATGAATGAAAATTGTTG 2492

Qy 2162 AATATCCCGACCTCAATAAATTGAAGGACATTCTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTTA 2221
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Db 2493 AATATCCCGACCTCAATAAATTGAAGGACATTCTTCTCACCTCAGGTTATAAAGTCAGCCCGGGTTA 2552

Qy 2222 GTGATCTTTTGGAGCTGGAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
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Db 2793 ATTTCCGAGTTATTGATTTAGGAGTCCATGACTCCATGACTCCGAGATACTGAAAGCTGTC 2852

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Db 2913 TGATTTTTGTTGTGCCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAG 2972

Qy 2642 GAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGCTCCGAGATACTGAAAATAGTCAGTGCACCTG 2701
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Db 2973 GAGCAACCACTTCAAAAACCCACAGCAGTTAAAATAGCTCCGAGATACTGAAAATAGTCAGTGCACCTG 3032

Qy 2702 TAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGTCGTGTTCCCAGCTGTTAGATGAAA 2761
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Db 3093 ATCTAAAGATGAATACTTTGAGGAAATCATGGAGAAATCATGGAAGAATATTAGACAGGNCC 3152

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Db 2881 ATTATCAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAANTNGTT 3212

Qy 3153 ATTATCAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAANTNGTT

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; Patent No. 6759200
; GENERAL INFORMATION:
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: THYMIDINE PHOSPHORYLASE GENE SEQUENCE
; TITLE OF INVENTION: VARIANCES HAVING UTILITY IN DETERMINING
; TITLE OF INVENTION: THE TREATMENT OF DISEASE
; FILE REFERENCE: 11926-015003
; CURRENT APPLICATION NUMBER: US/09/962,677
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/658,659
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/596,033
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/357,743
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/357,024
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 60/093,484
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 1
; LENGTH: 7224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 194, 3209
; OTHER INFORMATION: n = c or g
; NAME/KEY: misc_feature
; LOCATION: 1136, 1334, 3150, 5551, 5934
; OTHER INFORMATION: n = a or g
; NAME/KEY: misc_feature
; LOCATION: 284, 1252, 1699, 5573, 5659, 5678, 5874
; OTHER INFORMATION: n = c or t
; NAME/KEY: misc_feature
; LOCATION: 3207
; OTHER INFORMATION: n = g or t
; NAME/KEY: misc_feature
; LOCATION: 5444
; OTHER INFORMATION: n = c or a
; US-09-962-677-1

Query Match             79.3%;  Score 3109;  DB 3;  Length 7224;
Best Local Similarity   99.6%;
Matches 3859;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;
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Qy        2  GTCACCTGTGGAGCACGTCTTCTCGCCGGCCCTCCTTCGCGGCAAGGAGGAGACTCGACA   61
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Qy       62  ACATGTCACCCGGCTCCAAGACCTGTCGCAACCCGGAGGTCGAAGAAACCCTGCGGG  121
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Db      393  ACATGTCACCCGGCTCCAAGACCTGTCGCAACCCGGAGGTCGAAGAAACCCTGCGGG  452

Qy      122  ATGAGATCAATGCCATCTGCGAGAAGAGGATTATGGTGCTGATGGGATGGGGACCA  181
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Db      453  ATGAGATCAATGCCATCTGCGAGAAGAGGATTATGGTGCTGATGGGATGGGGACCA  512

Qy      182  TGATCCAGCGCGGAGAAGCTAAACGAAGAACACTTCCGAGGTGAGG AATTTAAAGATCATG  241
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Db      513  TGATCCAGCGCGGAGAAGCTAAACGAAGAACACTTCCGAGGTGAGGAATTTAAAGATCATG  572

Qy      242  CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      573  CCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCATTTACC  632

Qy      302  AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      633  AAATCCATAAGGAATACTTGCTGGCTGGGCAGATATCATTGAAACAAATACTTTTAGCA  692

Qy      362  GCACTAGTATTGCCCAAGCTGACTATGGCCCTTGAACACTTGGCCTATGGTGAACAATGT  421
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     2882  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG  2941
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3213  TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGG  3272

Qy     2942  TCTTTGAAGACTATGACCTGCAGAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG  3001
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3273  TCTTTGAAGACTATGACCTGCAGAGCTGGTGGACTACATTGACTGGAAGCCTTTCTTTG  3332

Qy     3002  ATGTCTGGCCAGCTCCGGGCAAGTACCCGAATGAGGCTTCCCCAAGATATTAACGACA  3061
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3333  ATGTCTGGCCAGCTCCGGGCAAGTACCCGAATGAGGCTTCCCCAAGATATTAACGACA  3392

Qy     3062  AAACAGTAGTGGAGAGGCCAGGAAGGTCACGACGATGAGCCCACAATATGCTGAACACAC  3121
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3393  AAACAGTAGTGGAGAGGCCAGGAAGGTCACGACGATGAGCCCACAATATGCTGAACACAC  3452

Qy     3122  TGATTAGTCAAAAGAAACTCCGGGCCCGGGTGTGGTTCGGTTCTGGCCAGCACAGAGTA  3181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3453  TGATTAGTCAAAAGAAACTCCGGGCCCGGGTGTGGTTCGGTTCTGGCCAGCACAGAGTA  3512

Qy     3182  TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAG  3241
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3513  TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCCAGGCTGCAGAGCCCATAG  3572

Qy     3242  CCACTTTCTATGGGTTAAGGCAACAGCTGAGAAGGACTCTGCCAGCACGGAGCACCATACT  3301
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3573  CCACCTTCTATGGGTTAAGGCAACAGCTGAGAAGGACTCTGCCAGCACGGAGCACCATACT  3632

Qy     3302  ACTGCCTCTCGAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3361
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3633  ACTGCCTCTCGAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGT  3692

Qy     3362  TTGCCGTTGCCGTCTGCTTTGGGGTAGAGAGCTGAGCAAGGCCTATGAGGATGGTGACG  3421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3693  TTGCCGTTGCCGTCTGCTTTGGGGTAGAGAGCTGAGCAAGGCCTATGAGGATGGTGACG  3752

Qy     3422  ACTACAGCAGCATCATGGTCAAGGGCGCTGGGGGACCCGGCTGGGCAGGGCCTTTGCAGAAG  3481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3753  ACTACAGCAGCATCATGGTCAAGGGCGCTGGGGGACCCGGCTGGGCAGGGCCTTTGCAGAAG  3812

Qy     3482  AGCTCCATGAAAGAGTTCGCCCGAGAACTGTGGCCTACTGTGTGGCAGTGAGCAGCTCGACG  3541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3813  AGCTCCATGAAAGAGTTCGCCCGAGAACTGTGGCCTACTGTGTGGCAGTGAGCAGCTGGACG  3872

Qy     3542  TCGCAGACCTGCGAAGGTTGCCGGTACAAGGGCATCCGCCCCGGCTCCTGGCTCACCCCAGCC  3601
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3873  TCGCAGACCTGCGAAGGTTGCCGGTACAAGGGCATCCGCCCCGGCTCCTGGCTCACCCCAGCC  3932

Qy     3602  AGCCCGACCACACCGAGAAGCTCACCATGTGGAGACTCGAGACATCGAGACAGTCTCACAG  3661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3933  AGCCCGACCACACCGAGAAGCTCACCATGTGGAGACTTGCAGACATCGAGACAGTCTCACAG  3992

Qy     3662  GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCCTCTACT  3721
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3993  GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCCTCTACT  4052

Qy     3722  TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGAAGATTTCCAAGGATCAGGTTGAGG  3781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4053  TCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGAAGATTTCCAAGGATCAGGTGTGAGG  4112

Qy     3782  ATTATGCATTGAGGAGAAGAACATAATCTGTGGCTGAGGTTGAGGAAATGGCTTGAGGACCCATTT  3841
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4113  ATTATGCATTGAGGAGAAGAACATAATCTGTGGCTGAGGTTGAGGAAATGGCTTGAGGACCCATTT  4172

Qy     3842  TCGGGATATGATGATACAGAGACTAACTTTTTTTTTTTTTTT  3875
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Db     4173  TCGGGATATGATGATACAGAGACTAACTTTTTTTTTTTTTTTTT  4206
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; RESULT 9
; US-09-962-677-1
; ; Sequence 1, Application US/09962677
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Qy 1502 ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1561
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1833 ACTTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAGCTGCTATGGTGGTCATGGCTT 1892

Qy 1562 TTGATGAAGAAGGACAGGCAACAGGAACACAGACACAAAAATCAGAGTGTGCACCCGGGCCT 1621
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1893 TTGATGAAGAAGGACAGGCAACAGGAACACAGACACAAAAATCAGAGTGTGCACCCGGGCCT 1952

Qy 1622 ACCATCTGCTTGTGTGAAAAACTGGCTTTAATCAAATGACATTATTTTTGACCCTAATA 1681
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Db 1953 ACCATCTGCTTGTGTGAAAAAACTGGCTTTAATCAAATGACATTATTTTTGACCCTAATA 2012

Qy 1682 TCCTAACCATTGGGACTGGGATGGAGGAACAACAACTTGTATGCCATTTTATCCATG 1741
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Db 2013 TCCTAACCATTGGGACTGGGATGGAGGAACACAACCTTGTATGCCATTTTATCCATG 2072

Qy 1742 CAACAAAAGTCATTAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTTCCAACT 1801
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Db 2073 CAACAAAAGTCATTAAGAAACATTACCTGGAGCCAGAATAAGTGAGGTCTTTCCAACT 2132

Qy 1802 TGTCCTTCTCCTCCGGAGGATGGAAGCCATTCGAGAAGCAATGCTGAAACCTCCCTGT 1861
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2133 TGTCCTTCTCCTCCGGAGGATGGAAGCCATTCGAGAAGCAATGCTGAAACCTCCCTGT 2192

Qy 1862 ACCATGCAATCAAGTCTGGCATGCAATGGACATGGGATCTCGTGTGAAGATCCATCTGT 1921
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2193 ACCATGCAATCAAGTCTGGCATGCAATGGACATGGGATCTCGTGTGAAGATCCATCTGT 2252

Qy 1922 ATGATGATATCCATAAGGAACTTCTGCAGCTCGTGTGAAGATCCATCTGGAATAAAGACC 1981
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2253 ATGATGATATCCATAAGGAACTTCTGCAGCTCGTGTGAAGATCCATCTGGAATAAAGACC 2312

Qy 1982 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAAGAAAG 2041
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2313 CTGAGGCCACTGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACAGGAAGAAAG 2372

Qy 2042 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACACGCCTGAGTATGCCCTTG 2101
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2373 TCATTCAGACTGATGAGTGAGAAATGGCCCTGTCGAAGAACACGCCTGAGTATGCCCTTG 2432

Qy 2102 TGAAAGGGCATTGAAAAACATATTATTGAGGATACTGAAGCCAGTTAAACCAAAAAA 2161
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2433 TGAAAGGGCATTGAAAAACATATTATTGAGGATACTGAAGCCAGTTAAACCAAAAAA 2492

Qy 2162 AATATCCCGACCTCTCAATATAATGAAGAACCCCTGATGAATGAAATGAAAATTGTTG 2221
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2493 AATATCCCGACCTCTCAATATAATGAAGAACCCCTGATGAATGAAATGAAAATTGTTG 2552

Qy 2222 GTGATCTTTTGGAGCTGGAAAAATGTTCACCTCAGGTTATAAAGTCAGCCCGGGTTA 2281
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2553 GTGATCTTTTGGAGCTGGAAAAATGTTCACCTCAGGTTATAAAGTCAGCCCGGGTTA 2612

Qy 2282 TGAAAGAGGCTGTTGGCCACCTTAATGGCAGAAAAAGAGAAGAACCAGAG 2341
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Db 2613 TGAAAGAGGCTGTTGGCCACCTTAATGGCAGAAAAAGAGAAGAACCAGAG 2672

Qy 2342 TGCTTAACGGCACAGTAGAAGAGGACCCATCCGTGCTGGCCACTG 2401
         |||||||||||||||||||||||||||||||||||||||||||||
Db 2673 TGCTTAACGGCACAGTAGAAGAGGACCCACCGTGCTGGCCACTG 2732

Qy 2402 TTAAAGGCGACGTGGCTGCACGACTAGGCAAGAACATAGTTGGAGTAGTGCTGCAATA 2461
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2733 TTAAAGGCGACGTGGCTGCACGACTAGGCAAGAACATAGTTGGAGTAGTGCTGCAATA 2792

Qy 2462 ATTTCCAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGTC 2521
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2793 ATTTCCAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGTC 2852

Qy 2522 TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTTCCCTGGATGAAA 2581
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2853 TTGACCACAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTTCCCTGGATGAAA 2912

Db 693 GCACTAGTATTGCCCAAGCTGACTATGGCCTTGAACACTTGGCTCTACCGGATGAACATGT 752
Qy 422 GCTCTGCAGGAGTGGCCAGAAAAGTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGA 481
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 753 GCTCTGCAGGAGTGGCCAGAAAAGTGCCGAGGAGTAACTCTCCAGACAGGAATTAAGA 812

Qy 482 GGTTTGTTGGCAGGGGCTCTGGTTCCGACTAATAAGACACTTCTCTGTCCCATCTGTGG 541
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 813 GGTTTGTTGGCAGGGGCTCTGGTTCCGACTAATAAGACACTTCTCTGTCCCATCTGTGG 872

Qy 542 AAAGGCCGGATTATAGGAACATCACATTTGTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 601
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 873 AAAGGCCGGATTATAGGAACATCACATTTGTGATGAGCTTGTTGAAGCATACCAAGAGCAGG 932

Qy 602 CCAAAGGACTTCTGGATGGCGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG 661
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 933 CCAAAGGACTTCTGGATGGCGCGGGGTTGATATCTTACTCATTGAAACTATTTTGATACTG 992

Qy 662 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC 721
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 993 CCAATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTGAGGAGAAATATGCTCCCC 1052

Qy 722 GGCCTATCTTTATTTCAGGGACGATCGTTGTCATCAGCGTGTCTCATGGAGAACCACCTCTGCATTGGATTAAAT 781
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Db 1053 GGCCTATCTTTATTTCAGGGACGATCGTTGTCATCAGCGTGTCTCATGGAGAACCACCTCTGCATTGGATTAAAT 1112

Qy 782 CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAAATAATTGGAAAATGTACAACAG 841
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1113 CAGGAGAGGGATTTGTCATCAGCGTGTCTCATGGAGAAATAATTGGAAAATGTACAACAG 1172

Qy 842 GTGCTTTGGGTGCAGCTGAGATGAGAACCTTTATTGAAATGACACCTTTGTGTGACTATGATGAAA 901
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Db 1173 GTGCTTTGGGTGCAGCTGAGATGAGAACCTTTATTGAAATGACACCTTTGTGTGACTATGATGAAA 1232

Qy 902 CCTATGTCCTCTGTTATCCCAATGCAGCTTAAAGGATTTTGCTATGGATGCTTCTATATAG 961
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Db 1233 CCTATGTCCTCTGTTATCCCAATGCAGCTTAAAGGATTTTGCTATGGATGCTTCTATATAG 1292

Qy 962 CGCCTTCTATGAATGGCCAAGCACCTAAAGCACCTAAAGGAAATTGCTAGAAGCTGTGAAAA 1021
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Db 1293 CGCCTTCTATGAATGGCCAAGCACCTAAAGCACCTAAAGGAAATTGCTAGAAGCTGTGAAAA 1352

Qy 1022 TTGGAGGATGCTGTGGGTCAACACCAGATCATCAGGGAAATTGCTAGAAGCTGTGAAAA 1081
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1353 TTGGAGGATGCTGTGGGTCAACACCAGATCATCAGGGAAATTGCTAGAAGCTGTGAAAA 1412

Qy 1082 ATTGTAAGCCTAGAGTTCCACCTGCCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTC 1141
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1413 ATTGTAAGCCTAGAGTTCCACCTGCCCACTGCTTTTGAAGGACATATGTTACTGTCTGGTC 1472

Qy 1142 TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGACGAGCGCTGTAATG 1201
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1473 TAGAGCCCTTCAGGATTGGACCGTACACCAACTTTGTTAACATTGGACGAGCGCTGTAATG 1532

Qy 1202 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACATGAAGAAGCCTTGT 1261
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Db 1533 TTGCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCAGGAAACATGAAGAAGCCTTGT 1592

Qy 1262 GTGTTGCCAAAGTGCAGGTGGAGCCCAGGTGGTTGGATGTCAACATGGATGATG 1321
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Db 1593 GTGTTGCCAAAGTGGTCAGGTGGAGCCCAGGTGTTGGATGTCAACATGGATGATG 1652

Qy 1322 GCATGCTAGATGGTCAAGTGCAATGCAGCCAGATTTTGCTAACTTAATTGCTTCCGAGCCAG 1381
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Db 1653 GCATGCTAGATGGTCAAGTGCAATGCAGCCAGATTTTGCTAACTTAATNGCTTCCGAGCCAG 1712

Qy 1382 ACATGCCAAAGTGCACCTTTGTGCATCGAATCCTCGACTTTGCTGTGAAGCTGGGT 1441
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1713 ACATGCCAAAGTGACCTTTGTGCATCGAATCCTCCAATTTTGCTGTGAAGCTGGGT 1772

Qy 1442 TAAAGTGCTGCCAAGGGAAGTGCATTGCATTGTCAATAGCATTAGTGCTGAAGGAAGGAGGACG 1501
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Db 1773 TAAAGTGCTGCCAAGGGAAGTGCATTGCATTGTCAATAGCATTAGTGCTGAAGGAAGGAGGACG 1832

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Qy   2582 TGATTTTGTGTGCCAAGGAAATGTGGAGAGATTAGCTATAAGGAGA 2641
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Qy   2642 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 2701
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Db   2973 GAGCAACCACTTCAAAAACCCACACAGCAGTTAAAATAGCTCCGAGATACAGTGCACCTG 3032

Qy   2702 TAATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTAGATGAAA 2761
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Db   3033 TAATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTGTTCCCAGCTGTTAGATGAAA 3092

Qy   2762 ATCTAAAGGATGAATACTTTGAGGAATCATGAGAGAATATGAACAGGACC 2821
          ||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   3093 ATCTAAAGGATGAATACTTTGAGGAATCATGAGAGAATATGAACAGGANCC 3152

Qy   2822 ATTATGAGTCTTCTCAAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTT 2881
          |||||||||||||||||||||||||||||||||||||||||| || ||||||||| ||||
Db   3153 ATTATGAGTCTTCTCAAGGAGGAGAGATACTTACCCTTAAGTCAAGCCAGAAAAANTNGTT 3212

Qy   2882 TCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCACGTTTATTGGGACCCAGG 2941
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Qy   2942 TCTTTGAAGACTATGACCTGCGAGAAGCTGGTGGACTACATTGACTGGAAGCTTTCTTTG 3001
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Db   3273 TCTTTGAAGACTATGACCTGCGAGAAGCTGGTGGACTACATTGACTGGAAGCTTTCTTTG 3332

Qy   3002 ATGTCTGGCAGCTCCCGGGCAAGTACCCGAATCGAGGCTTCCCCAAGATATTTAACGACA 3061
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3062 AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGACGTTGATGATGCCCACAATATGTGAACACAC 3121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3393 AAACAGTAGGTGGAGAGGCCAGGAAGTCTACGACGTTGATGATGCCCACAATATGTGAACACAC 3452

Qy   3122 TGATTAGTCAAAAGAAACTCCGGGGCGTGTGGTTCTGGCCAGCACAGAGTA 3181
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Qy   3182 TCCAAGACGACATTCACCTGTACGCAGAGGCTGCTGTGCCCCAGGCTGCGAGAGCCCATAG 3241
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Qy   3242 CCACTTTCTATGGGTTAAGGCAACAGCCTGAGAAGGACTCTGCCAGCACGGAGCCACCATACT 3301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3302 ACTGCCCTCAGACTTCATCGCTCCCCTTGCATTCTCGGCATCCGTGACTACCTGGGCCTGT 3361
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Qy   3362 TTGCCGTTGCCTTGCCTTTGGGGTAGAGAGCTGAGCAGGCAAGGCCTATGACGATGGTGACG 3421
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Db   3693 TTGCCGTTGCCTTGCCTTTGGGGTAGAGAGCTGAGCAGGCAAGGCCTATGACGATGGTGACG 3752

Qy   3422 ACTACAGCAGCATCATGGTCAAGGCCGCTGGGGGACCCGCTGCAGAGGCCTTTGCAGAAG 3481
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Db   3753 ACTACAGCAGCATCATGGTCAAGGCCGCTGCGGGGACCCGCTGCAGAGGCCTTTGCAGAAG 3812

Qy   3482 AGCTCCATGAAAGAGTTCGCGCGAGAAGCTTCACCATGTGGCCTTACTGTGGCAGCTGACG 3541
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Db   3813 AGCTCCATGAAAGAGTTCGCGCGAGAACTCGCCATGTGGCCTTACTGTGGCAGCTGACG 3872

Qy   3542 TCGGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGCCCGGCTCTGCGTACCCCAGCC 3601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3873 TCGGCAGACCTGCGCGCGGTCGCGTACAAAGGGCATCCGCCCGGCTACCCCAGCC 3932

Qy   3602 AGCCCGACCACCACCACGAGAAGCTTCACCATGTGGAGACTCGCAGACATCGAGACAGTCTACAG 3661
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3933 AGCCCGACCACCACCACGAGAAGCTCACATGTGAGACATCGAGACATCGAGCAGTCTACAG 3992

Qy   3662 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCAGGCCTCTACT 3721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3993 GCATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCAGGCCTCTACT 4052

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4053 TCTCCAATTGAAGTCCAAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGG 4112

Qy   3782 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT 3841
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Db   4113 ATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTT 4172

Qy   3842 TGGGATATGATACAGACTAACTTTTTTTTTTTT 3875
          ||||||||||||||||||||||||||||||
Db   4173 TGGGATATGATACAGACTAACTTTTTTTTTTTTTTT 4206
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RESULT 10
US-08-980-326-45/c
; Sequence 45, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-45

Query Match   0.7%; Score 28; DB 3; Length 28;
Best Local Similarity   100.0%; Pred. No. 0.049;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  2468 GAGTTATTGATTTAGGAGTCATGACTCC 2495
         ||||||||||||||||||||||||||||
Db    28 GAGTTATTGATTTAGGAGTCATGACTCC 1
```

RESULT 11
US-08-980-326-35
; Sequence 35, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27

```
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-35

Query Match             0.7%;    Score 26;   DB 3;   Length 26;
Best Local Similarity  100.0%;   Pred. No. 0.37;
Matches   26;  Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      214 TTCCGAGGTCAGGAATTAAAGATCA 239
                |||||||||||||||||||||||||
Db        1 TTCCGAGGTCAGGAATTAAAGATCA 26

RESULT 12
US-08-980-326-48
; Sequence 48, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-48

Query Match             0.7%;    Score 26;   DB 3;   Length 26;
Best Local Similarity  100.0%;   Pred. No. 0.37;
Matches   26;  Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     2422 ATAGGCAAGAACATAGTTGGAGTAGT 2447
                ||||||||||||||||||||||||||
Db        1 ATAGGCAAGAACATAGTTGGAGTAGT 26

RESULT 13
US-08-980-326-53
; Sequence 53, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964

; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-53

Query Match             0.7%;    Score 26;   DB 3;   Length 26;
Best Local Similarity  100.0%;   Pred. No. 0.37;
Matches   26;  Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     2790 CATGGAAGAATATGAAGATATTAGAC 2815
                ||||||||||||||||||||||||||
Db        1 CATGGAAGAATATGAAGATATTAGAC 26

RESULT 14
US-08-980-326-57/c
; Sequence 57, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-57

Query Match             0.7%;    Score 26;   DB 3;   Length 26;
Best Local Similarity  100.0%;   Pred. No. 0.37;
Matches   26;  Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     2496 ATGTGATAAGATACTGAAAGCTGCTC 2521
                ||||||||||||||||||||||||||
Db       26 ATGTGATAAGATACTGAAAGCTGCTC 1

RESULT 15
US-08-980-326-63/c
; Sequence 63, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1997-06-20
```

; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-63

Query Match   0.7%; Score 26; DB 3; Length 26;
Best Local Similarity   100.0%; Pred. No. 0.37;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1177 GTTAACATTGGAGAGGCGCTGTAATGT 1202
            ||||||||||||||||||||||||||
Db   26 GTTAACATTGGAGAGGCGCTGTAATGT 1

RESULT 16
US-09-949-016-162933/c
; Sequence 162933, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 162933
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-162933

Query Match   0.7%; Score 26; DB 3; Length 601;
Best Local Similarity   100.0%; Pred. No. 0.36;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTTGCCTTTTTA 3888
            ||||||||||||||||||||||||||
Db   299 TTTTTTTTTTTTTTTTTTGCCTTTTTA 274

RESULT 17
US-09-949-016-16297
; Sequence 16297, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16297

; LENGTH: 421118
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(421118)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16297

Query Match   0.7%; Score 26; DB 3; Length 421118;
Best Local Similarity   100.0%; Pred. No. 0.34;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTTGCCTTTTTA 3888
            ||||||||||||||||||||||||||
Db   321872 TTTTTTTTTTTTTTTTTTGCCTTTTTA 321897

RESULT 18
US-08-980-326-39
; Sequence 39, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-39

Query Match   0.6%; Score 25; DB 3; Length 25;
Best Local Similarity   100.0%; Pred. No. 1;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2233 GGAGCTGGAAAAATGTTTCTACCTC 2257
            |||||||||||||||||||||||||
Db   1 GGAGCTGGAAAAATGTTTCTACCTC 25

RESULT 19
US-08-980-326-41/c
; Sequence 41, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20

; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-41

Query Match 0.6%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2168 CCCGACCTCTCAATATAATTGAAGG 2192
         |||||||||||||||||||||||||
Db 25 CCCGACCTCTCAATATAATTGAAGG 1

RESULT 20
US-08-980-326-49/c
; Sequence 49, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-49

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2737 GTGTGTTCCCAGCTGTTAGATGAAA 2761
         |||||||||||||||||||||||||
Db 25 GTGTGTTCCCAGCTGTTAGATGAAA 1

RESULT 21
US-08-980-326-58/c
; Sequence 58, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310

; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-58

Query Match 0.6%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1696 ACTGGAATGAGGAGGAACACAACTTGT 1720
          |||||||||||||||||||||||||
Db 25 ACTGGGAATGGAGGAACACAACTTGT 1

RESULT 22
US-08-980-326-59
; Sequence 59, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-59

Query Match 0.6%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1188 AGAGCGCTGTAATGTTGCAGGATCA 1212
          |||||||||||||||||||||||||
Db 1 AGAGCGCTGTAATGTTGCAGGATCA 25

RESULT 23
US-08-980-326-60/c
; Sequence 60, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26

```
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-60

Query Match             0.6%;  Score 25;  DB 3;  Length 25;
Best Local Similarity  100.0%;  Pred. No. 1;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       2096 CCCTTGTGAAGGGCATTGAAAAACA 2120
              |||||||||||||||||||||||||
Db         25 CCCTTGTGAAGGGCATTGAAAAACA 1


RESULT 24
US-08-980-326-61
; Sequence 61, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-61

Query Match             0.6%;  Score 25;  DB 3;  Length 25;
Best Local Similarity  100.0%;  Pred. No. 1;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1527 TAAAAAGTATGGAGCTGCTATGGTG 1551
              |||||||||||||||||||||||||
Db          1 TAAAAAGTATGGAGCTGCTATGGTG 25


RESULT 25
US-08-980-326-62/c
; Sequence 62, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-62

Query Match             0.6%;  Score 25;  DB 3;  Length 25;
Best Local Similarity  100.0%;  Pred. No. 1;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1117 GAAGGACATATGTTACTGTCTGGTC 1141
              |||||||||||||||||||||||||
Db         25 GAAGGACATATGTTACTGTCTGGTC 1


RESULT 26
US-08-980-326-65/c
; Sequence 65, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-65

Query Match             0.6%;  Score 25;  DB 3;  Length 25;
Best Local Similarity  100.0%;  Pred. No. 1;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       3788 CATTGAGGAAGAACATATCTGTGGC 3812
              |||||||||||||||||||||||||
Db         25 CATTGAGGAAGAACATATCTGTGGC 1


RESULT 27
US-09-949-016-36633
; Sequence 36633, Application US/0994016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
```

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36633
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-36633

Query Match             0.6%;   Score 25;  DB 3;  Length 601;
Best Local Similarity  100.0%;  Pred. No. 0.97;
Matches   25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   3864 TTTTTTTTTTTTTTTGCCTTTTTTA 3888
          |||||||||||||||||||||||||
Db    287 TTTTTTTTTTTTTTTGCCTTTTTTA 311


RESULT 28
US-09-949-016-44805
; Sequence 44805, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44805
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44805

Query Match             0.6%;   Score 25;  DB 3;  Length 601;
Best Local Similarity  100.0%;  Pred. No. 0.97;
Matches   25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   3864 TTTTTTTTTTTTTTTGCCTTTTTTA 3888
          |||||||||||||||||||||||||
Db    287 TTTTTTTTTTTTTTTGCCTTTTTTA 311


RESULT 29
US-09-949-016-12696
; Sequence 12696, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12696
; LENGTH: 15546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12696

Query Match             0.6%;   Score 25;  DB 3;  Length 15546;
Best Local Similarity  100.0%;  Pred. No. 0.94;
Matches   25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   3864 TTTTTTTTTTTTTTTGCCTTTTTTA 3888
          |||||||||||||||||||||||||
Db   6839 TTTTTTTTTTTTTTTGCCTTTTTTA 6863


RESULT 30
US-09-949-016-13028
; Sequence 13028, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13028
; LENGTH: 15546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13028

Query Match             0.6%;   Score 25;  DB 3;  Length 15546;
Best Local Similarity  100.0%;  Pred. No. 0.94;
Matches   25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   3864 TTTTTTTTTTTTTTTGCCTTTTTTA 3888
          |||||||||||||||||||||||||
Db   6839 TTTTTTTTTTTTTTTGCCTTTTTTA 6863


RESULT 31
US-09-949-016-16005/c
; Sequence 16005, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16005
; LENGTH: 24508
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16005
```

```
Query Match           0.6%;    Score 25;   DB 3;   Length 24508;
Best Local Similarity 100.0%;  Pred. No. 0.94;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      3863 TTTTTTTTTTTTTTTTGCCTTTTTT 3887
             |||||||||||||||||||||||||
Db      1492 TTTTTTTTTTTTTTTTGCCTTTTTT 1468
```

RESULT 32
US-09-949-016-11864/c
; Sequence 11864, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11864
;   LENGTH: 24519
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-11864

```
Query Match           0.6%;    Score 25;   DB 3;   Length 24519;
Best Local Similarity 100.0%;  Pred. No. 0.94;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      3863 TTTTTTTTTTTTTTTTGCCTTTTTT 3887
             |||||||||||||||||||||||||
Db      1504 TTTTTTTTTTTTTTTTGCCTTTTTT 1480
```

RESULT 33
US-08-980-326-36/c
; Sequence 36, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-980-326-36

```
Query Match           0.6%;    Score 24;   DB 3;   Length 24;
```

```
Best Local Similarity 100.0%;  Pred. No. 2.7;
Matches   24;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       190 CGGGAGAAGCTAAACGAAGAACAC 213
             ||||||||||||||||||||||||
Db        24 CGGGAGAAGCTAAACGAAGAACAC 1
```

RESULT 34
US-08-980-326-37/c
; Sequence 37, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-980-326-37

```
Query Match           0.6%;    Score 24;   DB 3;   Length 24;
Best Local Similarity 100.0%;  Pred. No. 2.7;
Matches   24;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       308 ATAAGGAATACTTGCTGGCTGGGG 331
             ||||||||||||||||||||||||
Db        24 ATAAGGAATACTTGCTGGCTGGGG 1
```

RESULT 35
US-08-980-326-38/c
; Sequence 38, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-980-326-38

Query Match   0.6%;   Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3896 GATCCTCAAGGAAATACAACCTAG 3919
           ||||||||||||||||||||||||
Db   24 GATCCTCAAGGAAATACAACCTAG 1

RESULT 36
US-08-980-326-40
; Sequence 40, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-40

Query Match   0.6%;   Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   2026 ACAGGAGGGAAGAAAGTCATTCAG 2049
           ||||||||||||||||||||||||
Db   1 ACAGGAGGGAAGAAAGTCATTCAG 24

RESULT 37
US-08-980-326-42
; Sequence 42, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-42

Query Match   0.6%;   Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   91 CAACCCGAAGGTCTGAAGAAAACC 114
           ||||||||||||||||||||||||
Db   1 CAACCCGAAGGTCTGAAGAAAACC 24

RESULT 38
US-08-980-326-50
; Sequence 50, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-50

Query Match   0.6%;   Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3304 TGCCTCTCAGACTTCATCGCTCCC 3327
           ||||||||||||||||||||||||
Db   1 TGCCTCTCAGACTTCATCGCTCCC 24

RESULT 39
US-08-980-326-52
; Sequence 52, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens

US-08-980-326-52

Query Match   0.6%; Score 24; DB 3; Length 24;
Best Local Similarity   100.0%; Pred. No. 2.7;
Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2887 ATGGATTGGCTGTCTGAACCTCAC 2910
           ||||||||||||||||||||||||
Db   1 ATGGATTGGCTGTCTGAACCTCAC 24

RESULT 40
US-08-980-326-54/c
; Sequence 54, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-54

Query Match   0.6%; Score 24; DB 3; Length 24;
Best Local Similarity   100.0%; Pred. No. 2.7;
Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3394 AGCAAGGCCTATGAGGATGATGGT 3417
           ||||||||||||||||||||||||
Db   24 AGCAAGGCCTATGAGGATGATGGT 1

RESULT 41
US-08-980-326-56/c
; Sequence 56, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 24
; TYPE: DNA

; ORGANISM: Homo sapiens
US-08-980-326-56

Query Match   0.6%; Score 24; DB 3; Length 24;
Best Local Similarity   100.0%; Pred. No. 2.7;
Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2631 GTTGATTGGAGGAGCAACCACTTC 2654
           ||||||||||||||||||||||||
Db   24 GTTGATTGGAGGAGCAACCACTTC 1

RESULT 42
US-08-980-326-64
; Sequence 64, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-980-326-64

Query Match   0.6%; Score 24; DB 3; Length 24;
Best Local Similarity   100.0%; Pred. No. 2.7;
Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3813 TGAGGTTGAGAAATGGCTTGGACC 3836
           ||||||||||||||||||||||||
Db   1 TGAGGTTGAGAAATGGCTTGGACC 24

RESULT 43
US-08-980-326-66
; Sequence 66, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 24
; TYPE: DNA

```
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-08-980-326-66

Query Match     0.6%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches  24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy      8 TGTGGAGAGCACGTCTTCTCTGCC 31
            ||||||||||||||||||||||||
Db      1 TGTGGAGAGCACGTCTTCTCTGCC 24

RESULT 44
US-09-949-016-39482/c
;  Sequence 39482, Application US/09949016
;  Patent No. 6812339
;  GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 39482
;  LENGTH: 601
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-39482

Query Match     0.6%; Score 24; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches  24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTTGCCTTTTT 3886
            ||||||||||||||||||||
Db    100 TTTTTTTTTTTTTTTTTTGCCTTTTT 77

RESULT 45
US-09-949-016-39515/c
;  Sequence 39515, Application US/09949016
;  Patent No. 6812339
;  GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 39515
;  LENGTH: 601
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-39515

Query Match     0.6%; Score 24; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches  24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTGCCTTTTT 3886
            ||||||||||||||||||
Db    100 TTTTTTTTTTTTTTTTGCCTTTTT 77

RESULT 46
US-09-949-016-61884
;  Sequence 61884, Application US/09949016
;  Patent No. 6812339
;  GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 61884
;  LENGTH: 601
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-61884

Query Match     0.6%; Score 24; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches  24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3861 ACTTTTTTTTTTTTTTTTTTTGCCTTT 3884
            ||||||||||||||||||||||
Db    493 ACTTTTTTTTTTTTTTTTTTTGCCTTT 516

RESULT 47
US-09-949-016-63101/c
;  Sequence 63101, Application US/09949016
;  Patent No. 6812339
;  GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 63101
;  LENGTH: 601
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-63101

Query Match     0.6%; Score 24; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches  24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTTGCCTTTTT 3886
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Db          100 TTTTTTTTTTTTTTGCCTTTTT 77

RESULT 48
US-09-949-016-63123/c
; Sequence 63123, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63123
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-63123

Query Match             0.6%;  Score 24;  DB 3;  Length 601;
Best Local Similarity   100.0%;  Pred. No. 2.7;
Matches   24;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       3863 TTTTTTTTTTTTTTTGCCTTTTT 3886
              |||||||||||||||||||||||
Db        100 TTTTTTTTTTTTTTTGCCTTTTT 77


RESULT 49
US-09-949-016-118281/c
; Sequence 118281, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 118281
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-118281

Query Match             0.6%;  Score 24;  DB 3;  Length 601;
Best Local Similarity   100.0%;  Pred. No. 2.7;
Matches   24;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       3863 TTTTTTTTTTTTTTTGCCTTTTT 3886
              |||||||||||||||||||||||
Db        100 TTTTTTTTTTTTTTTGCCTTTTT 77


RESULT 50
US-09-949-016-118319/c
; Sequence 118319, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 118319
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-118319

Query Match             0.6%;  Score 24;  DB 3;  Length 601;
Best Local Similarity   100.0%;  Pred. No. 2.7;
Matches   24;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       3863 TTTTTTTTTTTTTTTGCCTTTTT 3886
              |||||||||||||||||||||||
Db        100 TTTTTTTTTTTTTTTGCCTTTTT 77

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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters:       57335

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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	4	318	8.1	420	5	US-10-040-862-8171	Sequence 8171, Ap
	5	318	8.1	420	6	US-10-057-475B-8171	Sequence 8171, Ap
	6	318	8.1	420	6	US-10-154-884B-8171	Sequence 8171, Ap
	7	318	8.1	420	8	US-10-764-324-8171	Sequence 8171, Ap
	8	222	5.7	305	5	US-10-040-739-642	Sequence 642, App
	9	124	3.2	901	6	US-10-027-632-121776	Sequence 121776,
	10	124	3.2	901	6	US-10-027-632-121776	Sequence 121776,
	11	124	3.2	1275	4	US-09-925-065A-727226	Sequence 727226,
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c	14	69	1.8	493	5	US-10-027-632-314464	Sequence 314464,
c	15	69	1.8	493	6	US-10-027-632-314465	Sequence 314465,
c	16	69	1.8	493	6	US-10-027-632-56722	Sequence 56722, A
c	17	69	1.8	493	6	US-10-027-632-314464	Sequence 314464,
c	18	69	1.8	493	6	US-10-027-632-314465	Sequence 314465,
c	19	69	1.8	627	5	US-10-027-632-3760	Sequence 3760, Ap
c	20	69	1.8	627	6	US-10-027-632-3760	Sequence 3760, Ap
c	21	39	1.0	611	4	US-09-925-065A-460077	Sequence 460077,
c	22	31	0.8	588	4	US-09-925-065A-39453	Sequence 39453, A
c	23	28	0.7	28	7	US-10-607-712-45	Sequence 45, Appl
	24	26	0.7	26	7	US-10-607-712-35	Sequence 35, Appl
	25	26	0.7	26	7	US-10-607-712-48	Sequence 48, Appl
	26	26	0.7	26	7	US-10-607-712-53	Sequence 53, Appl
	27	26	0.7	26	7	US-10-607-712-57	Sequence 57, Appl
	28	26	0.7	26	7	US-10-607-712-63	Sequence 63, Appl
c	29	26	0.7	559	4	US-09-925-065A-602656	Sequence 602656,
	30	26	0.7	595	4	US-09-925-065A-271845	Sequence 271845,
	31	26	0.7	649	4	US-10-437-961-1741	Sequence 1741, Ap
c	32	26	0.7	1374	4	US-09-925-065A-702090	Sequence 702090,
	33	25	0.6	25	7	US-10-607-712-39	Sequence 39, Appl
c	34	25	0.6	25	7	US-10-607-712-41	Sequence 41, Appl
c	35	25	0.6	25	7	US-10-607-712-49	Sequence 49, Appl
c	36	25	0.6	25	7	US-10-607-712-58	Sequence 58, Appl
	37	25	0.6	25	7	US-10-607-712-59	Sequence 59, Appl
c	38	25	0.6	25	7	US-10-607-712-60	Sequence 60, Appl
c	39	25	0.6	25	7	US-10-607-712-61	Sequence 61, Appl
c	40	25	0.6	25	7	US-10-607-712-62	Sequence 62, Appl
c	41	25	0.6	25	7	US-10-607-712-65	Sequence 65, Appl
c	42	25	0.6	237	8	US-10-357-930-61072	Sequence 61072, A
c	43	25	0.6	238	7	US-10-424-599-9150	Sequence 9150, Ap
c	44	25	0.6	262	8	US-10-424-599-13138	Sequence 13138, A
c	45	25	0.6	280	8	US-10-425-115-158147	Sequence 158147,
c	46	25	0.6	296	9	US-09-867-701-9532	Sequence 9532, Ap
c	47	25	0.6	343	9	US-10-756-149-3961	Sequence 3961, Ap
c	48	25	0.6	375	8	US-10-425-115-165833	Sequence 165833,
c	49	25	0.6	433	7	US-10-021-323-7632	Sequence 7632, Ap
c	50	25	0.6	442	8	US-10-425-115-111243	Sequence 111243,
c	51	25	0.6	475	8	US-10-021-323-7449	Sequence 7449, Ap
c	52	25	0.6	519	8	US-10-425-115-109290	Sequence 109290,
c	53	25	0.6	524	8	US-10-425-115-127511	Sequence 127511,
c	54	25	0.6	530	7	US-10-437-963-20808	Sequence 20808, A
c	55	25	0.6	542	8	US-09-925-065A-279223	Sequence 279223,
c	56	25	0.6	545	4	US-09-925-065A-936651	Sequence 936651,
c	57	25	0.6	630	4	US-09-925-065A-550047	Sequence 550047,
c	58	25	0.6	693	4	US-10-425-115-26647	Sequence 26647, A
c	59	25	0.6	1059	7	US-10-424-599-83851	Sequence 83851, A
c	60	25	0.6	1180	9	US-09-948-820-21	Sequence 21, Appl
c	61	25	0.6	1180	8	US-09-613-076-21	Sequence 21, Appl
c	62	25	0.6	1198	8	US-10-425-115-135465	Sequence 135465,
c	63	25	0.6	1312	8	US-10-425-115-13261	Sequence 13261, A
c	64	25	0.6	1374	8	US-10-425-115-35149	Sequence 35149, A
c	65	25	0.6	1385	8	US-10-425-115-148748	Sequence 148748,
c	66	25	0.6	1660	4	US-09-925-065A-34355	Sequence 34355, A
c	67	25	0.6	1660	4	US-09-925-065A-34356	Sequence 34356, A
c	68	25	0.6	1660	4	US-09-925-065A-34357	Sequence 34357, A
c	69	25	0.6	1660	4	US-09-925-065A-34358	Sequence 34358, A
c	70	25	0.6	1660	4	US-09-925-065A-34359	Sequence 34359, A
	71	25	0.6	1793	7	US-10-437-963-63954	Sequence 63954, A
	72	25	0.6	2050	3	US-09-940-240-15	Sequence 15, Appl
	73	25	0.6	2050	7	US-10-413-899-15	Sequence 15, Appl
	74	25	0.6	4959	8	US-10-425-115-97308	Sequence 97308, A
	75	25	0.6	142976	8	US-10-367-094-99	Sequence 99, Appl
c	76	25	0.6	251199	8	US-10-482-029-205	Sequence 205, App
	77	25	0.6	2140405	5	US-10-027-632-76212	Sequence 76212, A
	78	25	0.6	2140405	6	US-10-027-632-76212	Sequence 76212, A
	79	24	0.6	24	7	US-10-607-712-36	Sequence 36, Appl
c	80	24	0.6	24	7	US-10-607-712-37	Sequence 37, Appl
c	81	24	0.6	24	7	US-10-607-712-38	Sequence 38, Appl
	82	24	0.6	24	7	US-10-607-712-40	Sequence 40, Appl
	83	24	0.6	24	7	US-10-607-712-42	Sequence 42, Appl
	84	24	0.6	24	7	US-10-607-712-50	Sequence 50, Appl
	85	24	0.6	24	7	US-10-607-712-52	Sequence 52, Appl
c	86	24	0.6	24	7	US-10-607-712-54	Sequence 54, Appl
	87	24	0.6	24	7	US-10-607-712-56	Sequence 56, Appl
	88	24	0.6	24	7	US-10-607-712-64	Sequence 64, Appl
	89	24	0.6	24	7	US-10-607-712-66	Sequence 66, Appl
	90	24	0.6	199	3	US-09-867-701-9184	Sequence 9184, Ap
	91	24	0.6	199	8	US-09-867-701-10780	Sequence 10780, A
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c	94	24	0.6	341	8	US-10-674-124A-11000	Sequence 11000, A
c	95	24	0.6	374	8	US-10-357-930-54298	Sequence 54298, A
c	96	24	0.6	479	5	US-10-027-632-57379	Sequence 57379, A

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c	98	24	0.6	479	5	US-10-027-632-57379	Sequence 57379, A
c	99	24	0.6	479	6	US-10-027-632-310427	Sequence 310427,
c	100	24	0.6	489	6	US-10-027-632-412268	Sequence 412268,
	101	24	0.6	506	4	US-09-925-065A-270554	Sequence 270554,
	102	24	0.6	512	4	US-09-925-065A-620176	Sequence 620176,
	103	24	0.6	548	4	US-09-969-034-2933	Sequence 2933, Ap
	104	24	0.6	548	4	US-09-925-065A-424567	Sequence 424567,
c	105	24	0.6	549	4	US-09-925-065A-889241	Sequence 889241,
	106	24	0.6	585	4	US-09-925-065A-624935	Sequence 624935,
	107	24	0.6	626	4	US-09-925-065A-530520	Sequence 530520,
	108	24	0.6	655	5	US-10-027-632-27407	Sequence 27407, A
c	109	24	0.6	655	5	US-10-027-632-27407	Sequence 27407, A
	110	24	0.6	655	6	US-10-027-632-27408	Sequence 27408, A
	111	24	0.6	766	5	US-10-027-632-5085	Sequence 5085, Ap
	112	24	0.6	766	6	US-10-027-632-5085	Sequence 5085, Ap
	113	24	0.6	794	5	US-10-437-963-80007	Sequence 80007, A
c	114	24	0.6	890	7	US-10-011-585A-134	Sequence 134, App
c	115	24	0.6	9417	9	US-10-852-335A-22	Sequence 22, Appl
	116	24	0.6	32249	3	US-10-242-355-1132	Sequence 1132, Ap
c	117	24	0.6	86500	8	US-10-719-993-6771	Sequence 6771, Ap
	118	24	0.6	137908	9	US-10-287-436A-779	Sequence 779, App
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c	120	24	0.6	241805	7	US-10-741-601-5621	Sequence 5621, Ap
c	121	24	0.6	241805	8	US-10-741-600-17581	Sequence 17581, A
c	122	24	0.6	325446	7	US-10-719-993-6824	Sequence 6824, Ap
	123	23	0.6	23	7	US-10-607-712-46	Sequence 46, Appl
c	124	23	0.6	23	7	US-10-607-712-55	Sequence 55, Appl
c	125	23	0.6	201	7	US-10-741-601-14799	Sequence 14799, A
	126	23	0.6	201	7	US-10-741-600-25758	Sequence 25758, A
	127	23	0.6	201	8	US-10-741-600-25759	Sequence 25759, A
	128	23	0.6	201	8	US-10-741-600-25764	Sequence 25764, A
	129	23	0.6	201	8	US-10-741-600-37188	Sequence 37188, A
	130	23	0.6	225	9	US-10-933-118-3	Sequence 3, Appli
	131	23	0.6	270	8	US-10-425-115-158083	Sequence 158083,
	132	23	0.6	282	8	US-10-425-115-92332	Sequence 92332, A
	133	23	0.6	361	8	US-10-425-115-88628	Sequence 88628, A
c	134	23	0.6	376	7	US-09-925-065A-261182	Sequence 261182,
	135	23	0.6	385	3	US-10-152-319A-457	Sequence 457, Appl
	136	23	0.6	421	3	US-09-917-800A-831	Sequence 831, App
	137	23	0.6	421	8	US-10-741-600-37188	Sequence 31, Appl
	138	23	0.6	421	9	US-10-388-934-31	Sequence 174, App
	139	23	0.6	434	3	US-09-876-143-174	Sequence 262, App
	140	23	0.6	434	3	US-09-876-143-262	Sequence 351757,
c	141	23	0.6	451	7	US-09-925-065A-351757	Sequence 116134,
c	142	23	0.6	459	7	US-10-424-599-116134	Sequence 56449, A
c	143	23	0.6	460	8	US-10-357-930-56449	Sequence 18, Appl
	144	23	0.6	481	3	US-09-746-783-18	Sequence 98281, A
	145	23	0.6	498	4	US-09-925-065A-98281	Sequence 98282, A
	146	23	0.6	498	4	US-09-925-065A-98282	Sequence 925330,
	147	23	0.6	503	4	US-09-925-065A-925330	Sequence 828324,
	148	23	0.6	522	4	US-09-925-065A-828324	Sequence 819272,
	149	23	0.6	523	8	US-09-925-065A-819272	Sequence 105702,
	150	23	0.6	549	4	US-10-425-115-105702	Sequence 3410, Ap
	151	23	0.6	556	4	US-09-925-065A-3410	Sequence 755600,
c	152	23	0.6	574	4	US-09-925-065A-755600	Sequence 278724,
	153	23	0.6	575	4	US-09-925-065A-278724	Sequence 561677,
c	154	23	0.6	576	9	US-09-925-065A-561677	Sequence 24722, A
c	155	23	0.6	600	4	US-10-972-079-24722	Sequence 24723, A
c	156	23	0.6	600	9	US-10-972-079-24723	Sequence 73651, A
c	157	23	0.6	600	9	US-10-972-079-73651	Sequence 73652, A
c	158	23	0.6	600	9	US-10-972-079-73652	Sequence 478484,
	159	23	0.6	601	4	US-09-925-065A-478484	Sequence 478485,
c	160	23	0.6	601	4	US-09-925-065A-478485	Sequence 188252,
	161	23	0.6	611	4	US-09-925-065A-188252	Sequence 751693,
	162	23	0.6	613	3	US-09-925-065A-751693	Sequence 273790,
c	163	23	0.6	619	5	US-10-027-632-273790	Sequence 273790,
c	164	23	0.6	619	6	US-10-027-632-273790	Sequence 739010,
	165	23	0.6	634	4	US-09-925-065A-739010	Sequence 922916,
c	166	23	0.6	705	5	US-09-925-065A-922916	Sequence 159784,
c	167	23	0.6	716	4	US-10-027-632-159784	Sequence 159784,
	168	23	0.6	716	6	US-10-027-632-159784	Sequence 107262,
	169	23	0.6	717	5	US-10-027-632-107262	Sequence 107262,
	170	23	0.6	717	5	US-10-027-632-107263	Sequence 107263,
	171	23	0.6	717	6	US-10-027-632-107262	Sequence 107262,
	172	23	0.6	717	6	US-10-027-632-107263	Sequence 107263,
c	173	23	0.6	821	5	US-10-027-632-153100	Sequence 153100,
c	174	23	0.6	821	6	US-10-027-632-153101	Sequence 153101,
c	175	23	0.6	821	6	US-10-027-632-153100	Sequence 153100,
c	176	23	0.6	821	6	US-10-027-632-153101	Sequence 153101,
c	177	23	0.6	825	8	US-10-425-115-85657	Sequence 85657, A
	178	23	0.6	886	8	US-10-425-115-76054	Sequence 76054, A
	179	23	0.6	955	4	US-09-925-065A-72630	Sequence 72630, A
c	180	23	0.6	1395	4	US-09-925-065A-78441	Sequence 78441, A
c	181	23	0.6	1610	6	US-10-133-937-77	Sequence 77, Appl
c	182	23	0.6	1875	5	US-10-159-563-77	Sequence 77, Appl
c	183	23	0.6	2073	6	US-10-106-698-222	Sequence 222, App
c	184	23	0.6	3382	6	US-10-027-632-97481	Sequence 97481, A
c	185	23	0.6	4840	8	US-10-027-632-27	Sequence 27, Appl
c	186	23	0.6	5565	6	US-10-443-201-27	Sequence 27, Appl
c	187	23	0.6	9456	8	US-10-723-860-6164	Sequence 6164, Ap
c	188	23	0.6	10480	6	US-10-311-455-236	Sequence 236, App
c	189	23	0.6	14117	3	US-10-723-860-6147	Sequence 6147, Ap
c	190	23	0.6	14117	9	US-10-311-455-2174	Sequence 2174, Ap
c	191	23	0.6	17431	9	US-09-954-531-1377	Sequence 1377, Ap
c	192	23	0.6	17431	3	US-10-843-641A-2444	Sequence 2444, Ap
c	193	23	0.6	20486	5	US-10-764-855-247	Sequence 247, App
c	194	23	0.6	34245	7	US-10-072-349-247	Sequence 247, App
c	195	23	0.6	81924	7	US-10-240-485-102	Sequence 102, App
c	196	23	0.6	107910	9	US-10-367-094-102	Sequence 102, App
c	197	23	0.6	169659	7	US-10-741-601-5636	Sequence 5636, Ap
c	198	23	0.6	203127	7	US-10-981-277-19	Sequence 19, Appl
	199	23	0.6	203127	8	US-10-322-696-70	Sequence 70, Appl
	200	23	0.6	510510	7	US-10-741-601-5654	Sequence 5654, Ap
	201	22	0.6	22	8	US-10-741-600-17666	Sequence 17666, A
	202	22	0.6	194	7	US-10-741-600-17606	Sequence 17606, A
	203	22	0.6	201	3	US-10-607-712-47	Sequence 47, Appl
	204	22	0.6	201	8	US-09-867-701-9917	Sequence 9917, Ap
	205	22	0.6	244	8	US-10-719-993-30838	Sequence 30838, A
	206	22	0.6	250	8	US-10-719-993-31678	Sequence 31678, A
	207	22	0.6	250	7	US-10-425-115-98422	Sequence 98422, A
	208	22	0.6	250	7	US-10-242-535A-54640	Sequence 54640, A
	209	22	0.6	250	7	US-10-242-535A-54648	Sequence 54648, A
	210	22	0.6	287	7	US-10-085-783A-54640	Sequence 54640, A
	211	22	0.6	324	3	US-10-085-783A-54648	Sequence 54648, A
	212	22	0.6	339	7	US-09-867-701-8939	Sequence 8939, Ap
	213	22	0.6	350	7	US-09-917-800A-641	Sequence 641, App
	214	22	0.6	353	6	US-10-437-963-34514	Sequence 34514, A
	215	22	0.6	374	8	US-10-424-599-34827	Sequence 84827, A
	216	22	0.6	374	4	US-10-424-599-80394	Sequence 80394, A
	217	22	0.6	424	8	US-10-058-053A-4	Sequence 4, Appli
	218	22	0.6	424	4	US-10-838-226-4	Sequence 4, Appli
	219	22	0.6	424	4	US-09-925-065A-204738	Sequence 204738, A
	220	22	0.6	436	4	US-09-925-065A-204739	Sequence 204739, A
	221	22	0.6	452	8	US-10-357-930-13696	Sequence 13696, A
	222	22	0.6	468	7	US-10-357-930-34836	Sequence 34836, A
	223	22	0.6	468	5	US-10-424-599-67712	Sequence 67712, A
	224	22	0.6	481	9	US-10-027-632-201664	Sequence 201664, A
	225	22	0.6	488	3	US-10-027-632-201664	Sequence 201664, A
	226	22	0.6	493	7	US-09-925-065A-401865	Sequence 401865, A
	227	22	0.6	494	4	US-09-918-995-24463	Sequence 24463, A
	228	22	0.6	494	3	US-09-918-995-21166	Sequence 21166, A
c	229	22	0.6	494	4	US-09-925-065A-396325	Sequence 396325, A
c	230	22	0.6	494	4	US-09-925-065A-396326	Sequence 396326, A
c	231	22	0.6	505	5	US-10-027-632-231843	Sequence 231843, A
c	232	22	0.6	506	4	US-10-027-632-231843	Sequence 231843, A
	233	22	0.6	514	3	US-09-925-065A-77965	Sequence 77965, A
	234	22	0.6	518	9	US-09-814-353-13630	Sequence 13630, A
	235	22	0.6	518	3	US-09-925-065A-113707	Sequence 113707, A
c	236	22	0.6	519	9	US-09-873-367C-1045	Sequence 1045, Ap
	237	22	0.6	519	4	US-10-843-641A-1045	Sequence 1045, Ap
c	238	22	0.6	520	4	US-10-843-641A-417525	Sequence 417525, A
c	239	22	0.6	524	4	US-09-925-065A-417527	Sequence 417527, A
c	240	22	0.6	524	4	US-09-925-065A-42413	Sequence 42413, A
c	241	22	0.6	520	4	US-09-925-065A-583132	Sequence 583132, A
c	242	22	0.6	524	4	US-09-925-065A-650278	Sequence 650278, A

#						Accession	Sequence
c 243	22	0.6	531	5	US-10-027-632-210314	Sequence 210314,
c 244	22	0.6	531	6	US-10-027-632-210314	Sequence 210314,
c 245	22	0.6	535	4	US-09-925-065A-417523	Sequence 417523,
c 246	22	0.6	535	4	US-09-925-065A-417524	Sequence 417524,
247	22	0.6	536	4	US-09-925-065A-924158	Sequence 924158,
248	22	0.6	538	4	US-09-925-065A-102798	Sequence 102798,
249	22	0.6	538	4	US-09-925-065A-102799	Sequence 102799,
250	22	0.6	540	4	US-09-925-065A-11434	Sequence 11434, A
251	22	0.6	540	4	US-09-925-065A-105964	Sequence 105964,
c 252	22	0.6	550	4	US-09-925-065A-262968	Sequence 262968,
253	22	0.6	550	7	US-10-152-319A-825	Sequence 825, App
c 254	22	0.6	563	4	US-09-925-065A-898853	Sequence 898853,
255	22	0.6	569	4	US-09-925-065A-112247	Sequence 112247,
256	22	0.6	569	4	US-09-925-065A-112248	Sequence 112248,
257	22	0.6	569	6	US-10-101-510-99	Sequence 99, Appl
258	22	0.6	569	7	US-10-283-975A-32	Sequence 32, Appl
259	22	0.6	570	4	US-09-925-065A-314680	Sequence 314680,
260	22	0.6	570	4	US-09-925-065A-314681	Sequence 314681,
c 261	22	0.6	573	7	US-10-437-963-40312	Sequence 40312, A
c 262	22	0.6	578	7	US-09-925-065A-297980	Sequence 297980,
c 263	22	0.6	585	4	US-10-425-115-120425	Sequence 120425,
264	22	0.6	588	3	US-09-871-161-275	Sequence 275, App
265	22	0.6	589	4	US-09-925-065A-878937	Sequence 878937,
c 266	22	0.6	598	4	US-09-925-065A-539793	Sequence 539793,
267	22	0.6	598	8	US-10-357-930-56158	Sequence 56158, A
268	22	0.6	599	9	US-10-972-079-18874	Sequence 18874, A
269	22	0.6	600	4	US-09-925-065A-902706	Sequence 902706,
c 270	22	0.6	601	4	US-09-925-065A-575787	Sequence 575787,
271	22	0.6	605	4	US-09-925-065A-898473	Sequence 898473,
c 272	22	0.6	608	4	US-09-925-065A-637147	Sequence 637147,
273	22	0.6	609	4	US-09-925-065A-809765	Sequence 809765,
274	22	0.6	612	5	US-10-027-632-71623	Sequence 71623, A
275	22	0.6	612	6	US-10-027-632-71623	Sequence 71623, A
c 276	22	0.6	614	6	US-10-027-632-209251	Sequence 209251,
277	22	0.6	614	6	US-10-027-632-209252	Sequence 209252,
c 278	22	0.6	614	6	US-10-027-632-209251	Sequence 209251,
279	22	0.6	614	6	US-10-027-632-209252	Sequence 209252,
280	22	0.6	619	7	US-10-242-535A-13956	Sequence 13956, A
c 281	22	0.6	619	4	US-10-085-783A-13956	Sequence 13956,
282	22	0.6	635	4	US-09-925-065A-731865	Sequence 731865,
283	22	0.6	655	5	US-10-027-632-6052	Sequence 6052, Ap
284	22	0.6	655	5	US-10-027-632-6052	Sequence 6052, Ap
285	22	0.6	655	6	US-10-027-632-6053	Sequence 6053, Ap
286	22	0.6	655	6	US-10-027-632-6053	Sequence 6053, Ap
287	22	0.6	657	7	US-10-424-599-9950	Sequence 9950, Ap
288	22	0.6	659	8	US-10-425-115-148511	Sequence 148511,
289	22	0.6	666	5	US-10-027-632-110414	Sequence 110414,
290	22	0.6	666	6	US-10-027-632-110414	Sequence 110414,
291	22	0.6	688	3	US-10-066-543-1210	Sequence 1210, Ap
292	22	0.6	714	4	US-10-424-599-65277	Sequence 65277,
293	22	0.6	734	4	US-09-925-065A-80511	Sequence 80511, A
294	22	0.6	734	4	US-09-925-065A-80512	Sequence 80512, A
295	22	0.6	759	3	US-09-919-580-825	Sequence 825, App
296	22	0.6	795	5	US-10-027-632-163308	Sequence 163308,
297	22	0.6	795	6	US-10-027-632-163309	Sequence 163309,
298	22	0.6	795	6	US-10-027-632-163310	Sequence 163310,
299	22	0.6	795	5	US-10-027-632-142106	Sequence 142106,
300	22	0.6	795	6	US-10-027-632-163309	Sequence 163309,
301	22	0.6	796	6	US-10-027-632-163310	Sequence 163310,
302	22	0.6	796	5	US-10-027-632-142106	Sequence 142106,
303	22	0.6	796	6	US-10-027-632-165236	Sequence 165236,
304	22	0.6	796	5	US-10-027-632-165237	Sequence 165237,
305	22	0.6	796	6	US-10-027-632-142106	Sequence 142106,
306	22	0.6	796	6	US-10-027-632-165236	Sequence 165236,
307	22	0.6	796	5	US-10-027-632-165237	Sequence 165237,
308	22	0.6	810	8	US-10-425-115-71750	Sequence 71750, A
309	22	0.6	816	7	US-10-152-319A-1717	Sequence 1717, Ap
310	22	0.6	844	4	US-10-424-599-25219	Sequence 25219, A
311	22	0.6	876	7	US-10-425-114-30264	Sequence 30264, A
c 312	22	0.6	905	7	US-10-424-599-78300	Sequence 78300, A
c 313	22	0.6	905	7	US-10-437-963-80008	Sequence 80008, A
c 314	22	0.6	952	5	US-09-925-065A-701979	Sequence 701979,
c 315	22	0.6	980	4	US-09-925-065A-696097	Sequence 696097,

#						Accession	Sequence
c 316	22	0.6	982	4	US-09-925-065A-725590	Sequence 725590,
c 317	22	0.6	998	5	US-10-425-115-68031	Sequence 68031, A
c 318	22	0.6	1031	9	US-10-956-157-1760	Sequence 1760, Ap
c 319	22	0.6	1031	9	US-10-956-157-6995	Sequence 6995, App
c 320	22	0.6	1136	4	US-10-320-352-1	Sequence 1, Appl
c 321	22	0.6	1170	4	US-09-925-065A-297981	Sequence 297981,
c 322	22	0.6	1225	4	US-09-925-065A-703263	Sequence 703263,
c 323	22	0.6	1228	5	US-10-027-632-253407	Sequence 253407,
c 324	22	0.6	1228	6	US-10-027-632-253407	Sequence 253407,
c 325	22	0.6	1352	9	US-10-314-942-9	Sequence 9, Appli
c 326	22	0.6	1470	8	US-10-775-920-155	Sequence 155, App
c 327	22	0.6	1471	9	US-10-504-173-9	Sequence 9, Appli
c 328	22	0.6	1518	8	US-09-729-674-143	Sequence 143, App
c 329	22	0.6	1518	9	US-10-913-553-143	Sequence 143, App
c 330	22	0.6	1520	3	US-09-397-945-101	Sequence 101, App
c 331	22	0.6	1520	7	US-10-653-595-101	Sequence 101, App
c 332	22	0.6	1573	5	US-09-746-783-187	Sequence 187, App
c 333	22	0.6	1739	5	US-10-236-433-6	Sequence 6, Appli
c 334	22	0.6	1766	4	US-09-925-065A-30791	Sequence 30791, A
c 335	22	0.6	1791	4	US-10-425-114-32464	Sequence 32464, A
336	22	0.6	1808	8	US-10-425-115-59855	Sequence 59855, A
c 337	22	0.6	1809	8	US-10-723-860-5723	Sequence 5723, Ap
c 338	22	0.6	1809	8	US-10-723-860-6360	Sequence 6360, Ap
c 339	22	0.6	1999	3	US-09-873-367C-1065	Sequence 1065, Ap
c 340	22	0.6	1999	4	US-10-843-641A-1065	Sequence 1065, Ap
341	22	0.6	2274	10	US-11-097-143-31417	Sequence 31417, A
c 342	22	0.6	2315	4	US-09-925-065A-706810	Sequence 706810,
c 343	22	0.6	2315	4	US-09-925-065A-706811	Sequence 706811,
c 344	22	0.6	2351	5	US-10-108-260A-1701	Sequence 1701, Ap
c 345	22	0.6	2595	6	US-10-106-698-451	Sequence 451, App
c 346	22	0.6	2628	4	US-09-925-065A-676638	Sequence 676638,
c 347	22	0.6	3002	4	US-09-925-065A-674422	Sequence 674422,
c 348	22	0.6	3002	4	US-09-925-065A-674423	Sequence 674423,
c 349	22	0.6	3115	3	US-09-925-299-123	Sequence 123, App
c 350	22	0.6	3115	3	US-09-925-299-123	Sequence 123, App
351	22	0.6	3157	7	US-10-282-122A-36766	Sequence 36766, A
c 352	22	0.6	3265	5	US-10-027-632-115124	Sequence 115124,
c 353	22	0.6	3265	6	US-10-027-632-115124	Sequence 115124,
c 354	22	0.6	3452	8	US-10-723-860-7644	Sequence 7644, Ap
c 355	22	0.6	3788	3	US-10-425-115-45050	Sequence 45050, A
c 356	22	0.6	4182	3	US-10-814-353-20319	Sequence 20319, A
357	22	0.6	4256	10	US-11-097-143-34252	Sequence 34252, A
c 358	22	0.6	5413	7	US-10-221-714A-418	Sequence 418, App
c 359	22	0.6	6450	5	US-10-096-710-2	Sequence 2, Appli
c 360	22	0.6	6450	5	US-10-081-563-1	Sequence 1, Appli
c 361	22	0.6	6450	5	US-10-052-092-1	Sequence 1, Appli
c 362	22	0.6	6450	6	US-10-052-092-7	Sequence 7, Appli
c 363	22	0.6	6450	5	US-10-207-655-60	Sequence 60, App
c 364	22	0.6	6450	6	US-10-177-293-127	Sequence 127, App
c 365	22	0.6	6450	6	US-10-007-983-3	Sequence 3, Appli
c 366	22	0.6	6450	6	US-10-007-926A-422	Sequence 422, App
c 367	22	0.6	6450	6	US-10-437-107-1	Sequence 1, Appli
c 368	22	0.6	6450	6	US-10-437-107-7	Sequence 7, Appli
c 369	22	0.6	6450	6	US-10-896-419-1	Sequence 1, Appli
c 370	22	0.6	6450	6	US-10-392-274-1	Sequence 1, Appli
c 371	22	0.6	6450	5	US-10-448-753-3	Sequence 3, Appli
c 372	22	0.6	6450	6	US-10-172-118-435	Sequence 435, App
c 373	22	0.6	6450	6	US-10-388-360-303	Sequence 303, App
c 374	22	0.6	6450	6	US-10-342-887-435	Sequence 435, App
c 375	22	0.6	6450	7	US-10-370-715B-75	Sequence 75, App
c 376	22	0.6	6450	8	US-10-896-419-1	Sequence 1, Appli
c 377	22	0.6	6450	7	US-10-896-419-7	Sequence 7, Appli
c 378	22	0.6	6450	9	US-10-928-465-72	Sequence 72, App
c 379	22	0.6	6619	8	US-10-888-313A-100	Sequence 100, App
c 380	22	0.6	7510	5	US-10-723-860-6901	Sequence 6901, Ap
c 381	22	0.6	8042	6	US-10-001-835-113	Sequence 113, App
c 382	22	0.6	8168	7	US-10-311-455-900	Sequence 900, App
c 383	22	0.6	8168	8	US-10-311-455-901	Sequence 901, App
c 384	22	0.6	10957	8	US-10-311-455-1084	Sequence 1084, App
c 385	22	0.6	11036	5	US-10-239-676-118	Sequence 118, App
c 386	22	0.6	11036	6	US-10-240-453-138	Sequence 138, App
c 387	22	0.6	12405	6	US-10-239-676-35	Sequence 35, App
c 388	22	0.6	12405	6	US-10-240-453-43	Sequence 43, Appl

Left block

c	No			Value		Accession	Description
c	389	0.6	22	12405	7	US-10-221-613-101	Sequence 101, App
c	390	0.6	22	13182	3	US-09-817-199A-3	Sequence 3, Appli
	391	0.6	22	13182	10	US-11-043-964-3	Sequence 3, Appli
	392	0.6	22	17142	5	US-10-239-676-206	Sequence 206, App
c	393	0.6	22	17142	6	US-10-311-455-2080	Sequence 2080, Ap
c	394	0.6	22	17142	6	US-10-240-453-304	Sequence 304, Ap
	395	0.6	22	17200	3	US-09-764-877-3390	Sequence 3390, Ap
c	396	0.6	22	17200	6	US-10-242-515-3390	Sequence 3390, Ap
c	397	0.6	22	17528	6	US-10-311-455-574	Sequence 574, App
	398	0.6	22	19338	9	US-10-737-082-99	Sequence 99, Appl
c	399	0.6	22	19338	9	US-10-765-790-99	Sequence 99, Appl
c	400	0.6	22	22478	3	US-09-997-722-115	Sequence 115, Ap
	401	0.6	22	22609	6	US-09-764-877-2146	Sequence 2146, Ap
c	402	0.6	22	22609	6	US-10-242-515-2146	Sequence 2146, Ap
c	403	0.6	22	24707	3	US-09-740-027-3	Sequence 3, Appli
c	404	0.6	22	24707	5	US-10-274-968-3	Sequence 3, Appli
	405	0.6	22	24707	10	US-11-043-932-3	Sequence 3, Appli
c	406	0.6	22	32193	3	US-09-764-877-2147	Sequence 2147, Ap
c	407	0.6	22	32193	6	US-10-242-515-2147	Sequence 2147, Ap
	408	0.6	22	35000	3	US-09-793-807-10	Sequence 10, Appl
c	409	0.6	22	36645	10	US-11-097-143-24415	Sequence 24415, A
	410	0.6	22	38054	5	US-10-087-192-1720	Sequence 1720, Ap
c	411	0.6	22	38054	5	US-10-087-192-1720	Sequence 1720, Ap
c	412	0.6	22	41787	3	US-10-322-281-820	Sequence 820, App
c	413	0.6	22	42334	7	US-10-052-482-94	Sequence 94, Appl
	414	0.6	22	43887	7	US-10-322-281-109	Sequence 109, App
c	415	0.6	22	46148	8	US-10-719-993-7064	Sequence 7064, Ap
c	416	0.6	22	54016	8	US-10-741-600-17886	Sequence 17886, A
	417	0.6	22	59475	7	US-10-322-696-166	Sequence 166, App
c	418	0.6	22	61197	5	US-10-087-192-1924	Sequence 1924, Ap
	419	0.6	22	75252	3	US-10-087-192-904	Sequence 904, Appl
	420	0.6	22	76180	7	US-10-322-281-492	Sequence 492, App
c	421	0.6	22	79528	8	US-10-723-860-2621	Sequence 2621, Ap
	422	0.6	22	79528	9	US-10-756-149-2427	Sequence 2427, Ap
c	423	0.6	22	81210	7	US-10-741-600-5664	Sequence 5664, Ap
c	424	0.6	22	81210	8	US-10-741-600-17691	Sequence 17691, A
c	425	0.6	22	87467	7	US-10-741-600-5634	Sequence 5634, Ap
c	426	0.6	22	87467	8	US-10-741-600-17624	Sequence 17624, A
	427	0.6	22	105413	8	US-10-427-923-3	Sequence 3, Appli
	428	0.6	22	105413	10	US-11-124-082-3	Sequence 3, Appli
c	429	0.6	22	110096	3	US-09-880-177-1542	Sequence 1542, Ap
	430	0.6	22	150319	9	US-10-981-277-37	Sequence 37, Appl
c	431	0.6	22	156416	9	US-10-461-862-12	Sequence 12, Appl
	432	0.6	22	169659	7	US-10-322-696-70	Sequence 70, Appl
	433	0.6	22	170245	7	US-10-717-597-322	Sequence 322, App
c	434	0.6	22	176373	5	US-10-095-407-17	Sequence 17, Appl
c	435	0.6	22	180557	8	US-10-003-806-6	Sequence 6, Appli
c	436	0.6	22	180557	9	US-10-003-806-9	Sequence 9, Appli
	437	0.6	22	245531	5	US-10-737-318-16	Sequence 16, Appl
	438	0.6	22	251364	5	US-10-175-523-58	Sequence 58, Appl
	439	0.6	22	251364	5	US-10-175-523-61	Sequence 61, Appl
	440	0.6	22	251364	5	US-10-175-523-79	Sequence 79, Appl
	441	0.6	22	251364	10	US-11-099-266-58	Sequence 58, Appl
	442	0.6	22	251364	10	US-11-099-266-61	Sequence 61, Appl
	443	0.6	22	251364	10	US-11-099-266-79	Sequence 79, Appl
c	444	0.6	22	260160	8	US-10-723-860-2837	Sequence 2837, Ap
c	445	0.6	21	465237	7	US-09-933-267A-1	Sequence 1 Appli
c	446	0.6	21	744802	6	US-10-292-798-1369	Sequence 1369, Ap
c	447	0.6	21	775062	8	US-10-719-993-6844	Sequence 6844, Ap
c	448	0.6	21	783062	5	US-10-461-862-166	Sequence 166, App
	449	0.6	22	3673778	6	US-10-312-841-2	Sequence 2, Appli
c	450	0.5	21	21	7	US-10-607-712-43	Sequence 43, Appli
c	451	0.5	21	21	7	US-10-607-712-44	Sequence 44, Appli
c	452	0.5	21	21	7	US-10-607-712-51	Sequence 51, Appli
	453	0.5	21	39	6	US-10-219-195-37	Sequence 37, Appl
	454	0.5	21	39	6	US-10-219-195-38	Sequence 38, Appl
c	455	0.5	21	141	3	US-09-814-353-1383	Sequence 1383, Ap
	456	0.5	21	141	5	US-09-814-353-7746	Sequence 7746, Ap
c	457	0.5	21	170	7	US-09-437-963-56750	Sequence 56750, A
c	458	0.5	21	189	3	US-10-079-623-123	Sequence 123, App
c	459	0.5	21	200	3	US-09-814-353-1387	Sequence 1387, Ap
c	460	0.5	21	200	3	US-09-814-353-7750	Sequence 7750, Ap
c	461	0.5	21	201	7	US-10-741-601-6880	Sequence 6880, Ap

Right block

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c	462	21	0.5	201	7	US-10-741-601-6881	6881,	Sequence 6881, Ap
	463	21	0.5	201	8	US-10-719-993-18653	18653	Sequence 18653, A
	464	21	0.5	201	8	US-10-719-993-19852	19852	Sequence 19852, A
	465	21	0.5	201	8	US-10-719-993-19853	19853	Sequence 19853, A
	466	21	0.5	201	8	US-10-719-993-19854	19854	Sequence 19854, A
c	467	21	0.5	201	8	US-10-719-993-21639	21639	Sequence 21639, A
	468	21	0.5	201	8	US-10-719-993-25064	25064	Sequence 25064, A
	469	21	0.5	201	8	US-10-719-993-43378	43378	Sequence 43378, A
	470	21	0.5	201	8	US-10-719-993-45753	45753	Sequence 45753, A
	471	21	0.5	201	8	US-10-719-993-53040	53040	Sequence 53040, A
	472	21	0.5	201	8	US-10-719-993-53760	53760	Sequence 53760, A
	473	21	0.5	201	8	US-10-719-993-53762	53762	Sequence 53762, A
	474	21	0.5	201	8	US-10-719-993-53764	53764	Sequence 53764, A
	475	21	0.5	201	8	US-10-741-600-54312	54312	Sequence 54312, A
c	476	21	0.5	201	8	US-10-741-600-19377	19377	Sequence 19377, A
c	477	21	0.5	201	8	US-10-741-600-19378	19378	Sequence 19378, A
	478	21	0.5	201	8	US-10-741-600-38488	38488	Sequence 38488, A
	479	21	0.5	201	8	US-10-741-600-39687	39687	Sequence 39687, A
	480	21	0.5	201	8	US-10-741-600-39688	39688	Sequence 39688, A
	481	21	0.5	201	8	US-10-741-600-39689	39689	Sequence 39689, A
c	482	21	0.5	201	8	US-10-741-600-41472	41472	Sequence 41472, A
	483	21	0.5	201	8	US-10-741-600-65895	65895	Sequence 65895, A
	484	21	0.5	201	8	US-10-741-600-71170	71170	Sequence 71170, A
	485	21	0.5	201	8	US-10-741-600-71172	71172	Sequence 71172, A
	486	21	0.5	201	8	US-10-741-600-71174	71174	Sequence 71174, A
	487	21	0.5	201	8	US-10-741-600-71722	71722	Sequence 71722, A
c	488	21	0.5	220	7	US-10-242-535A-2201	2201,	Sequence 2201, Ap
c	489	21	0.5	220	7	US-10-085-783A-2201	2201,	Sequence 2201, Ap
	490	21	0.5	244	8	US-10-425-115-10205	10205	Sequence 10205, A
	491	21	0.5	248	8	US-10-425-115-140881	140881,	Sequence 140881,
c	492	21	0.5	285	4	US-09-925-065A-130263	130263	Sequence 130263,
	493	21	0.5	290	8	US-10-357-930-19399	19399	Sequence 19399, A
	494	21	0.5	292	4	US-10-357-930-7817	7817,	Sequence 7817, Ap
	495	21	0.5	296	7	US-10-242-535A-52499	52499	Sequence 52499, A
c	496	21	0.5	296	7	US-10-085-783A-52499	52499	Sequence 52499, A
c	497	21	0.5	300	5	US-10-191-803-311	311,	Sequence 311, App
c	498	21	0.5	310	7	US-10-191-803-856	856,	Sequence 856, App
	499	21	0.5	315	3	US-09-960-352-12366	12366	Sequence 12366, A
c	500	21	0.5	319	5	US-10-674-124A-4819	4819,	Sequence 4819, Ap
	501	21	0.5	327	3	US-09-960-352-14937	14937	Sequence 14937, A
	502	21	0.5	338	5	US-10-079-623-131	131,	Sequence 131, App
c	503	21	0.5	339	7	US-10-357-930-19627	19627	Sequence 19627, A
	504	21	0.5	343	7	US-10-424-599-51313	51313	Sequence 51313, A
c	505	21	0.5	345	4	US-09-925-065A-732590	732590	Sequence 732590,
	506	21	0.5	353	4	US-09-925-065A-149005	149005	Sequence 149005,
	507	21	0.5	355	3	US-09-867-701-6727	6727,	Sequence 6727, Ap
c	508	21	0.5	360	3	US-10-764-877-3230	3230,	Sequence 3230, Ap
c	509	21	0.5	360	6	US-10-242-515-3230	3230,	Sequence 3230, Ap
c	510	21	0.5	371	3	US-09-867-701-2936	2936,	Sequence 2936, Ap
	511	21	0.5	372	4	US-09-925-065A-554264	554264	Sequence 554264,
	512	21	0.5	378	3	US-09-925-115-80509	80509,	Sequence 80509, A
	513	21	0.5	379	4	US-09-960-352-3105	3105,	Sequence 3105, Ap
	514	21	0.5	385	3	US-09-991-936-938	938,	Sequence 938, App
	515	21	0.5	385	9	US-10-206-901B-14	14,	Sequence 14, Appl
	516	21	0.5	388	5	US-10-978-245-938	938,	Sequence 938, App
	517	21	0.5	390	7	US-10-424-599-105806	105806	Sequence 105806,
c	518	21	0.5	391	3	US-09-960-352-9287	9287,	Sequence 9287, Ap
c	519	21	0.5	392	5	US-10-079-623-320	320,	Sequence 320, App
	520	21	0.5	393	5	US-10-079-623-314	314,	Sequence 314, App
	521	21	0.5	393	8	US-10-357-930-13149	13149	Sequence 13149, A
	522	21	0.5	396	3	US-10-357-930-37770	37770	Sequence 37770, A
	523	21	0.5	398	4	US-09-925-065A-177621	177621	Sequence 177621,
c	524	21	0.5	398	4	US-09-925-065A-177622	177622	Sequence 177622,
	525	21	0.5	403	8	US-10-425-115-61402	61402	Sequence 61402, A
	526	21	0.5	406	3	US-09-965-965-4402	4402,	Sequence 4402, Ap
	527	21	0.5	410	3	US-10-767-795-977	977,	Sequence 977, App
	528	21	0.5	414	5	US-10-079-623-323	323,	Sequence 323, App
c	529	21	0.5	415	4	US-09-925-065A-518970	518970	Sequence 518970
c	530	21	0.5	418	7	US-10-021-323-6764	6764,	Sequence 6764, Ap
c	531	21	0.5	419	4	US-09-925-065A-222991	222991	Sequence 222991,
c	532	21	0.5	419	6	US-10-027-632-34810	34810,	Sequence 34810, A
	533	21	0.5	419	6	US-10-027-632-34810	34810,	Sequence 34810, A
	534	21	0.5	421	8	US-10-425-115-136043	136043	Sequence 136043

	No.					Accession	Sequence
c	535	0.5	21	422	8	US-10-357-930-48520	Sequence 48520, A
c	536	0.5	21	424	4	US-09-925-065A-219497	Sequence 219497, A
c	537	0.5	21	426	7	US-10-424-599-33658	Sequence 33658, A
c	538	0.5	21	427	4	US-10-925-065A-154328	Sequence 154328,
c	539	0.5	21	427	8	US-10-723-860-7253	Sequence 7253, Ap
c	540	0.5	21	430	7	US-10-424-599-136214	Sequence 136214,
c	541	0.5	21	431	3	US-09-918-995-8709	Sequence 8709, Ap
c	542	0.5	21	436	5	US-10-027-632-36674	Sequence 36674, Ap
c	543	0.5	21	436	5	US-10-027-632-68992	Sequence 68992, A
c	544	0.5	21	436	5	US-10-027-632-69538	Sequence 69538, A
c	545	0.5	21	436	6	US-10-027-632-311766	Sequence 311766,
c	546	0.5	21	436	6	US-10-027-632-36674	Sequence 36674, A
c	547	0.5	21	436	6	US-10-027-632-68992	Sequence 68992, A
c	548	0.5	21	436	6	US-10-027-632-69538	Sequence 69538, A
c	549	0.5	21	436	6	US-10-027-632-311766	Sequence 311766,
c	550	0.5	21	437	6	US-10-264-049-1763	Sequence 1763, Ap
c	551	0.5	21	442	7	US-10-021-323-16032	Sequence 16032, A
c	552	0.5	21	442	6	US-10-357-930-10102	Sequence 10102, A
c	553	0.5	21	444	8	US-09-814-353-14135	Sequence 14135, A
c	554	0.5	21	444	5	US-10-027-632-83811	Sequence 83811, A
c	555	0.5	21	444	5	US-10-027-632-83810	Sequence 83810, A
c	556	0.5	21	444	6	US-10-027-632-83811	Sequence 83811, A
c	557	0.5	21	444	6	US-10-357-930-49422	Sequence 49422, A
c	558	0.5	21	444	8	US-09-925-065A-349522	Sequence 349522,
c	559	0.5	21	445	4	US-10-027-632-281108	Sequence 281108,
c	560	0.5	21	446	5	US-10-027-632-281109	Sequence 281109,
c	561	0.5	21	446	5	US-10-027-632-281110	Sequence 281110,
c	562	0.5	21	446	5	US-10-027-632-281108	Sequence 281108,
c	563	0.5	21	446	6	US-10-027-632-281109	Sequence 281109,
c	564	0.5	21	446	6	US-10-027-632-281110	Sequence 281110,
c	565	0.5	21	446	6	US-10-027-632-281110	Sequence 281110,
c	566	0.5	21	455	3	US-09-833-790-69	Sequence 69, Appl
c	567	0.5	21	456	4	US-09-925-065A-513522	Sequence 513522,
c	568	0.5	21	456	4	US-09-925-065A-561045	Sequence 561045,
c	569	0.5	21	456	4	US-09-925-065A-561047	Sequence 561047,
c	570	0.5	21	456	4	US-09-925-065A-561048	Sequence 561048,
c	571	0.5	21	457	3	US-09-864-761-1586	Sequence 1586, Ap
c	572	0.5	21	463	7	US-10-437-963-7814	Sequence 7814, Ap
c	573	0.5	21	466	7	US-10-424-599-142436	Sequence 142436,
c	574	0.5	21	467	8	US-10-357-930-933	Sequence 933, App
c	575	0.5	21	470	7	US-09-925-065A-82797	Sequence 82797, A
c	576	0.5	21	471	4	US-09-925-065A-496565	Sequence 496565,
c	577	0.5	21	471	4	US-09-925-065A-496566	Sequence 496566,
c	578	0.5	21	472	3	US-09-814-353-14131	Sequence 14131, A
c	579	0.5	21	476	5	US-10-066-543-1608	Sequence 1608, Ap
c	580	0.5	21	476	4	US-10-027-632-282965	Sequence 282965,
c	581	0.5	21	478	3	US-10-027-632-282965	Sequence 282965,
c	582	0.5	21	482	5	US-10-198-846-1141	Sequence 1141, Ap
c	583	0.5	21	485	6	US-10-058-053A-220	Sequence 220, App
c	584	0.5	21	485	4	US-10-838-226-220	Sequence 220, App
c	585	0.5	21	486	8	US-10-424-599-90782	Sequence 90782, A
c	586	0.5	21	486	7	US-10-357-930-31301	Sequence 31301, A
c	587	0.5	21	486	8	US-10-357-930-40271	Sequence 40271, A
c	588	0.5	21	489	4	US-09-925-065A-289154	Sequence 289154,
c	589	0.5	21	489	6	US-10-027-632-37180	Sequence 37180, A
c	590	0.5	21	489	6	US-10-027-632-37180	Sequence 37180, A
c	591	0.5	21	493	8	US-10-357-930-40842	Sequence 40842, A
c	592	0.5	21	496	4	US-09-925-065A-753404	Sequence 753404,
c	593	0.5	21	496	8	US-09-925-065A-753405	Sequence 753405,
c	594	0.5	21	497	4	US-09-925-065A-260244	Sequence 260244,
c	595	0.5	21	498	7	US-10-424-599-56948	Sequence 56948, A
c	596	0.5	21	500	8	US-09-925-065A-252253	Sequence 252253,
c	597	0.5	21	500	5	US-10-060-830-40	Sequence 40, Appl
c	598	0.5	21	501	8	US-10-357-930-20613	Sequence 20613, A
c	599	0.5	21	501	8	US-10-357-930-26452	Sequence 26452, A
c	600	0.5	21	503	4	US-09-925-065A-387021	Sequence 387021,
c	601	0.5	21	503	8	US-10-027-632-387022	Sequence 387022,
c	602	0.5	21	503	4	US-09-925-065A-387022	Sequence 387022,
c	603	0.5	21	503	4	US-09-925-065A-751623	Sequence 751623,
c	604	0.5	21	505	4	US-09-925-065A-405485	Sequence 405485,
c	605	0.5	21	510	4	US-09-925-065A-405486	Sequence 405486,
c	606	0.5	21	510	4	US-09-925-065A-74198	Sequence 74198, A
c	607	0.5	21	511	4	US-09-925-065A-74199	Sequence 74199, A

	No.					Accession	Sequence
c	608	21	0.5	511	4	US-10-357-930-74200	Sequence 74200, A
c	609	21	0.5	511	4	US-09-925-065A-34296	Sequence 34296, A
c	610	21	0.5	511	8	US-10-357-930-43158	Sequence 43158, A
c	611	21	0.5	512	4	US-09-925-065A-580299	Sequence 580299,
c	612	21	0.5	512	4	US-09-925-065A-762931	Sequence 762931,
c	613	21	0.5	512	5	US-10-027-632-267388	Sequence 267388,
c	614	21	0.5	513	6	US-10-027-632-267388	Sequence 267388,
c	615	21	0.5	513	4	US-09-925-065A-358459	Sequence 358459,
c	616	21	0.5	513	4	US-09-925-065A-358460	Sequence 358460,
c	617	21	0.5	514	4	US-09-925-065A-358461	Sequence 358461,
c	618	21	0.5	516	4	US-09-925-065A-358462	Sequence 358462,
c	619	21	0.5	516	4	US-09-925-065A-763143	Sequence 763143,
c	620	21	0.5	516	6	US-10-027-632-484457	Sequence 484457,
c	621	21	0.5	521	4	US-10-027-632-237042	Sequence 237042,
c	622	21	0.5	524	6	US-10-027-632-237042	Sequence 237042,
c	623	21	0.5	525	3	US-09-925-065A-422732	Sequence 422732,
c	624	21	0.5	525	4	US-09-814-353-14057	Sequence 14057, A
c	625	21	0.5	526	7	US-09-925-065A-118032	Sequence 118032,
c	626	21	0.5	529	8	US-10-021-323-3074	Sequence 3074, Ap
c	627	21	0.5	530	7	US-10-357-930-56012	Sequence 56012, A
c	628	21	0.5	530	4	US-09-925-065A-320969	Sequence 320969,
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c	630	21	0.5	532	7	US-10-437-963-44744	Sequence 44744, A
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us-10-607-712-1.ol118.rnpbm

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988	21	0.5	1777	6	US-09-791-932-54	Sequence 54, Appl
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ALIGNMENTS

RESULT 1
US-10-607-712-1
; Sequence 1, Application US/10607712
; Publication No. US2004007301 8A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
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; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3919
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (1)...(3919)
; OTHER INFORMATION: Entire cloned cDNA encoding wild type methionine
; OTHER INFORMATION: synthase.
US-10-607-712-1

Query Match   100.0%; Score 3919; DB 7; Length 3919;
Best Local Similarity   100.0%;
Matches 3919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  2161  AAATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAAAATTGTT  2220
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Db  2161  AAATATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGAATGAAAATTGTT  2220
```

```
Qy  2221  GGTGATCTTTTTGGAGCTGGAAAATGTTCTACCTTCAGGTTATAAAGTCAGCCGCGGGTT  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGTGATCTTTTTGGAGCTGGAAAATGTTCTACCTTCAGGTTATAAAGTCAGCCCGGGGTT  2280

Qy  2281  ATGAAGAGAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAAGAAGAGAGAAACCAGA  2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  ATGAAGAGAGGCTGTTGGCCACCTTATCCCTTCATGGAAAAAGAAGAGAGAAACCAGA  2340

Qy  2341  GTGCTTAACGGCACAGTAGAAGAAGAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACT  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  GTGCTTAACGGCACAGTAGAAGAAGAGAGACCCTTACCAGGGCACCATCGTGCTGGCCACT  2400

Qy  2401  GTTAAAGGCGACGTGCGACGACATAGGCAAGAACACATAGTGGAGTAGTCCTTGCTGCGCAAT  2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GTTAAAGGCGACGTGCGACGACATAGGCAAGAACACATAGTGGAGTAGTCCTTGCTGCGCAAT  2460

Qy  2461  AATTCCGAGTTATTGATTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCT  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  AATTCCGAGTTATTGATTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCT  2520

Qy  2521  CTTGACCACCAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAA  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CTTGACCACCAAAGCAGATATAATTGGCCTGTCAGGACTCATCACTCCTTCCCTGGATGAA  2580

Qy  2581  ATGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATCCATGTTGATTGGA  2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  ATGATTTTGTTGCCAAGGAAATGGAGAGATTAGCTATAAGGATCCATGTTGATTGGA  2640

Qy  2641  GGAGCAACCACTTCAAAAACCCACACAGCAGTGTAAAATAGCTCCGAGATACAGTGCACCT  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GGAGCAACCACTTCAAAAACCCACACAGCAGTGTAAAATAGCTCCGAGATACAGTGCACCT  2700

Qy  2701  GTAATCCATGTCCTGACGCGTCCAAGAGTGTGGTGGTGTGTTCCCAGCTGTGTAGATGAA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  GTAATCCATGTCCTGGACGCGTCCAAGAGTGTGGTGGTGTGTTCCCAGCTGTGTAGATGAA  2760

Qy  2761  AATCTAAAGGATGAATACTTTGAGGAAATCATGAGGAATAATCATGGAAGAATATTAGACAGGAC  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  AATCTAAAGGATGAATACTTTGAGGAAATCATGAGGAATAATCATGGAAGAATATTAGACAGGAC  2820

Qy  2821  CATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGT  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  CATTATGAGTCTCTCAAGGAGGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGT  2880

Qy  2881  TTCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAG  2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TTCCAAATGGATTGGCTGTCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAG  2940

Qy  2941  GTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGACTGGAAGCCTTTCTTT  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  GTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGACTGGAAGCCTTTCTTT  3000

Qy  3001  GATGTCTGGCAGCTCCGGCAGTCAAGTACCCGAATCGGAGCTTCCCCAAGATCAATTAACGAC  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  GATGTCTGGCAGCTCCGGCAGTCAAGTACCCGAATCGGAGCTTCCCCAAGATCAATTAACGAC  3060

Qy  3061  AAAACAGTAGGTGGAGAGGCCAGGAAGTCTCACGATGCCCACAATTGCAACACA  3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  AAAACAGTAGGTGGAGAGGCCAGGAAGTCTCACGATGCCCACAATTGCAACACA  3120

Qy  3121  CTGATTAGTCAAAAGAGAACTCCCGGGGCGTGTGGTTCTGGCCACACAGAGT  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  CTGATTAGTCAAAAGAGAACTCCCGGGGCGTGTGGTTCTGGCCACACAGAGT  3180

Qy  3181  ATCCAAGACGACATTCACCTGTACGCAGAGGCTGCGAGCCCATA  3240
          |||||||||||||||||||||||||||||||||||||||||||||
Db  3181  ATCCAAGACGACATTCACCTGTACGCAGAGGCTGCGAGCCCATA  3240

Qy  3241  GCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGGAGCCATAC  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  GCCACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGGAGCCATAC  3300
```

```
;     FEATURE:
;     NAME/KEY: variation
;     LOCATION: (1)...(3856)
;     OTHER INFORMATION: nnn at positions 2640-2642 is either AAT or no
;     OTHER INFORMATION: nucleotides; n at position 2756 is either A or G;
;     OTHER INFORMATION: n at position 2758 is either C or G.
US-10-607-712-75

Query Match             91.9%;  Score 3601;  DB 7;  Length 3856;
Best Local Similarity   99.9%;  Pred. NO. 0;
Matches 3851;  Conservative  0;  Mismatches  0;  Indels  5;  Gaps  0;

Qy    64 ATGTCACCCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAGAGAAACCCTGCGGGAT 123
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGTCACCCGCTCCAAGACCTGTCGCAACCCGAAGGTCTGAGAGAAACCCTGCGGGAT 60

Qy   124 GAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGGATGGGGATGGGGACCATG 183
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGGATGGGGATGGGGACCATG 120

Qy   184 ATCCAGGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAATTTAAAGATCATGCC 243
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ATCCAGGGGAGAAGCTAAACGAAGAACACTTCCGAGTCAGGAATTTAAAGATCATGCC 180

Qy   244 AGGCCGCTGAAAGCAACAATGACATTTAAGTATAAACTCAGCCTGATGTCATTTACCAA 303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGGCCGCTGAAAGCAACAATGACATTTAAGTATAAACTCAGCCTGATGTCATTTACCAA 240

Qy   304 ATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCAGC 363
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATCCATAAGGAATACTTGCTGGCTGGGGCAGATATCATTGAAACAAATACTTTTAGCAGC 300

Qy   364 ACTAGTATTGCCCAAGCTGACTCATGGCCTGGCTTGGCTTCACCGGATGAACATGTGC 423
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACTAGTATTGCCCAAGCTGACTCATGGCCTGGCTTGGCTTCACCGGATGAACATGTGC 360

Qy   424 TCTGCAGGAGTGGCCAGAAAAGTGCCGCCGAGGAGTAACTCTCCAGACAGGAGGAGAGG 483
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCTGCAGGAGTGGCCAGAAAAGTGCCGCCGAGGAGTAACTCTCCAGACAGGAGGAGAGG 420

Qy   484 TTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGAA 543
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCATCTGTGAA 480

Qy   544 AGGCCGGATTATAGGAACATCACATTGATGAGCTTGTTGAAGCATCACCAAGAGCAGGCC 603
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGGCCGGATTATAGGAACATCACATTGATGAGCTTGTTGAAGCATCACCAAGAGCAGGCC 540

Qy   604 AAAGGACTTCTGGATGCGGCGGGTTGATATCTTGATATCTTACTCATTGAAACTATTTTTGATACTGCC 663
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGGACTTCTGGATGCGGCGGGTTGATATCTTGATATCTTACTCATTGAAACTATTTTTGATACTGCC 600

Qy   664 AATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCCCG 723
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AATGCCAAGGCAGCCTTGTTGCACTCCAAAATCTTTTTGAGGAGAAATATGCTCCCCCG 660

Qy   724 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGCGGACTCTTTCCGACAGACA 783
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CCTATCTTTATTTCAGGGACGATCGTTGATAAAAGTGGGCGCGGACTCTTTCCGACAGACA 720

Qy   784 GGAGAGGGATTTGTCATCACGCGTGTCTCATGGGAACCACTCTGCGATTGGATTAAATTGT 843
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GGAGAGGGATTTGTCATCACGCGTGTCTCATGGGAACCACTCTGCGATTGGATTAAATTGT 780

Qy   844 GCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAAATAGTACAACAGCC 903
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GCTTTGGGTGCAGCTGAGATGAGACCTTTATTGAAAATAGTACAACAGCC 840

Qy   904 TATGTCCCTGTATCCCAATGCAGGTCTTCCCAACACACTTTGGTGACTATGATGAAACG 963
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TATGTCCCTGTATCCCAATGCAGGTCTTCCCAACACACTTTGGTGACTATGATGAAACG 900

Qy   964 CCTTCTATGATGGCCAAGCACCTAAAGGATTTTCTATGGATGGCTTGGTCAATATAGTT 1023
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Qy  3301 TACTGCCTCTCAGACTTCATCGTCCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTG 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 TACTGCCTCTCAGACTTCATCGTCCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTG 3360

Qy  3361 TTTGCCGTGGCCTGCCTGCTTGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGAC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TTTGCCGTGGCCTGCCTGCTTGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGAC 3420

Qy  3421 GACTACAGCAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGGTCGCAGAGGCCTTTGCAGAA 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 GACTACAGCAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGGTCGCAGAGGCCTTTGCAGAA 3480

Qy  3481 GAGCTCCATGAAAGAGTTCGCCCAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGAC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GAGCTCCATGAAAGAGTTCGCCCAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGAC 3540

Qy  3541 GTCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGGCCTCCTGGCTACCCCAGC 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 GTCGCAGACCTGCGAAGGTTGCGGTACAAGGGCATCCGGCCTCCTGGCTACCCCAGC 3600

Qy  3601 CAGCCCGACCACCACCGAGAAGCTCGCAGAGACTCGAGACATCGAGACCGTCTACA 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CAGCCCGACCACCACCGAGAAGCTCGCAGAGACTCGAGACATCGAGACCGTCTACA 3660

Qy  3661 GGCATTAGGTTAACAGAATCATTAGCAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAG 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GGCATTAGGTTAACAGAATCATTAGCAATATTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAG 3720

Qy  3721 TTCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGC 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 TTCTCCAATTTGAAGTCCAAATATTTTGCTGTGTGGGGAAGATTTCCAAGGATCAGGTTGAGC 3780

Qy  3781 GATTATGCATTGAGGAGAAGAACATATCTGGCTGAGGTTGAGAAATGCTTGGACCCATT 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 GATTATGCATTGAGGAGAAGAACATATCTGGCTGAGGTTGAGAAATGCTTGGACCCATT 3840

Qy  3841 TTGGGATATGATACAGACTAACTTTTTTTTTTTTTGCCTTTTATCTTGATGATCC 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 TTGGGATATGATACAGACTAACTTTTTTTTTTTTTGCCTTTTATCTTGATGATCC 3900

Qy  3901 TCAAGGAAATACAACCTAG 3919
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Db  3901 TCAAGGAAATACAACCTAG 3919
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RESULT 2
US-10-607-712-75
; Sequence 75, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 3856
; TYPE: DNA
; ORGANISM: Homo sapiens
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Db  1981 ATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTGTGT 2040
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Qy  2104 AAGGGCCATTGAAAAACATATATTATTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAAA 2163
Db  2041 AAGGGCCATTGAAAAACATATATTATTGAGGATACTGAGGAAGCCAGTTAAACCAAAAAAA 2100

Qy  2164 TATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGGAATGAAAATTGTTGGT 2223
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TATCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGGAATGAAAATTGTTGGT 2160

Qy  2224 GATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCGGGGTTATG 2283
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GATCTTTTTGGAGCTGGAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGGGTTATG 2220

Qy  2284 AAGAAGGCTGTTGGCCACCTTATCCTTTCATGGAAAAAGAAGAGAAGAACCAGAGTG 2343
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AAGAAGGCGTTGGCCACCTTATCCTTTCATGGAAAAAGAAGAGAAGAAACCAGAGTG 2280

Qy  2344 CTTAACGGCACAGTAGAAGAAGAGACCCTTACCAGGGCACCATCGTGCTCGGCCACTGTT 2403
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CTTAACGGCACAGTAGAAGAAGAGACCCTTACCAGGGCACCATCGTGCTCGGCCACTCTT 2340

Qy  2404 AAAGGGGACGTGCACGACATAGGCAAGAACACATAGTTGGAGTAGTCCTTGGCTGCAATAT 2463
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 AAAGGGGACGTGCACGACATAGGCAAGAACACATAGTTGGAGTAGTCCTTGGCTCAATAAT 2400

Qy  2464 TTCCGAGTTATTGATTTAGGAGTCATGTCATGTGATAAGATACTGAAAGTGCTCTT 2523
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TTCCGAGTTATTGATTTAGGAGTCATGTCATGTGATAAGATACTGAAAGTGCTCTT 2460

Qy  2524 GACCACAAAGCAGATATAATTGGCTGTCAGGACTCATCCTTCCCTGGATGAAATG 2583
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 GACCACAAAGCAGATATAATTGGCTGTCAGGACTCATCCTTCCCTGGATGAAATG 2520

Qy  2584 ATTTTTGTTGCCAAGGAAATGGAGAAATCGGAGGATTAGCTATAAGGAGGTTAGCTATAATAGCT 2643
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Db  2521 ATTTTTGTTGCCAAGGAAATGGAGAAATCGGAGGATTAGCTATAAGGAGGATTCCATTGTTGATTGGAGGA 2580

Qy  2644 GCAACCACTTCAAAAACCCACACACAGTTAAAATAGCTCCGAGATACAGTGCACCTGTA 2703
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 GCAACCACTTCAAAAACCCACACACAGTTAAAATAGCTCCGAGATACAGTGCACCTGTN 2640

Qy  2704 ATCCATGTCCTGGACCGCGTCCAAGAGTGTGGTGTTCCCAGCTGTTAGATGAAAAT 2763
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 NNCCATGTCCTGGACCGCGTCCAAGAGTGTGGTGTTCCCAGCTGTTAGATGAAAAT 2700

Qy  2764 CTAAAGGATGAATACTTTGGAGGAGAGGAGAATCATGGAGAAATCATGGAGATATGAGAGATTAGACAGGACCAT 2823
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTAAAGGATGAATACTTTGGAGGAGAGGAGAATCATGGAGAAATCATGGAGATATGAGAGATATTAGACAGGACCAT 2760

Qy  2824 TATGAGTCTCTCAAGGAGGAGCCAGAATAAGTGGAGGTCTTCTTAAGTCAAGCCAGAAAAGTGGTTTC 2883
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TATGAGTCTCTCAAGGAGGAGCCAGAATAAGTGGAGGTCTTCTTAAGTCAAGCCAGAAAAGTGGTTTC 2820

Qy  2884 CAAATGATTGGCTGTCTGCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGTC 2943
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Db  2821 CAAATGATTGGCTGTCTGCTGAACCTCACCCAGTGAAGCCCACGTTTATTGGGACCCAGTC 2880

Qy  2944 TTTGAAGACTATGACCTGCGAGAAGCTGGTGACTGACTGGAAGCCTTTCTTTGAT 3003
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TTTGAAGACTATGACCTGCGAGAAGCTGGTGACTGACTGGAAGCCTTTCTTTGAT 2940

Qy  3004 GTCTGGCAGCTCCGGGGCAAGTCACCCGAATCGAGGCTTCCCCAAGATATTTAACGACAAA 3063
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 GTCTGGCAGCTCCGGGGCAAGTCACCCGAATCGAGGCTTCCCCAAGATATTTAACGACAAA 3000

Qy  3064 ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACACTG 3123
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAATATGCTGAACACACTG 3060

Qy  3124 ATTAGTCAAAAGAAACTCCGGCGCCCGGGGTGTGGTTCGGGTGTGGTTCGGCCAGCACAGAGTATC 3183
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Db  3061 ATTAGTCAAAAGAAACTCCGGCGCCCGGGGTGTGGTTCGGGTGTGGTTCGGCCAGCACAGAGTATC 3120
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Db   901                                                        CCTTCTATGATGATGGGCCAAGCACCTAAAGGATTTGCTATGATGGGCTTGGGTCAATATAGTT  960
                                                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1024 GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTAGCAGGTGTGAAAAAT 1083
Db  1021 GGAGGATGCTGTGGGTCAACACCAGATCATATCAGGGAAATTGCTAGCAGGTGTGAAAAAT  961

Qy  1084 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTTCTCGGTCTA 1143
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAAGGACATATGTTACTTCTCGGTCTA 1080

Qy  1144 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATGTT 1203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GAGCCCTTCAGGATTGGACCGTACACCAACTTGTTAACATTGGAGAGCGCTGTAATGTT 1140

Qy  1204 GCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCGCAGGAAACTATGAAGAAGCCTTGTGT 1263
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GCAGGATCAAGGAAGTTTGCTAAACTCATCATGGCGCAGGAAACTATGAAGAAGCCCTTGTGT 1200

Qy  1264 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTGTGGATGTCAACATGATGATGGC 1323
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GTTGCCAAAGTGCAGGTGGAAATGGGAGCCCAGGTGTGTGGATGTCAACATGATGATGGC 1260

Qy  1324 ATGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTAATTGCTTCCGAGCCAGAC 1383
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ATGCTAGATGGTCCAAGTGCAATGACCAGATTTTGCAACTAATTGCTTCCGAGCCAGAC 1320

Qy  1384 ATCGCAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGTTA 1443
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ATCGCAAAAGGTACCTTTGTGCATCGACTCCTCCAATTTTGCTGTGATTGAAGCTGGGTTA 1380

Qy  1444 AAGTGCTGCCAAGGAAGTGCAGCAGGACAACAGAACAGAAAATCAGAGTGTGCACCCGGCCTAC 1503
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 AAGTGCTGCCAAGGAAGTGCAGCAGGACAACAGAACAGAAAATCAGAGTGTGCACCCGGCCTAC 1440

Qy  1504 TTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAAGCTGCTGTCATGGTCATGGCTTTT 1563
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 TTCTTGGAGAAGGCCAGGAAGATTAAAAAGTATGGAAGCTGCTGTCATGGTCATGGCTTTT 1500

Qy  1564 GATGAAGAAGGACAGCCGCAACAGAAATCAGAGTGTGCACCCGGCCTAC 1623
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 GATGAAGAAGGACAGCCGCAACAGAAATCAGAGTGTGCACCCGGCCTAC 1560

Qy  1624 CATCTGCTTGTGAAAAAACTGGGCTTAATCAAATGACATTATTTTGACCCTAATATC 1683
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 CATCTGCTTGTGAAAAAACTGGGCTTAATCAAATGACATTATTTTGACCCTAATATC 1620

Qy  1684 CTAACCATTGGGACTGAGGAACACAACTTGTATGCCATTAATTTTATCCATGCA 1743
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 CTAACCATTGGGACTGAGGAACACAACTTGTATGCCATTAATTTTATCCATGCA 1680

Qy  1744 ACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTCTTCCAACTTG 1803
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 ACAAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTCTTCCAACTTG 1740

Qy  1804 TCCTTCTCCTTCCGAGGAGTTCCATCATGGGGTTTTCCTTTAC 1863
         |||||||||||||||||||||||||||||||||||||||||||
Db  1741 TCCTTCTCCTTCCGAGGAGTTCCATCATGGGGTTTTCCTTTAC 1800

Qy  1864 CATGCAATCAAGTCTGCGATGACATGGAGATAGTGAATGCTGGAAACCTCCCTGTGTAT 1923
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CATGCAATCAAGTCTGCGATGACATGGAGATAGTGAATGCTGGAAACCTCCCTGTGTAT 1860

Qy  1924 GATGATATCCATAAGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCT 1983
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GATGATATCCATAAGAACTTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCT 1920

Qy  1984 GAGGCCACTCGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACACAGGGAAGAAAGTC 2043
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 GAGGCCACTCGAGAAGCTCTTACGTTATGCCCAGACTCAAGGCACACAGGGAAGAAAGTC 1980

Qy  2044 ATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTGTG 2103
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2044 ATTCAGACTGATGAGTGGAGAAATGGCCCTGTCGAAGAACGCCTTGAGTATGCCCTGTG 2103
```

Qy 3184 CAAGACGACATTCACCTGTACGAGAGCTGCTGTGCCCAGGCTGCGAGAGCCCATAGCC 3243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3121 CAAGACGACATTCACCTGTACGAGAGCTGCTGTGCCCAGGCTGCGAGAGCCCATAGCC 3180

Qy 3244 ACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACTAC 3303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3181 ACTTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCACGGAGCCATACTAC 3240

Qy 3304 TGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTT 3363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 TGCCTCTCAGACTTCATCGCTCCCTTGCATTCTGGCATCCGTGACTACCTGGGCCTGTTT 3300

Qy 3364 GCCGTTGCCTGCTTGTTGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGAC 3423
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3301 GCCGTTGCCTGCTTGTTGGGTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGAC 3360

Qy 3424 TACAGCAGCATCATGGTCAAGGCGCGCTGGCAGAGCCTTTGCAGAAGAG 3483
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 TACAGCAGCATCATGGTCAAGGCGCGCTGGCAGAGCCTTTGCAGAAGAG 3420

Qy 3484 CTCCATGAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGCTGGAGCGTC 3543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3421 CTCCATGAAAGAGTTCGCCGAGAACTGTGGCCTACTGTGGCAGCTGGACGTC 3480

Qy 3544 GCAGACCTGCGAAGGTTGCGGTACAAGGGCATCGCCCGGCTCCTGGCTACCCCAGCCAG 3603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3481 GCAGACCTGCGAAGGTTGCGGTACAAGGGCATCGCCCGGCTCCTGGCTACCCCAGCCAG 3540

Qy 3604 CCCGACCACCGAGAAGCTCACCATGTGGAGACTCGAGCAGTCTACAGGC 3663
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 3541 CCCGACCACCGAGAAGCTCACCATGTGGAGACTCGAGCAGTCTACAGGC 3600

Qy 3664 ATTAGGTTAACAGAACATTAGCAATGGCAATGGCACCTGTTCAGCGCCTCACTTC 3723
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3601 ATTAGGTTAACAGAACATTAGCAATGGCAATGGCACCTGTTCAGCGCCTCACTTC 3660

Qy 3724 TCCAATTGAAGTCCAAATATTTTGCTGTGGGGAAGATTCCAAGAATCAGGTTGAGGAT 3783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3661 TCCAATTGAAGTCCAAATATTTTGCTGTGGGGAAGATTCCAAGAATCAGGTTGAGGAT 3720

Qy 3784 TATGCAATTGAGGAAGAACATATCTGTGCGCTGAGGTTGAGAAATGGCTTGGACCCATTTG 3843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3721 TATGCAATTGAGGAAGAACATATCTGTGCGCTGAGGTTGAGAAATGGCTTGGACCCATTTG 3780

Qy 3844 GGATATGATACAGACTAACTTTTTTTTTTTTTTTATCTTGATGATCCTCA 3903
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3781 GGATATGATACAGACTAACTTTTTTTTTTTTTTTATCTTGATGATCCTCA 3840

Qy 3904 AGGAAATACAACCTAG 3919
          ||||||||||||||||
Db 3841 AGGAAATACAACCTAG 3856

RESULT 3
US-09-796-692-8171
; Sequence 8171, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Geiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8171
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-8171

Query Match   8.1%; Score 318; DB 3; Length 420;
Best Local Similarity   99.5%; Pred. No. 3.5e-153;
Matches 418; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2749 CTGTTAGATGAAAATCTAAAGGATGAATCATTGAGGAAATCATGGAAGAATATGAAGAT 2808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CTGTTAGATGAAAATCTAAAGGATGAATCATTGAGGAAATCATGGAAGAATATGAAGAT 60

Qy 2809 ATTAGACAGGACCATTATGAGTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCC 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATTAGACAGGACCATTATGAGTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCC 120

Qy 2869 AGAAAAAGTGGTTTCCAAATGATTGGCTGTCTGAAACTTCACCCAGTGAAGCCCACGTTT 2928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGAAAAAGTGGTTTCCAAATGATTGGCTGTCTGAAACTTCACCCAGTGAAGCCCACGTTT 180

Qy 2929 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGG 2988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGG 240

Qy 2989 AAGCCTTTCTTTGATGTCTGGCAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCCAAG 3048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 AAGCCTTTCTTTGATGTCTGGCAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCCAAG 300

Qy 3049 ATATTTAACGACAAAAACAGTAGGTGGAGGCCAGGAGGTCTACGATGATGCCCACAAT 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 ATATTTAACGACAAAAACAGTAGGTGGAGGCCAGGAGGTCTACGATGATGCCCACAAT 360

Qy 3109 ATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGGGTTCTGG 3168
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 ATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGCCCGGGGTGTGGGTTCTGG 420

RESULT 4
US-10-040-862-8171
; Sequence 8171, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Geiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-01352US
; CURRENT APPLICATION NUMBER: US/10/040,862

; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8171
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-8171

Query Match   8.1%;   Score 318;   DB 5;   Length 420;
Best Local Similarity   99.5%;   Pred. No. 3.5e-153;
Matches 418;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy   2749 CTGTTAGTAGTGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAT 2808
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CTGTTAGTAGTGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAT 60

Qy   2809 ATTAGACAGGACCATTATGAGTCTTCAAGGAGAGAGATACTTACCCTTAAGTCAAGCC 2868
                ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATTAGACAGGGCCATTATGAGTCTTCAAGGAGAGAGATACTTACCCTTAAGTCAAGCC 120

Qy   2869 AGAAAAAGTGGTTTCCAAATGATTGGCTCGTCTGACCTCACCCGAGCCCACGTTT 2928
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGAAAAAGTGGTTTCCAAATGATTGGCTCGTCTGACCTCACCCGAGCCCACGTTT 180

Qy   2929 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGG 2988
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGG 240

Qy   2989 AAGCCTTTCTTTGATGTCTGGCCAGCTCCGGGGCAAGTCGAGGCTTCCCAAG 3048
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGCCTTTCTTTGATGTCTGGCCAGCTCCGGGGCAAGTCGAGGCTTCCCAAG 300

Qy   3049 ATATTTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAAT 3108
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ATATTTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAAT 360

Qy   3109 ATGCTGAACACACTGATTAGTCAAAGAAAACTCCGGGCCCGGGGTGTGGGTTCTGG 3168
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8171
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-475B-8171

Query Match   8.1%;   Score 318;   DB 6;   Length 420;
Best Local Similarity   99.5%;   Pred. No. 3.5e-153;
Matches 418;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy   2749 CTGTTAGTAGTGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAT 2808
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CTGTTAGTAGTGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAT 60

Qy   2809 ATTAGACAGGACCATTATGAGTCTCTCAAGAGAGAGAGATACTTACCCTTAAGTCAAGCC 2868
                ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATTAGACAGGGCCATTATGAGTCTCTCAAGAGAGAGAGATACTTACCCTTAAGTCAAGCC 120

Qy   2869 AGAAAAAGTGGTTTCCAAATGATTGGCTCGTCTGACCTCACCCGAGCCCACGTTT 2928
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGAAAAAGTGGTTTCCAAATGATTGGCTCGTCTGACCTCACCCGAGCCCACGTTT 180

Qy   2929 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGG 2988
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGG 240

Qy   2989 AAGCCTTTCTTTGATGTCTGGCCAGCTCCGGGGCAAGTCGAGGCTTCCCAAG 3048
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGCCTTTCTTTGATGTCTGGCCAGCTCCGGGGCAAGTCGAGGCTTCCCAAG 300

Qy   3049 ATATTTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAAT 3108
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ATATTTAACGACAAAACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAAT 360

Qy   3109 ATGCTGAACACACTGATTAGTCAAAGAAAACTCCGGGCCCGGGGTGTGGGTTCTGG 3168
                ||||||

RESULT 5
US-10-057-475B-8171
; Sequence 8171, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:

Db 301 ATATTTAACGACAAAACAGTAGGTGGAGGAGGCCAGGAAGTCTACGATGATGCCACAAT 360
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 3109 ATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGCGCCCGGGGTGTGGTTCTGG 3168
||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 361 ATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGGCCCGGGGTGTGGTTGGGTTCTGG 420

RESULT 7
US-10-764-324-8171
; Sequence 8171, Application US/10764324
; Publication No. US2004017573 9A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8171
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-764-324-8171

Query Match 8.1%; Score 318; DB 8; Length 420;
Best Local Similarity 99.5%; Pred. No. 3.5e-153;
Matches 418; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2749 CTGTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAT 2808
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 CTGTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAT 60

Qy 2809 ATTAGACAGGACCATTATGAGTCTTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCC 2868
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 ATTAGACAGGGCCATTATGAGTCTTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCC 120

Qy 2869 AGAAAAAGTGGTTTCCAAATGGCTGTCTCGAACCTGCGAGAGCTGGTGGACTACATTGACTGG 2928
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGAAAAAGTGGTTTCCAAATGGCTGTCTCGAACCTGCGAGAGCTGGTGGACTACATTGACTGG 180

Qy 2929 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGG 2988
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGG 240

Qy 2989 AAGCCTTTCTTTGATGTCTGGCAGCTCCGGGGCAAGTACCGGGGCAAGTACCGGAGGCTTCCCCAAG 3048
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 AAGCCTTTCTTTGATGTCTGGCAGCTCCGGGGCAAGTACCGGGGCAAGTACCGGGGCTTTCCCAAG 300

Db 361 ATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGGGCCCGGGGTGTGGTTGGGTTCTGG 420

RESULT 6
US-10-154-884B-8171
; Sequence 8171, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8171
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-154-884B-8171

Query Match 8.1%; Score 318; DB 6; Length 420;
Best Local Similarity 99.5%; Pred. No. 3.5e-153;
Matches 418; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2749 CTGTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAT 2808
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 CTGTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGAT 60

Qy 2809 ATTAGACAGGACCATTATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCC 2868
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 ATTAGACAGGGCCATTATGAGTCTCTCAAGGAGGAGATACTTACCCTTAAGTCAAGCC 120

Qy 2869 AGAAAAAGTGGTTTCCAAATGGCTGTCTCGAACCTGCGAGAGCTGGTGGACTACATTGACTGG 2928
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGAAAAAGTGGTTTCCAAATGGCTGTCTCGAACCTGCGAGAGCTGGTGGACTACATTGACTGG 180

Qy 2929 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTTCCCCAAG 2988
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ATTGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTTCCCCAAG 240

Qy 2989 AAGCCTTTCTTTGATGTCTGGCAGCTCCGGGGCAAGTACCGGGGCAAGTACCGGAGGCTTCCCCAAG 3048
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 AAGCCTTTCTTTGATGTCTGGCAGCTCGGGGCAGCTCCGGGGCAAGTACCGGAGGCGCTTTCCCAAG 300

Qy 3049 ATATTTAACGACAAAACAGTAGGTGGAGGAGGCCAGGAAGTCTACGATGATGCCACAAT 3108
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db    241 AAGCCTTTCTTCTTGATGTCTGGCAGCTCCGGGCGGAAGTACCCGAATCGAGGCTTTCCCAAG 300
                                                                         |||||||||||||||||||||||||||||||||||||||||||||||
Db    142 AAAAAGTGGTTTCCAAATGATTGGCTGTCTGCTGAACCTCACCCAGTGAGCCCACGTTTAT 201

Qy   3049 ATATTTAACGACAAAACAGTAGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAAT 3108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATATTTAACGACAAAACAGTAGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCACAAT 360
                                                                         |||||||||||||||||||||||||||||||||||
Qy   2931 TGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAA 2990
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 TGGGACCCAGGTCTTTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAA 261

Qy   3109 ATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGCCCGGGGTGTGGTTCGGTTCTGG 3168
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGCTGAACACACTGATTAGTCAAAAGAAACTCCGGCCCGGGGTGTGGTTCGGTTCTGG 420
                                                                         |||||||||||||||||||||||||||||||||||
Qy   2991 GCCTTTCTTTGATGTCTGGCAGCTCCGGGCAA 3023
          ||||||||||||||||||||||||||||||||
Db    262 GCCTTTCTTTGATGTCTGGCAGCTCCGGGCAA 294
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RESULT 8
US-10-040-739-642
; Sequence 642, Application US/10040739
; Publication No. US20020173635A1
; GENERAL INFORMATION:
;   APPLICANT: Jacobs, Kenneth
;   McCoy, John
;   LaVallie, Edward
;   Racie, Lisa
;   Merberg, David
;   Treacy, Maurice
;   Spaulding, Vikki
;   TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
;   NUMBER OF SEQUENCES: 1519
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genetics Institute, Inc.
;   STREET: 87 CambridgePark Drive
;   CITY: Cambridge
;   STATE: Massachusetts
;   COUNTRY: U.S.A
;   ZIP: 02140
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy Disk
;   COMPUTER: IBM PC Compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/040,739
;   FILING DATE: 07-Jan-2002
;   CLASSIFICATION: .<Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/036,520
;   FILING DATE: 03-JUN-1998
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Brown, Scott A.
;   REGISTRATION NUMBER: 32,724
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 498-8224
;   TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 642:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 305 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 642:
US-10-040-739-642

Query Match   5.7%; Score 222; DB 5; Length 305;
Best Local Similarity 99.6%; Pred. No. 1.9e-103;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy   2751 GTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAGAATCATGGAAGAATATGAAGATAT 2810
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 GTTAGATGAAAATCTAAAGGATGAATACTTTGAGGAAGAATCATGGAAGAATATGAAGATAT 81

Qy   2811 TAGACAGGACCATTATGAGTCTCTCAAGGAGGAGGAGACTTACCCTTAAGTCAAGCCAG 2870
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db     82 TAGACAGGGCCATTATGAGTCTCTCAAGGAGGAGGAGACTTACCCTTAAGTCAAGCCAG 141

Qy   2871 AAAAAGTGGTTTCCAAATGATTGGCTGTCTGCTGAACCTCACCCAGTGAGCCCACGTTTAT 2930
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RESULT 9
US-10-027-632-121776
; Sequence 121776, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;   TITLE OF INVENTION: Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.129
;   CURRENT APPLICATION NUMBER: US/10/027,632
;   CURRENT FILING DATE: 2002-04-30
;   PRIOR APPLICATION NUMBER: US 60/218,006
;   PRIOR FILING DATE: 2000-07-12
;   PRIOR APPLICATION NUMBER: US 60/198,676
;   PRIOR FILING DATE: 2000-04-20
;   PRIOR APPLICATION NUMBER: US 60/193,483
;   PRIOR FILING DATE: 2000-03-29
;   PRIOR APPLICATION NUMBER: US 60/185,218
;   PRIOR FILING DATE: 2000-02-24
;   PRIOR APPLICATION NUMBER: US 60/167,363
;   PRIOR FILING DATE: 1999-11-23
;   PRIOR APPLICATION NUMBER: US 60/156,358
;   PRIOR FILING DATE: 1999-09-28
;   PRIOR APPLICATION NUMBER: US 60/146,002
;   PRIOR FILING DATE: 1999-08-09
;   NUMBER OF SEQ ID NOS: 325720
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 121776
;   LENGTH: 901
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(901)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-121776

Query Match   3.2%; Score 124; DB 5; Length 901;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1893 GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT 1952
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT 418

Qy   1953 CTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGGAAGCTCTTACGTTATGC 2012
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 CTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGGAAGCTCTTACGTTATGC 478

Qy   2013 CCAG 2016
          ||||
Db    479 CCAG 482
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RESULT 10
US-10-027-632-121776
; Sequence 121776, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```
;   TITLE OF INVENTION:  Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.129
;   CURRENT APPLICATION NUMBER: US/10/027,632
;   CURRENT FILING DATE:  2002-04-30
;   PRIOR APPLICATION NUMBER: US 60/218,006
;   PRIOR FILING DATE:  2000-07-12
;   PRIOR APPLICATION NUMBER: US 60/198,676
;   PRIOR FILING DATE:  2000-04-20
;   PRIOR APPLICATION NUMBER: US 60/193,483
;   PRIOR FILING DATE:  2000-03-29
;   PRIOR APPLICATION NUMBER: US 60/185,218
;   PRIOR FILING DATE:  2000-02-24
;   PRIOR APPLICATION NUMBER: US 60/167,363
;   PRIOR FILING DATE:  1999-11-23
;   PRIOR APPLICATION NUMBER: US 60/156,358
;   PRIOR FILING DATE:  1999-09-28
;   PRIOR APPLICATION NUMBER: US 60/146,002
;   PRIOR FILING DATE:  1999-08-09
;   NUMBER OF SEQ ID NOS: 325720
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 121776
;   LENGTH: 901
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(901)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-121776

  Query Match             3.2%;  Score 124;  DB 6;  Length 901;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-52;
  Matches  124;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1893 GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT 1952
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      359 GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT 418

Qy     1953 CTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTTATGC 2012
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      419 CTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTTATGC 478

Qy     2013 CCAG 2016
            ||||
Db      479 CCAG 482

RESULT 11
US-09-925-065A-727226/c
;   Sequence 727226, Application US/09925065A
;   Publication No. US20050228172A9
;   GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 727226
;   LENGTH: 1275
;   TYPE: DNA
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;   ORGANISM: Homo sapiens
US-09-925-065A-727226

  Query Match             3.2%;  Score 124;  DB 4;  Length 1275;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-52;
  Matches  124;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1893 GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT 1952
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      543 GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT 484

Qy     1953 CTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTTATGC 2012
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      483 CTGTGAAGATCTCATCTGGAATAAAGACCCTGAGGCCACTGAGAAGCTCTTACGTTATGC 424

Qy     2013 CCAG 2016
            ||||
Db      423 CCAG 420

RESULT 12
US-09-925-065A-697175/c
;   Sequence 697175, Application US/09925065A
;   Publication No. US20050228172A9
;   GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 697175
;   LENGTH: 616
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-697175

  Query Match             2.0%;  Score 80;  DB 4;  Length 616;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-30;
  Matches   80;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     2739 GTGTTCCCAGCTGTTAGATGAAAATCTAAAGGATGAAATCATGGAAGA 2798
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db      134 GTGTTCCCAGCTGTTAGATGAAAATCTAAAGGATGAAATCATGGAAGA 75

Qy     2799 ATATGAAGATATTAGACAGG 2818
            ||||||||||||||||||||
Db       74 ATATGAAGATATTAGACAGG 55

RESULT 13
US-10-027-632-56722/c
;   Sequence 56722, Application US/10027632
;   Publication No. US20020198371A1
;   GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;   TITLE OF INVENTION:  Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.129
;   CURRENT APPLICATION NUMBER: US/10/027,632
;   CURRENT FILING DATE: 2002-04-30
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;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 56722
;  LENGTH: 493
;  TYPE: DNA
;  ORGANISM: Human
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(493)
;  OTHER INFORMATION: n = A,T,C or G
US-10-027-632-56722

Query Match       1.8%;   Score 69;   DB 5;   Length 493;
Best Local Similarity  100.0%;   Pred. No. 3.8e-24;
Matches   69;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   862 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 921
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 73

Qy   922 AATGCAGGT 930
         |||||||||
Db    72 AATGCAGGT 64

RESULT 14
US-10-027-632-314464/c
;  Sequence 314464, Application US/10027632
;  Publication No. US2002019837lA1
;  GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION: Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE: 2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 314464
;  LENGTH: 493
;  TYPE: DNA
;  ORGANISM: Human
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(493)
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;  OTHER INFORMATION: n = A,T,C or G
US-10-027-632-314464

Query Match       1.8%;   Score 69;   DB 5;   Length 493;
Best Local Similarity  100.0%;   Pred. No. 3.8e-24;
Matches   69;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   862 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 921
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 73

Qy   922 AATGCAGGT 930
         |||||||||
Db    72 AATGCAGGT 64

RESULT 15
US-10-027-632-314465/c
;  Sequence 314465, Application US/10027632
;  Publication No. US2002019837lA1
;  GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION: Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE: 2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 314465
;  LENGTH: 493
;  TYPE: DNA
;  ORGANISM: Human
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(493)
;  OTHER INFORMATION: n = A,T,C or G
US-10-027-632-314465

Query Match       1.8%;   Score 69;   DB 5;   Length 493;
Best Local Similarity  100.0%;   Pred. No. 3.8e-24;
Matches   69;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   862 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 921
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 73

Qy   922 AATGCAGGT 930
         |||||||||
Db    72 AATGCAGGT 64

RESULT 16
US-10-027-632-56722/c
;  Sequence 56722, Application US/10027632
;  Publication No. US20030204075A9
;  GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56722
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(493)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-56722

Query Match   1.8%; Score 69; DB 6; Pred. No. 3.8e-24; Length 493;
Best Local Similarity   100.0%;
Matches   69; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   862 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCGTTATCCC 921
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCGTTATCCC 73

Qy   922 AATGCAGGT 930
            |||||||||
Db   72 AATGCAGGT 64

RESULT 17
US-10-027-632-314464/c
; Sequence 314464, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 314464
; LENGTH: 493
; TYPE: DNA

; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(493)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-314464

Query Match   1.8%; Score 69; DB 6; Pred. No. 3.8e-24; Length 493;
Best Local Similarity   100.0%;
Matches   69; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   862 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCGTTATCCC 921
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCGTTATCCC 73

Qy   922 AATGCAGGT 930
            |||||||||
Db   72 AATGCAGGT 64

RESULT 18
US-10-027-632-314465/c
; Sequence 314465, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 314465
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(493)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-314465

Query Match   1.8%; Score 69; DB 6; Pred. No. 3.8e-24; Length 493;
Best Local Similarity   100.0%;
Matches   69; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   862 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCGTTATCCC 921
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132 ATGAGACCTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCGTTATCCC 73

Qy   922 AATGCAGGT 930
            |||||||||
Db   72 AATGCAGGT 64

RESULT 19
US-10-027-632-3760/c
; Sequence 3760, Application US/10027632

; Publication No.US2002019837lAl
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3760
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(627)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-3760

Qy   Query Match   1.8%;   Score 69; DB 5; Length 627;
Best Local Similarity 100.0%; Pred. No. 3.8e-24;
Matches   69; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   862 ATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 921
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 212

Qy   922 AATGCAGGT 930
          |||||||||
Db   211 AATGCAGGT 203

RESULT 20
US-10-027-632-3760/c
; Sequence 3760, Application US/10027632
; Publication No. US2003020407SA9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3760
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(627)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-3760

Query Match   1.8%;   Score 69; DB 6; Length 627;
Best Local Similarity 100.0%; Pred. No. 3.8e-24;
Matches   69; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   862 ATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 921
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ATGAGACCTTTTATTGAAATAATTGGAAAATGTACAACAGCCTATGTCCTCTGTTATCCC 212

Qy   922 AATGCAGGT 930
          |||||||||
Db   211 AATGCAGGT 203

RESULT 21
US-09-925-065A-460077/c
; Sequence 460077, Application US/09925065A
; Publication No. US2005022817ZA9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 460077
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-460077

Query Match   1.0%;   Score 39; DB 4; Length 611;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches   39; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   989 AGGATTTGCTATGGATGGCTTGGTCAATATAGTTGGAG 1027
          ||||||||||||||||||||||||||||||||||||||
Db   39 AGGATTTGCTATGGATGGCTTGGTCAATATAGTTGGAG 1

RESULT 22
US-09-925-065A-39453/c
; Sequence 39453, Application US/09925065A
; Publication No. US2005022817ZA9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08

```
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39453
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-39453

Query Match             0.8%;  Score 31;  DB 4;  Length 588;
Best Local Similarity   100.0%;  Pred. No. 0.00019;
Matches    31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        3889 TCTTGATGATCCTCAAGGAAATACAACCTAG 3919
               |||||||||||||||||||||||||||||||
Db         570 TCTTGATGATCCTCAAGGAAATACAACCTAG 540


RESULT 23
US-10-607-712-45/c
; Sequence 45, Application US/10607712
; Publication No. US2004007301841
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-45

Query Match             0.7%;  Score 28;  DB 7;  Length 28;
Best Local Similarity   100.0%;  Pred. No. 0.0063;
Matches    28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        2468 GAGTTATTGATTTAGGAGTCATGACTCC 2495
               ||||||||||||||||||||||||||||
Db          28 GAGTTATTGATTTAGGAGTCATGACTCC 1


RESULT 24
US-10-607-712-35
; Sequence 35, Application US/10607712
; Publication No. US2004007301841
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
```

```
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-35

Query Match             0.7%;  Score 26;  DB 7;  Length 26;
Best Local Similarity   100.0%;  Pred. No. 0.069;
Matches    26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         214 TTCCGAGGTCAGGAATTTAAAGATCA 239
               ||||||||||||||||||||||||||
Db           1 TTCCGAGGTCAGGAATTTAAAGATCA 26


RESULT 25
US-10-607-712-48
; Sequence 48, Application US/10607712
; Publication No. US2004007301841
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-48

Query Match             0.7%;  Score 26;  DB 7;  Length 26;
Best Local Similarity   100.0%;  Pred. No. 0.069;
Matches    26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        2422 ATAGGCAAGAACATAGTTGGAGTAGT 2447
               ||||||||||||||||||||||||||
Db           1 ATAGGCAAGAACATAGTTGGAGTAGT 26


RESULT 26
US-10-607-712-53
```

```
; Sequence 53, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
;  APPLICANT: Gravel, Roy A.
;  APPLICANT: Rozen, Rima
;  APPLICANT: LeClerc, Daniel
;  APPLICANT: Goyette, Philippe
;  APPLICANT: Campeau, Eric
;  TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
;  TITLE OF INVENTION:  METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE, AND CANCER
;  FILE REFERENCE: 50004/002005
;  CURRENT APPLICATION NUMBER: US/10/607,712
;  CURRENT FILING DATE: 2003-06-27
;  PRIOR APPLICATION NUMBER: 08/980,326
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: 60/031,964
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: 60/050,310
;  PRIOR FILING DATE: 1997-06-20
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
;  LENGTH: 26
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-607-712-53

Query Match             0.7%;  Score 26;  DB 7;  Length 26;
Best Local Similarity   100.0%; Pred. No. 0.069;
Matches  26;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       2790 CATGGAAGAATATGAAGAGATATTAGAC 2815
              ||||||||||||||||||||||||||
Db          1 CATGGAAGAATATGAAGAGATATTAGAC 26


RESULT 27
US-10-607-712-57/c
; Sequence 57, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
;  APPLICANT: Gravel, Roy A.
;  APPLICANT: Rozen, Rima
;  APPLICANT: LeClerc, Daniel
;  APPLICANT: Goyette, Philippe
;  APPLICANT: Campeau, Eric
;  TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
;  TITLE OF INVENTION:  METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE, AND CANCER
;  FILE REFERENCE: 50004/002005
;  CURRENT APPLICATION NUMBER: US/10/607,712
;  CURRENT FILING DATE: 2003-06-27
;  PRIOR APPLICATION NUMBER: 08/980,326
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: 60/031,964
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: 60/050,310
;  PRIOR FILING DATE: 1997-06-20
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
;  LENGTH: 26
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-607-712-57

Query Match             0.7%;  Score 26;  DB 7;  Length 26;
Best Local Similarity   100.0%; Pred. No. 0.069;
Matches  26;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       2496 ATGTGATAAGATACTGAAAGCTGCTC 2521
              |||||||||||||||||||||||||
```

```
Db         26 ATGTGATAAGATACTGAAAGCTGCTC 1


RESULT 28
US-10-607-712-63/c
; Sequence 63, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
;  APPLICANT: Gravel, Roy A.
;  APPLICANT: Rozen, Rima
;  APPLICANT: LeClerc, Daniel
;  APPLICANT: Goyette, Philippe
;  APPLICANT: Campeau, Eric
;  TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
;  TITLE OF INVENTION:  METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE, AND CANCER
;  FILE REFERENCE: 50004/002005
;  CURRENT APPLICATION NUMBER: US/10/607,712
;  CURRENT FILING DATE: 2003-06-27
;  PRIOR APPLICATION NUMBER: 08/980,326
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: 60/031,964
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: 60/050,310
;  PRIOR FILING DATE: 1997-06-20
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
;  LENGTH: 26
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-607-712-63

Query Match             0.7%;  Score 26;  DB 7;  Length 26;
Best Local Similarity   100.0%; Pred. No. 0.069;
Matches  26;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1177 GTTAACATTGGAGAGCGCTGTAATGT 1202
              ||||||||||||||||||||||||||
Db         26 GTTAACATTGGAGAGCGCTGTAATGT 1


RESULT 29
US-09-925-065A-602656
; Sequence 602656, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602656
;  LENGTH: 559
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-925-065A-602656

Query Match             0.7%;  Score 26;  DB 4;  Length 559;
Best Local Similarity   100.0%; Pred. No. 0.074;
```

Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3864 TTTTTTTTTTTTTTGCCTTTTTAT 3889
             ||||||||||||||||||||||||
Db   21 TTTTTTTTTTTTTTGCCTTTTTAT 46

RESULT 30
US-09-925-065A-271845
; Sequence 271845, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 271845
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-271845

Query Match   0.7%; Score 26; DB 4; Length 595;
Best Local Similarity   100.0%; Pred. No. 0.074;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTGCCTTTTTA 3888
             ||||||||||||||||||||||
Db   378 TTTTTTTTTTTTTTGCCTTTTTA 403

RESULT 31
US-10-437-963-1741/c
; Sequence 1741, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;   APPLICANT: La Rosa, Thomas J.
;   APPLICANT: Kovalic, David K.
;   APPLICANT: Zhou, Yihua
;   APPLICANT: Cao, Yongwei
;   APPLICANT: Wu, Wei
;   APPLICANT: Boukharov, Andrey A.
;   APPLICANT: Barbazuk, Brad
;   APPLICANT: Li, Ping
;   TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;   TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;   FILE REFERENCE: 38-21(53221)B
;   CURRENT APPLICATION NUMBER: US/10/437,963
;   CURRENT FILING DATE: 2003-05-14
;   NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 1741
;   LENGTH: 649
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_101579C.1
US-10-437-963-1741

Query Match   0.7%; Score 26; DB 7; Length 649;

Best Local Similarity   100.0%; Pred. No. 0.074;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3862 CTTTTTTTTTTTTTTGCCTTTTTT 3887
             ||||||||||||||||||||||||
Db   305 CTTTTTTTTTTTTTTGCCTTTTTT 280

RESULT 32
US-09-925-065A-702090
; Sequence 702090, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 702090
;   LENGTH: 1374
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-702090

Query Match   0.7%; Score 26; DB 4; Length 1374;
Best Local Similarity   100.0%; Pred. No. 0.075;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3862 CTTTTTTTTTTTTTTGCCTTTTTT 3887
             ||||||||||||||||||||||||
Db   204 CTTTTTTTTTTTTTTGCCTTTTTT 229

RESULT 33
US-10-607-712-39
; Sequence 39, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
;   APPLICANT: Gravel, Roy A.
;   APPLICANT: Rozen, Rima
;   APPLICANT: LeClerc, Daniel
;   APPLICANT: Goyette, Philippe
;   APPLICANT: Campeau, Eric
;   TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
;   TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
;   TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
;   FILE REFERENCE: 50004/002005
;   CURRENT APPLICATION NUMBER: US/10/607,712
;   CURRENT FILING DATE: 2003-06-27
;   PRIOR APPLICATION NUMBER: 08/980,326
;   PRIOR FILING DATE: 1997-11-26
;   PRIOR APPLICATION NUMBER: 60/031,964
;   PRIOR FILING DATE: 1996-11-27
;   PRIOR APPLICATION NUMBER: 60/050,310
;   PRIOR FILING DATE: 1997-06-20
;   NUMBER OF SEQ ID NOS: 76
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
;   LENGTH: 25
;   TYPE: DNA

; ORGANISM: Homo sapiens
US-10-607-712-39

```
Query Match             0.6%;    Score 25;   DB 7;   Length 25;
Best Local Similarity   100.0%;  Pred. No. 0.23;
Matches   25;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy    2233 GGAGCTGGAAAAATGTTCTACCTC 2257
           |||||||||||||||||||||||||
Db       1 GGAGCTGGAAAAATGTTCTACCTC 25
```

RESULT 34
US-10-607-712-41/c
; Sequence 41, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-41

```
Query Match             0.6%;    Score 25;   DB 7;   Length 25;
Best Local Similarity   100.0%;  Pred. No. 0.23;
Matches   25;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy    2168 CCCGACCTCTCAATATAATTGAAGG 2192
           |||||||||||||||||||||||||
Db      25 CCCGACCTCTCAATATAATTGAAGG 1
```

RESULT 35
US-10-607-712-49/c
; Sequence 49, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20

; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-49

```
Query Match             0.6%;    Score 25;   DB 7;   Length 25;
Best Local Similarity   100.0%;  Pred. No. 0.23;
Matches   25;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy    2737 GTGTGTTCCCAGCTGTTAGATGAAA 2761
           |||||||||||||||||||||||||
Db      25 GTGTGTTCCCAGCTGTTAGATGAAA 1
```

RESULT 36
US-10-607-712-58/c
; Sequence 58, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-58

```
Query Match             0.6%;    Score 25;   DB 7;   Length 25;
Best Local Similarity   100.0%;  Pred. No. 0.23;
Matches   25;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy    1696 ACTGGAATGGGAGGAACACAACTTGT 1720
           |||||||||||||||||||||||||
Db      25 ACTGGAATGGGAGGAACACAACTTGT 1
```

RESULT 37
US-10-607-712-59
; Sequence 59, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326

```
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-59

Query Match             0.6%;  Score 25;  DB 7;  Length 25;
Best Local Similarity   100.0%;  Pred. No. 0.23;
Matches   25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         1188 AGAGCGCTGTAATGTTGCAGGATCA 1212
                |||||||||||||||||||||||||
Db            1 AGAGCGCTGTAATGTTGCAGGATCA 25

RESULT 38
US-10-607-712-60/c
; Sequence 60, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-60

Query Match             0.6%;  Score 25;  DB 7;  Length 25;
Best Local Similarity   100.0%;  Pred. No. 0.23;
Matches   25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         2096 CCCTTGTGAAGGGCATTGAAAAACA 2120
                |||||||||||||||||||||||||
Db           25 CCCTTGTGAAGGGCATTGAAAAACA 1

RESULT 39
US-10-607-712-61
; Sequence 61, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-61

Query Match             0.6%;  Score 25;  DB 7;  Length 25;
Best Local Similarity   100.0%;  Pred. No. 0.23;
Matches   25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         1527 TAAAAAGTATGGAGCTGCTATGGTG 1551
                |||||||||||||||||||||||||
Db            1 TAAAAAGTATGGAGCTGCTATGGTG 25

RESULT 40
US-10-607-712-62/c
; Sequence 62, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-62

Query Match             0.6%;  Score 25;  DB 7;  Length 25;
Best Local Similarity   100.0%;  Pred. No. 0.23;
Matches   25;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         1117 GAAGGACATATGTTACTGTCTGGTC 1141
                |||||||||||||||||||||||||
Db           25 GAAGGACATATGTTACTGTCTGGTC 1

RESULT 41
US-10-607-712-65/c
; Sequence 65, Application US/10607712
; Publication No. US20040073018A1
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
```

; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-712-65

Query Match   0.6%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches   25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3788 CATTGAGGAAGAACATATCTGTGGC 3812
          |||||||||||||||||||||||||
Db   25 CATTGAGGAAGAACATATCTGTGGC 1

RESULT 42
US-10-357-930-61072
; Sequence 61072, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61072
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-61072

Query Match   0.6%; Score 25; DB 8; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches   25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3863 TTTTTTTTTTTTTTTGCCTTTTTT 3887

Db   10 TTTTTTTTTTTTTTTGCCTTTTTT 34
          |||||||||||||||||||||||||

RESULT 43
US-10-424-599-9150/c
; Sequence 9150, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 9150
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108272C.1
US-10-424-599-9150

Query Match   0.6%; Score 25; DB 7; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches   25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3863 TTTTTTTTTTTTTTTGCCTTTTTT 3887
          |||||||||||||||||||||||||
Db   81 TTTTTTTTTTTTTTTGCCTTTTTT 57

RESULT 44
US-10-424-599-13138
; Sequence 13138, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 13138
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(262)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_111870C.1
US-10-424-599-13138

Query Match   0.6%; Score 25; DB 7; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches   25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3863 TTTTTTTTTTTTTTTGCCTTTTTT 3887
          |||||||||||||||||||||||||
Db   190 TTTTTTTTTTTTTTTGCCTTTTTT 214

RESULT 45

US-10-425-115-158147
; Sequence 158147, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 158147
; LENGTH: 280
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_75807C.1
US-10-425-115-158147

Query Match   0.6%; Score 25; DB 8; Length 280;
Best Local Similarity   100.0%; Pred. No. 0.24;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTGCCTTTTTT 3887
              |||||||||||||||||||||||
Db   6 TTTTTTTTTTTTTTTGCCTTTTTT 30

RESULT 46
US-09-867-701-9532/c
; Sequence 9532, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9532
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-9532

Query Match   0.6%; Score 25; DB 3; Length 296;
Best Local Similarity   100.0%; Pred. No. 0.24;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTGCCTTTTTT 3887
              |||||||||||||||||||||||
Db   288 TTTTTTTTTTTTTTTGCCTTTTTT 264

RESULT 47
US-10-756-149-3961/c
; Sequence 3961, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12

; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3961
; LENGTH: 343
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-3961

Query Match   0.6%; Score 25; DB 9; Length 343;
Best Local Similarity   100.0%; Pred. No. 0.24;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTGCCTTTTTT 3887
              |||||||||||||||||||||||
Db   329 TTTTTTTTTTTTTTTGCCTTTTTT 305

RESULT 48
US-10-425-115-165833/c
; Sequence 165833, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 165833
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_82824C.1
US-10-425-115-165833

Query Match   0.6%; Score 25; DB 8; Length 375;
Best Local Similarity   100.0%; Pred. No. 0.24;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTGCCTTTTTT 3887
              |||||||||||||||||||||||
Db   162 TTTTTTTTTTTTTTTGCCTTTTTT 138

RESULT 49
US-10-021-323-7632/c
; Sequence 7632, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
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; PRIOR FILING DATE: 2000-12-14
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; FEATURE:
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US-10-021-323-7632

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Db   188 TTTTTTTTTTTTTTGCCTTTTTT 164

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; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
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; OTHER INFORMATION: Clone ID: MRT45577_32945C.1
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Search completed: March 7, 2006, 03:38:15
Job time : 2731 secs

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                GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:   March 7, 2006, 02:21:39 ; Search time 1025 Seconds
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Searched:       721B535 seqs, 1096242582 residues

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Total number of hits satisfying chosen parameters:    14824

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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	6	26	0.7	595	6	US-09-925-065A-271845	Sequence 271845,
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c	18	25	0.6	156544	12	US-11-121-086-81	Sequence 81, Appl
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	38	23	0.6	491	12	US-11-136-527-1395	Sequence 1395, Ap
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	58	23	0.6	1395	8	US-10-750-623-53615	Sequence 53615, A
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	73	22	0.6	143947	12	US-11-193-771-37	Sequence 37, Appl
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	105	22	0.6	540	US-09-925-065A-102799	Sequence 102799,
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c	151	22	0.6	6450	US-10-955-054A-30	Sequence 30, Appl
c	152	22	0.6	22475	US-10-330-773-975	Sequence 975, App
c	153	22	0.6	79528	US-10-276-233A-6	Sequence 6, Appl
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	155	22	0.6	87672	US-10-995-561-13237	Sequence 13237, A
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	166	21	0.5	23	US-10-310-914A-882784	Sequence 882784,

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	174	21	0.5	201	US-10-995-561-23938	Sequence 23938, A
	175	21	0.5	201	US-10-995-561-23940	Sequence 23940, A
	176	21	0.5	201	US-10-995-561-24041	Sequence 24041, A
	177	21	0.5	201	US-10-995-561-28047	Sequence 28047, A
	178	21	0.5	201	US-10-995-561-32660	Sequence 32660, A
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	213	21	0.5	511	US-09-925-065A-74198	Sequence 74198, A
	214	21	0.5	511	US-09-925-065A-74199	Sequence 74199, A
	215	21	0.5	511	US-09-925-065A-74200	Sequence 74200, A
c	216	21	0.5	512	US-09-925-065A-580299	Sequence 580299,
c	217	21	0.5	512	US-09-925-065A-762931	Sequence 762931,
c	218	21	0.5	513	US-09-925-065A-358459	Sequence 358459,
c	219	21	0.5	513	US-09-925-065A-358460	Sequence 358460,
c	220	21	0.5	513	US-09-925-065A-358461	Sequence 358461,
c	221	21	0.5	513	US-09-925-065A-358462	Sequence 358462,
c	222	21	0.5	513	US-09-925-065A-763143	Sequence 763143,
	223	21	0.5	514	US-09-925-065A-484457	Sequence 484457,
	224	21	0.5	521	US-09-925-065A-422732	Sequence 422732,
	225	21	0.5	524	US-09-925-065A-118032	Sequence 118032,
	226	21	0.5	526	US-09-925-065A-320969	Sequence 320969,
	227	21	0.5	526	US-09-925-065A-320970	Sequence 320970,
	228	21	0.5	530	US-09-925-065A-318951	Sequence 318951,
c	229	21	0.5	530	US-09-925-065A-318953	Sequence 318953,
c	230	21	0.5	530	US-09-925-065A-318954	Sequence 318954,
c	231	21	0.5	532	US-09-925-065A-557580	Sequence 557580,
c	232	21	0.5	532	US-09-925-065A-610344	Sequence 610344,
c	233	21	0.5	532	US-09-925-065A-610345	Sequence 610345,
c	234	21	0.5	532	US-09-925-065A-610346	Sequence 610346,
c	235	21	0.5	533	US-09-925-065A-610347	Sequence 610347,
c	236	21	0.5	533	US-09-925-065A-526099	Sequence 526099, A
c	237	21	0.5	534	US-09-925-065A-10121	Sequence 10121, A
c	238	21	0.5	534	US-09-925-065A-33898	Sequence 33898,
c	239	21	0.5	537	US-09-925-065A-230349	Sequence 230349,

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	241	21	0.5	537	6	US-09-925-065A-489873	Sequence 489873,
	242	21	0.5	537	6	US-09-925-065A-489874	Sequence 489874,
c	243	21	0.5	538	6	US-09-925-065A-340190	Sequence 340190,
	244	21	0.5	546	6	US-09-925-065A-71178	Sequence 71178, A
c	245	21	0.5	547	6	US-09-925-065A-71179	Sequence 71179, A
	246	21	0.5	550	6	US-09-925-065A-589347	Sequence 589347,
c	247	21	0.5	550	6	US-09-925-065A-319926	Sequence 319926,
	248	21	0.5	556	6	US-09-925-065A-319927	Sequence 319927,
c	249	21	0.5	557	6	US-09-925-065A-591297	Sequence 591297,
	250	21	0.5	558	6	US-09-925-065A-123387	Sequence 123387,
c	251	21	0.5	558	6	US-09-925-065A-293387	Sequence 293387,
	252	21	0.5	560	6	US-09-925-065A-454776	Sequence 454776,
c	253	21	0.5	562	6	US-09-925-065A-454777	Sequence 454777, A
	254	21	0.5	575	6	US-09-925-065A-17376	Sequence 17376,
	255	21	0.5	577	6	US-09-925-065A-158888	Sequence 158888,
	256	21	0.5	577	6	US-09-925-065A-938868	Sequence 938868,
	257	21	0.5	579	6	US-09-925-065A-938869	Sequence 938869,
c	258	21	0.5	580	6	US-09-925-065A-258961	Sequence 258961,
c	259	21	0.5	582	6	US-09-925-065A-258962	Sequence 258962,
c	260	21	0.5	582	6	US-09-925-065A-954549	Sequence 954549,
c	261	21	0.5	583	6	US-09-925-065A-296463	Sequence 296463,
	262	21	0.5	583	6	US-09-925-065A-899637	Sequence 899637,
	263	21	0.5	585	6	US-09-925-065A-899638	Sequence 899638, A
c	264	21	0.5	585	6	US-09-925-065A-40758	Sequence 40758,
	265	21	0.5	585	6	US-09-925-065A-558657	Sequence 558657,
c	266	21	0.5	585	6	US-09-925-065A-172098	Sequence 172098,
c	267	21	0.5	585	6	US-09-925-065A-172099	Sequence 172099,
c	268	21	0.5	585	6	US-09-925-065A-172100	Sequence 172100,
c	269	21	0.5	585	6	US-09-925-065A-294385	Sequence 294385,
c	270	21	0.5	585	6	US-09-925-065A-294386	Sequence 294386,
	271	21	0.5	587	6	US-09-925-065A-774157	Sequence 774157,
	272	21	0.5	587	6	US-09-925-065A-774158	Sequence 774158,
c	273	21	0.5	587	6	US-09-925-065A-670881	Sequence 670881,
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	276	21	0.5	589	6	US-09-925-065A-588995	Sequence 588995,
	277	21	0.5	592	6	US-09-925-065A-588996	Sequence 588996,
	278	21	0.5	595	6	US-09-925-065A-588997	Sequence 588997,
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c	280	21	0.5	597	6	US-09-925-065A-472185	Sequence 472185,
c	281	21	0.5	598	6	US-09-925-065A-886355	Sequence 886355,
c	282	21	0.5	599	6	US-09-925-065A-911361	Sequence 911361,
	283	21	0.5	599	6	US-09-925-065A-762930	Sequence 762930,
c	284	21	0.5	600	6	US-09-925-065A-816088	Sequence 816088,
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	286	21	0.5	610	6	US-09-925-065A-399184	Sequence 399184,
	287	21	0.5	611	6	US-09-925-065A-690628	Sequence 690628,
	288	21	0.5	612	6	US-09-925-065A-319246	Sequence 319246,
c	289	21	0.5	612	6	US-09-925-065A-580587	Sequence 580587,
c	290	21	0.5	612	6	US-09-925-065A-885141	Sequence 885141,
c	291	21	0.5	612	6	US-09-925-065A-910826	Sequence 910826,
	292	21	0.5	613	6	US-09-925-065A-161287	Sequence 161287,
	293	21	0.5	619	6	US-09-925-065A-161288	Sequence 161288,
	294	21	0.5	619	6	US-09-925-065A-247900	Sequence 247900,
	295	21	0.5	620	6	US-09-925-065A-343174	Sequence 343174,
	296	21	0.5	620	6	US-09-925-065A-343175	Sequence 343175,
	297	21	0.5	620	6	US-09-925-065A-343176	Sequence 343176,
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	299	21	0.5	622	6	US-09-925-065A-770572	Sequence 770572, A
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c	302	21	0.5	625	6	US-09-925-065A-866942	Sequence 866942,
c	303	21	0.5	626	6	US-09-925-065A-866943	Sequence 866943,
c	304	21	0.5	626	6	US-09-925-065A-899725	Sequence 899725,
	305	21	0.5	626	6	US-09-925-065A-501311	Sequence 501311,
c	306	21	0.5	626	6	US-09-925-065A-501312	Sequence 501312,
	307	21	0.5	626	6	US-09-925-065A-264948	Sequence 264948,
c	308	21	0.5	626	6	US-09-925-065A-15616	Sequence 15616, A
c	309	21	0.5	626	6	US-09-925-065A-158695	Sequence 158695,
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c	314	21	0.5	627	6	US-09-925-065A-878744	Sequence 878744,
c	315	21	0.5	627	6	US-09-925-065A-878745	Sequence 878745,
c	316	21	0.5	628	6	US-09-925-065A-559335	Sequence 559335,
	317	21	0.5	633	6	US-09-925-065A-875899	Sequence 875899,
c	318	21	0.5	636	6	US-09-925-065A-731134	Sequence 731134,
	319	21	0.5	636	6	US-09-925-065A-731135	Sequence 731135,
	320	21	0.5	637	6	US-09-925-065A-932840	Sequence 932840,
	321	21	0.5	638	6	US-09-925-065A-548422	Sequence 548422,
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	323	21	0.5	640	6	US-09-925-065A-822586	Sequence 822586,
	324	21	0.5	640	6	US-09-925-065A-688042	Sequence 688042,
	325	21	0.5	640	6	US-09-925-065A-688043	Sequence 688043,
	326	21	0.5	640	6	US-09-925-065A-862829	Sequence 862829,
	327	21	0.5	640	6	US-09-925-065A-862830	Sequence 862830,
	328	21	0.5	650	6	US-09-925-065A-897747	Sequence 897747,
	329	21	0.5	653	6	US-09-925-065A-701394	Sequence 701394,
	330	21	0.5	653	6	US-09-925-065A-748516	Sequence 748516,
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c	333	21	0.5	668	6	US-09-925-065A-41772	Sequence 41772, A
	334	21	0.5	672	6	US-09-925-065A-41773	Sequence 41773, A
c	335	21	0.5	673	6	US-09-925-065A-691735	Sequence 691735,
c	336	21	0.5	700	6	US-09-925-065A-682472	Sequence 682472,
c	337	21	0.5	710	6	US-09-925-065A-680053	Sequence 680053, A
	338	21	0.5	726	6	US-09-925-065A-540081	Sequence 540081,
c	339	21	0.5	732	6	US-09-925-065A-65701	Sequence 65701, A
c	340	21	0.5	762	6	US-09-925-065A-63027	Sequence 63027, A
c	341	21	0.5	762	6	US-09-925-065A-57310	Sequence 57310, A
c	342	21	0.5	801	6	US-09-925-065A-59562	Sequence 59562, A
c	343	21	0.5	895	6	US-09-925-065A-59563	Sequence 59563, A
c	344	21	0.5	895	6	US-09-925-065A-678775	Sequence 678775, A
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c	346	21	0.5	907	8	US-10-750-623-61125	Sequence 61125, A
c	347	21	0.5	1002	6	US-09-925-065A-68283	Sequence 68283, A
c	348	21	0.5	1027	6	US-09-925-065A-68284	Sequence 68284, A
c	349	21	0.5	1027	6	US-09-925-065A-68285	Sequence 68285, A
	350	21	0.5	1027	6	US-09-925-065A-31170	Sequence 31170, A
c	351	21	0.5	1070	6	US-09-925-065A-3659	Sequence 3659, Ap
c	352	21	0.5	1087	6	US-09-925-065A-3660	Sequence 3660, Ap
c	353	21	0.5	1087	6	US-09-925-065A-3661	Sequence 3661, Ap
c	354	21	0.5	1092	6	US-09-925-065A-3662	Sequence 3662, Ap
	355	21	0.5	1130	6	US-09-925-065A-686010	Sequence 686010,
	356	21	0.5	1131	6	US-09-925-065A-686011	Sequence 686011,
	357	21	0.5	1131	6	US-09-925-065A-709482	Sequence 709482,
	358	21	0.5	1139	6	US-09-925-065A-709483	Sequence 709483,
	359	21	0.5	1139	6	US-09-925-065A-689194	Sequence 689194,
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	361	21	0.5	1167	6	US-09-925-065A-719121	Sequence 719121,
	362	21	0.5	1190	6	US-09-925-065A-718023	Sequence 718023,
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c	364	21	0.5	1284	6	US-09-925-065A-28729	Sequence 28729, A
	365	21	0.5	1284	6	US-09-925-065A-28730	Sequence 28730,
	366	21	0.5	1331	6	US-09-925-065A-28731	Sequence 28731,
	367	21	0.5	1382	6	US-09-925-065A-28732	Sequence 28732, A
	368	21	0.5	1382	6	US-09-925-065A-670666	Sequence 670666,
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	370	21	0.5	1382	6	US-09-925-065A-681170	Sequence 681170,
	371	21	0.5	1393	6	US-09-925-065A-681171	Sequence 681171,
	372	21	0.5	1393	6	US-09-925-065A-681172	Sequence 681172,
	373	21	0.5	1393	6	US-09-925-065A-47638	Sequence 47638, A
	374	21	0.5	1398	6	US-09-925-065A-69581	Sequence 69581, A
	375	21	0.5	1496	6	US-09-925-065A-69582	Sequence 69582, A
	376	21	0.5	1496	6	US-09-925-065A-69583	Sequence 69583, A
	377	21	0.5	1496	6	US-09-925-065A-69584	Sequence 69584, A
	378	21	0.5	1496	6	US-09-925-065A-550969	Sequence 550969,
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c	380	21	0.5	1512	8	US-10-750-623-54425	Sequence 54425, A
c	381	21	0.5	1512	12	US-11-149-403-3	Sequence 3, Appli
	382	21	0.5	1512	8	US-10-750-185-55271	Sequence 55271, A
	383	21	0.5	1512	8	US-10-750-623-55271	Sequence 55271, A
c	384	21	0.5	1512	6	US-09-925-065A-704680	Sequence 704680,
c	385	21	0.5	1512	6	US-09-925-065A-704681	Sequence 704681,

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c	386	21	0.5	1673	6	US-09-925-065A-73000	Sequence 73000, A
c	387	21	0.5	1694	6	US-09-925-065A-699512	Sequence 699512,
c	388	21	0.5	1694	6	US-09-925-065A-699513	Sequence 699513,
	389	21	0.5	1760	6	US-09-925-065A-714280	Sequence 714280,
c	390	21	0.5	1761	8	US-10-750-185-32845	Sequence 32845, A
c	391	21	0.5	1761	8	US-10-750-185-32845	Sequence 32845, A
	392	21	0.5	1774	8	US-10-750-623-62002	Sequence 62002, A
c	393	21	0.5	1774	8	US-10-750-623-62002	Sequence 62002, A
c	394	21	0.5	1778	8	US-10-980-388-54	Sequence 54, Appl
c	395	21	0.5	1798	6	US-09-925-065A-685610	Sequence 685610,
	396	21	0.5	1824	8	US-10-750-185-55137	Sequence 55137, A
	397	21	0.5	1824	8	US-10-750-623-55137	Sequence 55137, A
	398	21	0.5	1831	8	US-10-750-185-34142	Sequence 34142, A
c	399	21	0.5	1831	8	US-10-750-623-34142	Sequence 34142, A
c	400	21	0.5	1962	8	US-10-750-185-31991	Sequence 31991, A
c	401	21	0.5	1962	8	US-10-750-623-31991	Sequence 31991, A
c	402	21	0.5	2195	6	US-09-925-065A-13945	Sequence 13945, A
c	403	21	0.5	2195	6	US-09-925-065A-13946	Sequence 13946, A
c	404	21	0.5	2260	6	US-09-925-065A-690385	Sequence 690385,
c	405	21	0.5	2260	6	US-09-925-065A-690386	Sequence 690386,
c	406	21	0.5	2277	6	US-09-925-065A-685269	Sequence 685269,
c	407	21	0.5	2277	6	US-09-925-065A-685270	Sequence 685270,
c	408	21	0.5	2277	6	US-09-925-065A-685271	Sequence 685271,
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c	410	21	0.5	2369	6	US-09-925-065A-707979	Sequence 707979,
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c	412	21	0.5	2369	6	US-09-925-065A-707981	Sequence 707981,
c	413	21	0.5	2369	6	US-09-925-065A-707982	Sequence 707982,
c	414	21	0.5	2369	6	US-09-925-065A-707983	Sequence 707983,
c	415	21	0.5	2369	6	US-09-925-065A-707984	Sequence 707984,
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c	417	21	0.5	2498	6	US-09-925-065A-685840	Sequence 685840,
c	418	21	0.5	2498	6	US-09-925-065A-685841	Sequence 685841,
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c	420	21	0.5	2723	8	US-10-750-623-54580	Sequence 54580, A
c	421	21	0.5	2731	9	US-11-072-512-284	Sequence 284, App
c	422	21	0.5	2765	6	US-09-925-065A-677497	Sequence 677497,
c	423	21	0.5	2941	9	US-11-072-512-723375	Sequence 723375,
c	424	21	0.5	3227	9	US-11-245-147-112	Sequence 112, App
c	425	21	0.5	3576	8	US-10-750-185-33942	Sequence 33942, A
c	426	21	0.5	3576	8	US-10-750-623-33942	Sequence 33942, A
c	427	21	0.5	3711	6	US-09-925-065A-717787	Sequence 717787,
c	428	21	0.5	3711	6	US-09-925-065A-717788	Sequence 717788,
c	429	21	0.5	3711	6	US-09-925-065A-717789	Sequence 717789,
c	430	21	0.5	3711	6	US-09-925-065A-717790	Sequence 717790,
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c	432	21	0.5	4105	8	US-10-750-623-37015	Sequence 37015, A
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c	434	21	0.5	4295	8	US-10-750-623-55549	Sequence 55549, A
c	435	21	0.5	4619	8	US-10-750-185-57460	Sequence 57460, A
c	436	21	0.5	4619	8	US-10-750-623-57460	Sequence 57460, A
c	437	21	0.5	5585	8	US-10-750-185-47879	Sequence 47879, A
c	438	21	0.5	5585	8	US-10-750-623-47879	Sequence 47879, A
c	439	21	0.5	10467	8	US-10-240-708-1	Sequence 1, Appli
c	440	21	0.5	20317	8	US-10-995-561-13460	Sequence 13460, A
c	441	21	0.5	26354	7	US-10-330-773-444	Sequence 444, App
c	442	21	0.5	27902	8	US-10-995-561-13462	Sequence 13462, A
c	443	21	0.5	65931	8	US-10-893-483-105	Sequence 105, App
c	444	21	0.5	69648	7	US-10-330-773-278	Sequence 278, App
	445	21	0.5	77246	12	US-11-124-368A-2907	Sequence 2907, Ap
	446	21	0.5	98638	7	US-10-330-773-896	Sequence 896, App
	447	21	0.5	100000	12	US-11-124-368A-2890	Sequence 2890, Ap
	448	21	0.5	101169	7	US-10-330-773-561	Sequence 561, App
	449	21	0.5	124285	7	US-10-893-483-105	Sequence 105, App
	450	21	0.5	127722	7	US-10-330-773-278	Sequence 278, App
	451	21	0.5	151052	7	US-10-330-773-503	Sequence 503, App
	452	21	0.5	151870	8	US-10-995-561-13199	Sequence 13199,
	453	21	0.5	152096	7	US-10-330-773-942	Sequence 942, App
	454	21	0.5	157230	12	US-11-121-086-64	Sequence 64, Appl
	455	21	0.5	166639	12	US-11-121-086-52	Sequence 52, Appl
	456	21	0.5	168516	12	US-11-121-086-3	Sequence 3, Appli
	457	21	0.5	168656	12	US-11-112-908-59	Sequence 59, Appli
	458	21	0.5	170285	12	US-11-112-908-58	Sequence 58, Appli
c	459	21	0.5	170508	12	US-11-112-908-62	Sequence 62, Appl
c	460	21	0.5	171162	12	US-11-112-908-38	Sequence 38, Appl
c	461	21	0.5	173115	12	US-11-112-908-65	Sequence 65, Appl
	462	21	0.5	173120	9	US-11-114-798-55	Sequence 55, Appl
c	463	21	0.5	176503	12	US-11-121-086-53	Sequence 53, Appl
c	464	21	0.5	178024	12	US-11-330-773-698	Sequence 698, App
c	465	21	0.5	182303	12	US-11-121-086-45	Sequence 45, Appl
c	466	21	0.5	196200	12	US-11-121-086-9	Sequence 9, Appli
	467	21	0.5	197241	9	US-11-114-798-47	Sequence 47, Appl
c	468	21	0.5	218821	12	US-11-121-086-31	Sequence 31, Appl
	469	21	0.5	222094	8	US-10-995-561-13244	Sequence 13244, A
	470	21	0.5	225033	12	US-11-157-389-1	Sequence 1, Appli
	471	21	0.5	237326	12	US-11-157-389-2	Sequence 2, Appli
c	472	21	0.5	246960	12	US-11-121-086-8	Sequence 8, Appli
	473	21	0.5	257645	7	US-10-330-773-266	Sequence 266, App
	474	21	0.5	355211	7	US-10-330-773-242	Sequence 242, App
	475	21	0.5	440684	7	US-10-330-773-114	Sequence 114, App
c	476	21	0.5	440684	7	US-10-330-773-114	Sequence 114, App
c	477	21	0.5	1125000	8	US-10-995-561-13286	Sequence 13286, A
c	478	21	0.5	1125000	8	US-10-995-561-13286	Sequence 13286, A
c	479	20	0.5	20	8	US-10-310-914A-46760	Sequence 46760, A
c	480	20	0.5	20	8	US-10-310-914A-979695	Sequence 979695, A
c	481	20	0.5	21	8	US-10-310-914A-84873	Sequence 84873, A
c	482	20	0.5	21	8	US-10-310-914A-179443	Sequence 179443, A
c	483	20	0.5	21	8	US-10-310-914A-191734	Sequence 191734, A
c	484	20	0.5	21	8	US-10-310-914A-224007	Sequence 224007, A
c	485	20	0.5	21	8	US-10-310-914A-432268	Sequence 432268, A
c	486	20	0.5	21	8	US-10-310-914A-454705	Sequence 454705, A
c	487	20	0.5	21	8	US-10-310-914A-466979	Sequence 466979, A
c	488	20	0.5	21	8	US-10-310-914A-661429	Sequence 661429, A
c	489	20	0.5	21	8	US-10-310-914A-670173	Sequence 670173, A
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c	493	20	0.5	21	8	US-10-310-914A-1335405	Sequence 1335405, A
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c	498	20	0.5	23	8	US-10-310-914A-979696	Sequence 979696, A
c	499	20	0.5	23	8	US-10-310-914A-84871	Sequence 84871, A
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c	525	20	0.5	201	8	US-10-995-561-40250	Sequence 40250, A
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c	527	20	0.5	201	8	US-10-995-561-44270	Sequence 44270, A
c	528	20	0.5	201	8	US-10-995-561-44527	Sequence 44527, A
c	529	20	0.5	201	8	US-10-995-561-49557	Sequence 49557, A
c	530	20	0.5	201	8	US-10-995-561-49557	Sequence 49557, A
c	531	20	0.5	201	8	US-10-995-561-52271	Sequence 52271, A

Idx	Length	n	0.5	20	Identifier	Sequence
c 532	201	8	0.5	20	US-10-995-561-52622	Sequence 52622, A
c 533	201	8	0.5	20	US-10-995-561-53793	Sequence 53793, A
c 534	201	8	0.5	20	US-10-995-561-53851	Sequence 53851, A
c 535	201	8	0.5	20	US-10-995-561-58398	Sequence 58398, A
c 536	201	8	0.5	20	US-10-995-561-59543	Sequence 59543, A
c 537	201	8	0.5	20	US-10-995-561-63343	Sequence 63343, A
c 538	201	8	0.5	20	US-10-995-561-68821	Sequence 68821, A
c 539	201	8	0.5	20	US-10-995-561-69966	Sequence 69966, A
c 540	201	8	0.5	20	US-10-995-561-70143	Sequence 70143, A
c 541	201	12	0.5	20	US-11-124-368A-3007	Sequence 3007, Ap
c 542	201	12	0.5	20	US-11-124-368A-3008	Sequence 3008, Ap
c 543	201	12	0.5	20	US-11-124-368A-3932	Sequence 3932, Ap
c 544	201	12	0.5	20	US-11-124-368A-3933	Sequence 3933, Ap
c 545	201	12	0.5	20	US-11-124-368A-5831	Sequence 5831, Ap
c 546	201	12	0.5	20	US-11-124-368A-5832	Sequence 5832, Ap
c 547	201	12	0.5	20	US-11-124-368A-5872	Sequence 5872, Ap
c 548	201	12	0.5	20	US-11-124-368A-5873	Sequence 5873, Ap
c 549	201	12	0.5	20	US-11-124-368A-6015	Sequence 6015, Ap
c 550	201	12	0.5	20	US-11-124-368A-6016	Sequence 6016, Ap
c 551	201	12	0.5	20	US-11-124-368A-9444	Sequence 9444, Ap
c 552	201	12	0.5	20	US-11-124-368A-11180	Sequence 11180, A
c 553	201	12	0.5	20	US-11-124-368A-11181	Sequence 11181, A
c 554	201	12	0.5	20	US-11-124-368A-11274	Sequence 11274, A
c 555	201	12	0.5	20	US-11-124-368A-11275	Sequence 11275, A
c 556	201	12	0.5	20	US-11-124-368A-11451	Sequence 11451, A
c 557	201	12	0.5	20	US-11-124-368A-11452	Sequence 11452, A
c 558	201	12	0.5	20	US-11-124-368A-12335	Sequence 12335, A
c 559	201	12	0.5	20	US-11-124-368A-12336	Sequence 12336, A
c 560	201	12	0.5	20	US-11-124-368A-14951	Sequence 14951, A
c 561	201	12	0.5	20	US-11-124-368A-16389	Sequence 16389, A
c 562	201	12	0.5	20	US-11-124-368A-16390	Sequence 16390, A
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c 564	201	12	0.5	20	US-11-124-368A-19762	Sequence 19762, A
c 565	201	12	0.5	20	US-11-124-367A-7142	Sequence 7142, Ap
c 566	201	12	0.5	20	US-11-124-367A-8503	Sequence 8503, Ap
c 567	201	12	0.5	20	US-11-124-367A-8540	Sequence 8540, Ap
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c 571	201	12	0.5	20	US-11-124-367A-9938	Sequence 9938, Ap
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c 573	201	12	0.5	20	US-11-124-367A-10556	Sequence 10556, A
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c 576	201	12	0.5	20	US-11-124-367A-15496	Sequence 15496, A
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c 578	201	12	0.5	20	US-11-124-367A-20895	Sequence 20895, A
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c 580	201	12	0.5	20	US-11-124-367A-21408	Sequence 21408, A
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c 582	201	12	0.5	20	US-11-124-367A-22987	Sequence 22987, A
c 583	201	12	0.5	20	US-11-124-367A-24501	Sequence 24501, A
c 584	201	12	0.5	20	US-11-124-367A-27827	Sequence 27827, A
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c 586	201	12	0.5	20	US-11-124-367A-28174	Sequence 28174, A
c 587	201	12	0.5	20	US-11-124-367A-28212	Sequence 28212, A
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c 591	201	12	0.5	20	US-11-124-367A-32573	Sequence 32573, A
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c 593	209	6	0.5	20	US-09-925-065A-196854	Sequence 196854, A
c 594	209	6	0.5	20	US-09-925-065A-196855	Sequence 196855, A
c 595	281	6	0.5	20	US-09-925-065A-311771	Sequence 311771, A
c 596	281	6	0.5	20	US-09-925-065A-311772	Sequence 311772, A
c 597	281	6	0.5	20	US-09-925-065A-311773	Sequence 311773, A
c 598	281	6	0.5	20	US-09-925-065A-311774	Sequence 311774, A
c 599	309	6	0.5	20	US-09-925-065A-239880	Sequence 239880, A
c 600	318	6	0.5	20	US-09-925-065A-452194	Sequence 452194, A
c 601	330	6	0.5	20	US-09-925-065A-145591	Sequence 145591, A
c 602	349	8	0.5	20	US-10-508-424-3	Sequence 3, Appli
c 603	352	6	0.5	20	US-09-925-065A-605018	Sequence 605018, A
c 604	352	6	0.5	20	US-09-925-065A-605019	Sequence 605019, A
c 605	393	6	0.5	20	US-09-925-065A-576379	Sequence 576379,
c 606	396	6	0.5	20	US-09-925-065A-370032	Sequence 370032,
c 607	397	6	0.5	20	US-09-925-065A-176025	Sequence 176025,
c 608	400	6	0.5	20	US-09-925-065A-224389	Sequence 224389,
c 609	414	6	0.5	20	US-09-925-065A-224390	Sequence 224390,
c 610	417	6	0.5	20	US-09-925-065A-659623	Sequence 659623,
c 611	419	8	0.5	20	US-10-775-169-209	Sequence 209, App
c 612	422	6	0.5	20	US-09-925-065A-224941	Sequence 224941,
c 613	423	6	0.5	20	US-09-925-065A-224942	Sequence 224942,
c 614	423	6	0.5	20	US-09-925-065A-477261	Sequence 477261,
c 615	423	6	0.5	20	US-09-925-065A-580505	Sequence 580505,
c 616	424	6	0.5	20	US-09-925-065A-580506	Sequence 580506,
c 617	424	6	0.5	20	US-09-925-065A-580507	Sequence 580507,
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c 619	429	6	0.5	20	US-09-925-065A-186016	Sequence 186016,
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c 621	434	6	0.5	20	US-09-925-065A-186018	Sequence 186018,
c 622	435	6	0.5	20	US-09-925-065A-186019	Sequence 186019,
c 623	439	6	0.5	20	US-09-925-065A-577307	Sequence 577307,
c 624	439	6	0.5	20	US-09-925-065A-173179	Sequence 173179,
c 625	439	6	0.5	20	US-09-925-065A-191228	Sequence 191228,
c 626	440	6	0.5	20	US-09-925-065A-325438	Sequence 325438,
c 627	442	6	0.5	20	US-09-925-065A-168831	Sequence 168831,
c 628	446	6	0.5	20	US-09-925-065A-168832	Sequence 168832,
c 629	446	6	0.5	20	US-09-925-065A-561020	Sequence 561020,
c 630	450	8	0.5	20	US-10-821-234-374	Sequence 374, App
c 631	452	6	0.5	20	US-09-925-065A-393355	Sequence 393355,
c 632	465	6	0.5	20	US-09-925-065A-418222	Sequence 418222,
c 633	471	6	0.5	20	US-09-925-065A-445201	Sequence 445201,
c 634	473	6	0.5	20	US-09-925-065A-445202	Sequence 445202,
c 635	475	6	0.5	20	US-09-925-065A-126170	Sequence 126170,
c 636	475	6	0.5	20	US-09-925-065A-814223	Sequence 814223,
c 637	476	6	0.5	20	US-09-925-065A-111854	Sequence 111854,
c 638	478	6	0.5	20	US-09-925-065A-876285	Sequence 876285,
c 639	480	6	0.5	20	US-09-925-065A-274464	Sequence 274464,
c 640	481	6	0.5	20	US-09-925-065A-455964	Sequence 455964,
c 641	481	6	0.5	20	US-09-925-065A-519059	Sequence 519059,
c 642	481	6	0.5	20	US-09-925-065A-884545	Sequence 884545,
c 643	482	6	0.5	20	US-09-925-065A-295118	Sequence 295118,
c 644	482	6	0.5	20	US-09-925-065A-787904	Sequence 787904,
c 645	483	6	0.5	20	US-09-925-065A-565124	Sequence 565124,
c 646	483	6	0.5	20	US-09-925-065A-239905	Sequence 239905,
c 647	484	6	0.5	20	US-09-925-065A-239506	Sequence 239506,
c 648	489	6	0.5	20	US-09-925-065A-277231	Sequence 277231,
c 649	490	6	0.5	20	US-09-925-065A-616435	Sequence 616435,
c 650	490	6	0.5	20	US-09-925-065A-616436	Sequence 616436,
c 651	493	6	0.5	20	US-09-925-065A-49808	Sequence 49808, A
c 652	494	6	0.5	20	US-09-925-065A-205573	Sequence 205573,
c 653	494	6	0.5	20	US-09-925-065A-184098	Sequence 184098,
c 654	495	6	0.5	20	US-09-925-065A-420033	Sequence 420033,
c 655	495	6	0.5	20	US-09-925-065A-249720	Sequence 249720,
c 656	495	6	0.5	20	US-09-925-065A-642169	Sequence 642169,
c 657	497	6	0.5	20	US-09-925-065A-97802	Sequence 97802, A
c 658	498	6	0.5	20	US-09-925-065A-97803	Sequence 97803, A
c 659	501	6	0.5	20	US-09-925-065A-519299	Sequence 519299,
c 660	501	6	0.5	20	US-09-925-065A-519300	Sequence 519300,
c 661	501	6	0.5	20	US-09-925-065A-569095	Sequence 569095,
c 662	503	6	0.5	20	US-09-925-065A-569096	Sequence 569096,
c 663	505	6	0.5	20	US-09-925-065A-173150	Sequence 173150,
c 664	506	6	0.5	20	US-09-925-065A-173152	Sequence 173152,
c 665	507	6	0.5	20	US-09-925-065A-173153	Sequence 173153,
c 666	508	6	0.5	20	US-09-925-065A-173154	Sequence 173154,
c 667	510	6	0.5	20	US-09-925-065A-9781	Sequence 9781, Ap
c 668		6	0.5	20	US-09-925-065A-413104	Sequence 413104,
c 669		6	0.5	20	US-09-925-065A-28311	Sequence 28311, A
c 670		6	0.5	20	US-09-925-065A-158135	Sequence 158135,
c 671		6	0.5	20	US-09-925-065A-516142	Sequence 516142,
c 672		6	0.5	20	US-09-925-065A-664563	Sequence 664563,
c 673		6	0.5	20	US-09-925-065A-694214	Sequence 694214,
c 674		6	0.5	20	US-09-925-065A-824298	Sequence 824298,
c 675		6	0.5	20	US-09-925-065A-507282	Sequence 507282,
c 676		6	0.5	20	US-09-925-065A-13624	Sequence 13624, A
c 677		6	0.5	20	US-09-925-065A-199354	Sequence 199354,

#					Accession	Sequence
678	20	0.5	510	6	US-09-925-065A-199355	Sequence 199355,
679	20	0.5	510	6	US-09-925-065A-199356	Sequence 199356,
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682	20	0.5	514	6	US-09-925-065A-837112	Sequence 837112,
c 683	20	0.5	516	6	US-09-925-065A-185890	Sequence 185890,
684	20	0.5	516	6	US-09-925-065A-185891	Sequence 185891,
685	20	0.5	516	6	US-09-925-065A-622900	Sequence 622900,
686	20	0.5	517	6	US-09-925-065A-596198	Sequence 596198,
687	20	0.5	519	6	US-09-925-065A-435920	Sequence 435920,
688	20	0.5	520	6	US-09-925-065A-42513	Sequence 42513, A
c 689	20	0.5	520	6	US-09-925-065A-651813	Sequence 651813,
c 690	20	0.5	521	6	US-09-925-065A-100028	Sequence 100028,
691	20	0.5	521	6	US-09-925-065A-207449	Sequence 207449,
692	20	0.5	522	6	US-09-925-065A-475183	Sequence 475183,
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697	20	0.5	523	6	US-09-925-065A-330400	Sequence 330400,
698	20	0.5	523	6	US-09-925-065A-330401	Sequence 330401,
699	20	0.5	523	6	US-09-925-065A-901309	Sequence 901309,
c 700	20	0.5	524	6	US-09-925-065A-151888	Sequence 151888,
c 701	20	0.5	524	6	US-09-925-065A-164525	Sequence 164525,
c 702	20	0.5	524	6	US-09-925-065A-514873	Sequence 514873,
703	20	0.5	525	6	US-09-925-065A-322765	Sequence 322765,
704	20	0.5	526	6	US-09-925-065A-564079	Sequence 564079,
705	20	0.5	526	6	US-09-925-065A-340981	Sequence 340981,
c 706	20	0.5	528	6	US-09-925-065A-193474	Sequence 193474,
707	20	0.5	528	6	US-09-925-065A-493300	Sequence 493300,
c 708	20	0.5	528	6	US-09-925-065A-645698	Sequence 645698,
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712	20	0.5	530	6	US-09-925-065A-37063	Sequence 37063, A
713	20	0.5	530	6	US-09-925-065A-37064	Sequence 37064, A
714	20	0.5	530	6	US-09-925-065A-37065	Sequence 37065, A
c 715	20	0.5	530	6	US-09-925-065A-37066	Sequence 37066, A
716	20	0.5	532	6	US-09-925-065A-204619	Sequence 204619,
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718	20	0.5	534	6	US-09-925-065A-474669	Sequence 474669,
719	20	0.5	534	6	US-09-925-065A-597928	Sequence 597928,
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721	20	0.5	535	6	US-09-925-065A-417526	Sequence 417526,
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723	20	0.5	537	6	US-09-925-065A-382127	Sequence 382127,
724	20	0.5	538	6	US-09-925-065A-546150	Sequence 546150,
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726	20	0.5	540	6	US-09-925-065A-244555	Sequence 244555,
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736	20	0.5	543	6	US-09-925-065A-106383	Sequence 106383,
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775	20	0.5	556	6	US-09-925-065A-481203	Sequence 481203,
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787	20	0.5	561	6	US-09-925-065A-439874	Sequence 439874,
c 788	20	0.5	561	6	US-09-925-065A-16247	Sequence 16247, A
c 789	20	0.5	561	6	US-09-925-065A-141833	Sequence 141833,
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793	20	0.5	564	6	US-09-925-065A-20067	Sequence 20067, A
794	20	0.5	564	6	US-09-925-065A-219003	Sequence 219003,
795	20	0.5	564	6	US-09-925-065A-294101	Sequence 294101,
796	20	0.5	564	6	US-09-925-065A-294102	Sequence 294102,
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c 812	20	0.5	570	6	US-09-925-065A-507552	Sequence 507552,
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	873	20	0.5	US-09-925-065A-144689	6	587	0.5	20	Sequence 144689,
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	893	20	0.5	US-09-925-065A-882181	6	595	0.5	20	Sequence 882181,
	894	20	0.5	US-09-925-065A-187708	6	596	0.5	20	Sequence 187708,
	895	20	0.5	US-09-925-065A-333100	6	596	0.5	20	Sequence 333100,
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c	903	20	0.5	600	8	US-09-925-065A-723981	Sequence 723981,
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c	906	20	0.5	601	12	US-11-136-527-5874	Sequence 5874, Ap
c	907	20	0.5	601	6	US-09-925-065A-609447	Sequence 609447,
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	913	20	0.5	602	6	US-09-925-065A-728590	Sequence 728590,
	914	20	0.5	602	6	US-09-925-065A-745421	Sequence 745421,
	915	20	0.5	603	6	US-09-925-065A-349601	Sequence 349601,
	916	20	0.5	603	6	US-09-925-065A-349602	Sequence 349602,
	917	20	0.5	604	6	US-09-925-065A-188736	Sequence 188736,
	918	20	0.5	604	6	US-09-925-065A-678632	Sequence 678632,
	919	20	0.5	604	6	US-09-925-065A-764789	Sequence 764789,
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	922	20	0.5	605	6	US-09-925-065A-572277	Sequence 572277,
	923	20	0.5	605	6	US-09-925-065A-764788	Sequence 764788,
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	925	20	0.5	606	6	US-09-925-065A-907929	Sequence 907929,
	926	20	0.5	607	6	US-09-925-065A-405550	Sequence 405550,
	927	20	0.5	607	6	US-09-925-065A-405551	Sequence 405551,
	928	20	0.5	607	6	US-09-925-065A-754660	Sequence 754660,
	929	20	0.5	607	6	US-09-925-065A-825392	Sequence 825392,
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	940	20	0.5	610	6	US-09-925-065A-508515	Sequence 508515,
c	941	20	0.5	610	6	US-09-925-065A-917540	Sequence 917540,
	942	20	0.5	611	6	US-09-925-065A-797466	Sequence 797466,
	943	20	0.5	611	6	US-09-925-065A-842985	Sequence 842985,
c	944	20	0.5	611	6	US-09-925-065A-848653	Sequence 848653,
	945	20	0.5	612	6	US-09-925-065A-504072	Sequence 504072,
c	946	20	0.5	612	6	US-09-925-065A-783786	Sequence 783786,
c	947	20	0.5	612	6	US-09-925-065A-938133	Sequence 938133,
	948	20	0.5	612	6	US-09-925-065A-938134	Sequence 938134,
	949	20	0.5	613	6	US-09-925-065A-107683	Sequence 107683,
c	950	20	0.5	614	6	US-09-925-065A-743489	Sequence 743489,
c	951	20	0.5	615	6	US-09-925-065A-516141	Sequence 516141,
c	952	20	0.5	616	6	US-09-925-065A-787828	Sequence 787828,
	953	20	0.5	618	6	US-09-925-065A-897959	Sequence 897959,
c	954	20	0.5	619	6	US-09-925-065A-110476	Sequence 110476,
	955	20	0.5	619	6	US-09-925-065A-110477	Sequence 110477,
	956	20	0.5	619	6	US-09-925-065A-292244	Sequence 292244,
	957	20	0.5	619	6	US-09-925-065A-761988	Sequence 761988,
c	958	20	0.5	619	6	US-09-925-065A-761989	Sequence 761989,
c	959	20	0.5	619	6	US-09-925-065A-774097	Sequence 774097,
c	960	20	0.5	619	6	US-09-925-065A-830263	Sequence 830263,
	961	20	0.5	619	6	US-09-925-065A-830264	Sequence 830264,
	962	20	0.5	620	6	US-09-925-065A-196761	Sequence 196761,
c	963	20	0.5	620	6	US-09-925-065A-832218	Sequence 832218,
c	964	20	0.5	621	6	US-09-925-065A-798426	Sequence 798426,
c	965	20	0.5	623	6	US-09-925-065A-725778	Sequence 725778,
	966	20	0.5	625	6	US-09-925-065A-242563	Sequence 242563,
	967	20	0.5	625	6	US-09-925-065A-670349	Sequence 670349,
c	968	20	0.5	625	6	US-09-925-065A-705261	Sequence 705261,
c	969	20	0.5	625	6	US-09-925-065A-705262	Sequence 705262,

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  970  20  0.5  US-09-925-065A-874597  Sequence 874597,
c 971  20  0.5  US-09-925-065A-716165  Sequence 716165,
c 972  20  0.5  US-09-925-065A-716166  Sequence 716166,
  973  20  0.5  US-09-925-065A-716167  Sequence 716167,
c 974  20  0.5  US-09-925-065A-716168  Sequence 716168,
  975  20  0.5  US-09-925-065A-544464  Sequence 544464,
  976  20  0.5  US-09-925-065A-230271  Sequence 230271, A
  977  20  0.5  US-09-925-065A-37838   Sequence 37838,  A
c 978  20  0.5  US-09-925-065A-37839   Sequence 37839,  A
c 979  20  0.5  US-09-925-065A-37840   Sequence 37840,  A
c 980  20  0.5  US-09-925-065A-386701  Sequence 386701,
  981  20  0.5  US-09-925-065A-677057  Sequence 677057,
  982  20  0.5  US-09-925-065A-677058  Sequence 677058,
  983  20  0.5  US-09-925-065A-773381  Sequence 773381,
  984  20  0.5  US-09-925-065A-900492  Sequence 900492,
c 985  20  0.5  US-09-925-065A-318173  Sequence 318173,
c 986  20  0.5  US-09-925-065A-745004  Sequence 745004,
  987  20  0.5  US-09-925-065A-777105  Sequence 777105,
c 988  20  0.5  US-10-973-115B-507     Sequence 507, App
c 989  20  0.5  US-10-131-826A-507     Sequence 507, App
c 990  20  0.5  US-09-925-065A-948087  Sequence 948087,
  991  20  0.5  US-09-925-065A-956472  Sequence 956472,
c 992  20  0.5  US-09-925-065A-727734  Sequence 727734,
c 993  20  0.5  US-09-925-065A-759540  Sequence 759540,
  994  20  0.5  US-09-925-065A-506407  Sequence 506407,
  995  20  0.5  US-09-925-065A-743657  Sequence 743657,
c 996  20  0.5  US-09-925-065A-787827  Sequence 787827,
c 997  20  0.5  US-09-925-065A-747816  Sequence 747816,
  998  20  0.5  US-09-925-065A-821187  Sequence 821187,
c 999  20  0.5  US-09-925-065A-935392  Sequence 935392,
 1000  20  0.5  US-09-925-065A-72710   Sequence 72710, A
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ALIGNMENTS

RESULT 1
US-09-925-065A-727226/c
; Sequence 727226, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 727226
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-727226

Query Match   3.2%;   Score 124;   DB 6;   Length 1275;
Best Local Similarity   100.0%;   Pred. No. 1.5e-29;
Matches   124;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1893 GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT 1952
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543 GATAGTGAATGCTGGAAACCTCCCTGTGTATGATGATATCCATAAGGAACTTCTGCAGCT 484

Qy   1953 CTGTGAAGATCTCATCTGGAATAAGACCCTGAGGCCACTGAGGAAGCTCTTACGTTATGC 2012
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 CTGTGAAGATCTCATCTGGAATAAGACCCTGAGGCCACTGAGGAAGCTCTTACGTTATGC 424

Qy   2013 CCAG 2016
         ||||
Db   423 CCAG 420

RESULT 2
US-09-925-065A-697175/c
; Sequence 697175, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 697175
;   LENGTH: 616
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-697175

Query Match   2.0%;   Score 80;   DB 6;   Length 616;
Best Local Similarity   100.0%;   Pred. No. 8.2e-16;
Matches   80;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   2739 GTGTTCCCAGCTGTTAGATGAAATCTAAAGGATGAAATCATGGAAGA 2798
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   134 GTGTTCCCAGCTGTTAGATGAAATCTAAAGGATGAAATCATGGAAGA 75

Qy   2799 ATATGAAGATATTAGACACAGG 2818
         ||||||||||||||||||||||
Db   74 ATATGAAGATATTAGACACAGG 55

RESULT 3
US-09-925-065A-460077/c
; Sequence 460077, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 460077
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-460077

Query Match   1.0%; Score 39; DB 6; Length 611;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches   39; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   989 AGGATTTGCTATGGATGGCTTGGTCAATATAGTTCGAG 1027
           ||||||||||||||||||||||||||||||||||||||
Db   39 AGGATTTGCTATGGATGGCTTGGTCAATATAGTTCGAG 1

RESULT 4
US-09-925-065A-39453/c
; Sequence 39453, Application US/09925065A
; Publication No. US2004018104A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39453
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-39453

Query Match   0.8%; Score 31; DB 6; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches   31; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3889 TCTTGATGATCCTCAAGGAAATACAACCTAG 3919
           |||||||||||||||||||||||||||||||
Db   570 TCTTGATGATCCTCAAGGAAATACAACCTAG 540

RESULT 5
US-09-925-065A-602656
; Sequence 602656, Application US/09925065A
; Publication No. US2004018104A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602656
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-602656

Query Match   0.7%; Score 26; DB 6; Length 559;
Best Local Similarity 100.0%; Pred. No. 49;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3864 TTTTTTTTTTTTTTTGCCTTTTTAT 3889
           |||||||||||||||||||||||||
Db   21 TTTTTTTTTTTTTTTGCCTTTTTAT 46

RESULT 6
US-09-925-065A-271845
; Sequence 271845, Application US/09925065A
; Publication No. US2004018104A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 271845
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-271845

Query Match   0.7%; Score 26; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 48;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTGCCTTTTTTA 3888
           |||||||||||||||||||||||||||
Db   378 TTTTTTTTTTTTTTTTTGCCTTTTTTA 403

RESULT 7
US-09-925-065A-702090
; Sequence 702090, Application US/09925065A
; Publication No. US2004018104A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092

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  ; PRIOR FILING DATE: 2000-11-30
  ; PRIOR APPLICATION NUMBER: US 60/261,766
  ; PRIOR FILING DATE: 2001-01-16
  ; PRIOR APPLICATION NUMBER: US 60/289,846
  ; PRIOR FILING DATE: 2001-05-09
  ; NUMBER OF SEQ ID NOS: 957086
  ; SOFTWARE: FastSEQ for Windows Version 4.0
  ; SEQ ID NO 702090
  ; LENGTH: 1374
  ; TYPE: DNA
  ; ORGANISM: Homo sapiens
US-09-925-065A-702090

Query Match             0.7%;  Score 26;  DB 6;  Length 1374;
Best Local Similarity   100.0%;  Pred. No. 40;
Matches   26;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   3862 CTTTTTTTTTTTTTTTTGCCTTTTTT 3887
          ||||||||||||||||||||||||||
Db    204 CTTTTTTTTTTTTTTTTGCCTTTTTT 229

RESULT 8
US-11-175-859-4373
; Sequence 4373, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; SOFTWARE: PatentIn version 3.2
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 4373
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-4373

Query Match             0.6%;  Score 25;  DB 12;  Length 50;
Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   2794 GAAGAATATGAAGAATATTAGACAGG 2818
          |||||||||||||||||||||||||
Db      1 GAAGAATATGAAGAATATTAGACAGG 25

RESULT 9
US-09-925-065A-279223/c
; Sequence 279223, Application US09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09


  ; NUMBER OF SEQ ID NOS: 957086
  ; SOFTWARE: FastSEQ for Windows Version 4.0
  ; SEQ ID NO 279223
  ; LENGTH: 542
  ; TYPE: DNA
  ; ORGANISM: Homo sapiens
US-09-925-065A-279223

Query Match             0.6%;  Score 25;  DB 6;  Length 542;
Best Local Similarity   100.0%;  Pred. No. 1e+02;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   3855 AGACTAACTTTTTTTTTTTTTTTTG 3879
          |||||||||||||||||||||||||
Db    435 AGACTAACTTTTTTTTTTTTTTTTG 411

RESULT 10
US-09-925-065A-936651/c
; Sequence 936651, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 936651
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-936651

Query Match             0.6%;  Score 25;  DB 6;  Length 545;
Best Local Similarity   100.0%;  Pred. No. 1e+02;
Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTGCCTTTTTT 3887
          |||||||||||||||||||||||||
Db    157 TTTTTTTTTTTTTTTTGCCTTTTTT 133

RESULT 11
US-09-925-065A-550047/c
; Sequence 550047, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
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; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550047
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-550047

Query Match   0.6%;   Score 25;   DB 6;   Length 630;
Best Local Similarity   100.0%;   Pred. No. 97;
Matches   25;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3855 AGACTAACTTTTTTTTTTTTTTTTG 3879
           ||||||||||||||||||||||||
Db   582 AGACTAACTTTTTTTTTTTTTTTTG 558

RESULT 12
US-09-925-065A-34355
; Sequence 34355, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,096
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34355
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-34355

Query Match   0.6%;   Score 25;   DB 6;   Length 1660;
Best Local Similarity   100.0%;   Pred. No. 78;
Matches   25;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3855 AGACTAACTTTTTTTTTTTTTTTTG 3879
           ||||||||||||||||||||||||
Db   692 AGACTAACTTTTTTTTTTTTTTTTG 716

RESULT 13
US-09-925-065A-34356
; Sequence 34356, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,096
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34356
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-34356

Query Match   0.6%;   Score 25;   DB 6;   Length 1660;
Best Local Similarity   100.0%;   Pred. No. 78;
Matches   25;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3855 AGACTAACTTTTTTTTTTTTTTTTG 3879
           ||||||||||||||||||||||||
Db   692 AGACTAACTTTTTTTTTTTTTTTTG 716

RESULT 14
US-09-925-065A-34357
; Sequence 34357, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,096
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34357
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-34357

Query Match   0.6%;   Score 25;   DB 6;   Length 1660;
Best Local Similarity   100.0%;   Pred. No. 78;
Matches   25;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3855 AGACTAACTTTTTTTTTTTTTTTTG 3879
           ||||||||||||||||||||||||
Db   692 AGACTAACTTTTTTTTTTTTTTTTG 716

RESULT 15
US-09-925-065A-34358
; Sequence 34358, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,096
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34358
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-34358

Query Match   0.6%; Score 25; DB 6; Pred. No. 78; Length 1660;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3855 AGACTAACTTTTTTTTTTTTTTTTTG 3879
          |||||||||||||||||||||||||
Db   692 AGACTAACTTTTTTTTTTTTTTTTTG 716

RESULT 16
US-09-925-065A-34359
; Sequence 34359, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34359
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-34359

Query Match   0.6%; Score 25; DB 6; Pred. No. 78; Length 1660;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3855 AGACTAACTTTTTTTTTTTTTTTTTG 3879
          |||||||||||||||||||||||||
Db   692 AGACTAACTTTTTTTTTTTTTTTTTG 716

RESULT 17
US-11-112-908-63
; Sequence 63, Application US/1112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 149111
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-63

Query Match   0.6%; Score 25; DB 12; Length 149111;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3863 TTTTTTTTTTTTTTTTTTGCCTTTTTT 3887
           ||||||||||||||||||||||||||
Db 148340 TTTTTTTTTTTTTTTTTTGCCTTTTTT 148364

RESULT 18
US-11-121-086-81/c
; Sequence 81, Application US/1121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 156544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-81

Query Match   0.6%; Score 25; DB 12; Length 156544;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3863 TTTTTTTTTTTTTTTTTTTGCCTTTTTT 3887
          ||||||||||||||||||||||||||
Db 27199 TTTTTTTTTTTTTTTTTTTGCCTTTTTT 27175

RESULT 19
US-11-112-908-64
; Sequence 64, Application US/1112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702

```
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
; LENGTH: 157230
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-64

Query Match    0.6%;   Score 25;   DB 12;   Length 157230;
Best Local Similarity  100.0%;   Pred. No. 29;
Matches  25;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy   3863  TTTTTTTTTTTTTTTTGCCTTTTTT  3887
           |||||||||||||||||||||||||
Db   95686 TTTTTTTTTTTTTTTTGCCTTTTTT  95710


RESULT 20
US-11-112-908-62
; Sequence 62, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 170508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-62

Query Match    0.6%;   Score 25;   DB 12;   Length 170508;
Best Local Similarity  100.0%;   Pred. No. 28;
Matches  25;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy   3863  TTTTTTTTTTTTTTTTGCCTTTTTT  3887
           |||||||||||||||||||||||||
Db   79442 TTTTTTTTTTTTTTTTGCCTTTTTT  79466


RESULT 21
US-11-112-908-65
; Sequence 65, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 173115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-65

Query Match    0.6%;   Score 25;   DB 12;   Length 173115;
Best Local Similarity  100.0%;   Pred. No. 28;
Matches  25;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy   3863  TTTTTTTTTTTTTTTTGCCTTTTTT  3887
           |||||||||||||||||||||||||
Db   31197 TTTTTTTTTTTTTTTTGCCTTTTTT  31221


RESULT 22
US-09-925-065A-412268/c
; Sequence 412268, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 412268
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-412268

Query Match    0.6%;   Score 24;   DB 6;   Length 489;
Best Local Similarity  100.0%;   Pred. No. 2.1e+02;
Matches  24;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy   3862  CTTTTTTTTTTTTTTTTTGCCTTTT  3885
           |||||||||||||||||||||||||
Db   136   CTTTTTTTTTTTTTTTTTGCCTTTT  113


RESULT 23
US-09-925-065A-270554/c
; Sequence 270554, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
```

```
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 270554
;     LENGTH: 506
;     TYPE: DNA
;     ORGANISM: Homo sapiens
US-09-925-065A-270554

Query Match        0.6%;  Score 24;  DB 6;  Length 506;
Best Local Similarity  100.0%;  Pred. No. 2.1e+02;
Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3863 TTTTTTTTTTTTTTTGCCTTTTT 3886
           ||||||||||||||||||||||
Db     268 TTTTTTTTTTTTTTTGCCTTTTT 245

RESULT 24
US-09-925-065A-620176/C
; Sequence 620176, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 620176
;   LENGTH: 512
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-620176

Query Match        0.6%;  Score 24;  DB 6;  Length 512;
Best Local Similarity  100.0%;  Pred. No. 2.1e+02;
Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3863 TTTTTTTTTTTTTTTGCCTTTTT 3886
           ||||||||||||||||||||||
Db     245 TTTTTTTTTTTTTTTGCCTTTTT 222

RESULT 25
US-09-925-065A-424567
; Sequence 424567, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 424567
;     LENGTH: 548
;     TYPE: DNA
;     ORGANISM: Homo sapiens
US-09-925-065A-424567

Query Match        0.6%;  Score 24;  DB 6;  Length 548;
Best Local Similarity  100.0%;  Pred. No. 2e+02;
Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3864 TTTTTTTTTTTTTTTGCCTTTTT 3887
           ||||||||||||||||||||||
Db     116 TTTTTTTTTTTTTTTGCCTTTTT 139

RESULT 26
US-09-925-065A-889241/C
; Sequence 889241, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 889241
;   LENGTH: 549
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-889241

Query Match        0.6%;  Score 24;  DB 6;  Length 549;
Best Local Similarity  100.0%;  Pred. No. 2e+02;
Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3864 TTTTTTTTTTTTTTTGCCTTTTT 3887
           ||||||||||||||||||||
Db      46 TTTTTTTTTTTTTTTGCCTTTTT 23

RESULT 27
US-09-925-065A-624935
; Sequence 624935, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
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; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 624935
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-624935

Query Match   0.6%; Score 24; DB 6; Length 585;
Best Local Similarity   100.0%; Pred. No. 2e+02;
Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 3865 TTTTTTTTTTTTTTTTGCCTTTTTTA 3888
         |||||||||||||||||||||||||
Db   126 TTTTTTTTTTTTTTTTGCCTTTTTTA 149

RESULT 28
US-09-925-065A-530520
; Sequence 530520, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 530520
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-530520

Query Match   0.6%; Score 24; DB 6; Length 626;
Best Local Similarity   100.0%; Pred. No. 2e+02;
Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 3863 TTTTTTTTTTTTTTTTTGCCTTTTT 3886
         |||||||||||||||||||||||||
Db   53 TTTTTTTTTTTTTTTTTGCCTTTTT 76

RESULT 29
US-10-995-561-13215/c
; Sequence 13215, Application US/1095561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13215
; LENGTH: 241805
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(241805)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13215

Query Match   0.6%; Score 24; DB 8; Length 241805;
Best Local Similarity   100.0%; Pred. No. 53;
Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3862 CTTTTTTTTTTTTTTTTTGCCTTTT 3885
           ||||||||||||||||||||||||
Db 188249 CTTTTTTTTTTTTTTTTTGCCTTTT 188226

RESULT 30
US-10-995-561-13259
; Sequence 13259, Application US/1095561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13259
; LENGTH: 387780
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(387780)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13259

Query Match   0.6%; Score 24; DB 8; Length 387780;
Best Local Similarity   100.0%; Pred. No. 48;
Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTGCCTTTTT 3886
           |||||||||||||||||||||||||
Db 250861 TTTTTTTTTTTTTTTTTGCCTTTTT 250884

RESULT 31
US-10-310-914A-496602
; Sequence 496602, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 496602
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-496602

Query Match   0.6%; Score 23; DB 8; Length 25;
Best Local Similarity   13.0%; Pred. No. 8.2e+02;
Matches   3; Conservative   20; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTGCCTTTT 3885
              ::::::::::::::::|||::::
Db   3 UUUUUUUUUUUUUUUGCCUUUU 25

RESULT 32
US-10-310-914A-859043
; Sequence 859043, Application US/10310914A
; Publication No. US2006000332A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 859043
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-859043

Query Match   0.6%; Score 23; DB 8; Length 25;
Best Local Similarity   13.0%; Pred. No. 8.2e+02;
Matches   3; Conservative   20; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTGCCTTTT 3885
              ::::::::::::::::|||::::
Db   3 UUUUUUUUUUUUUUUGCCUUUU 25

RESULT 33
US-11-124-367A-12473
; Sequence 12473, Application US/11124367A
; Publication No. US2006024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12473
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-12473

Query Match   0.6%; Score 23; DB 12; Length 201;
Best Local Similarity   100.0%; Pred. No. 5.2e+02;
Matches   23; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTTTGCCTTTT 3885
              |||||||||||||||||||||||||
Db   133 TTTTTTTTTTTTTTTTTTTGCCTTTT 133

RESULT 34
US-11-124-367A-12474
; Sequence 12474, Application US/11124367A
; Publication No. US2006024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12474
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-12474

Query Match   0.6%; Score 23; DB 12; Length 201;
Best Local Similarity   100.0%; Pred. No. 5.2e+02;
Matches   23; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTTTGCCTTTT 3885
              |||||||||||||||||||||||||
Db   111 TTTTTTTTTTTTTTTTTTTGCCTTTT 129

RESULT 35
US-09-925-065A-261182/c
; Sequence 261182, Application US/09925065A
; Publication No. US2004018104BA1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261182
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-261182

Query Match   0.6%; Score 23; DB 6; Length 376;
Best Local Similarity   100.0%; Pred. No. 4.5e+02;
Matches   23; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTTTGCCTTTT 3885
              |||||||||||||||||||||||||
Db   107 TTTTTTTTTTTTTTTTTTTGCCTTTT 129

```
Qy   3863  TTTTTTTTTTTTTTTTGCCTTTT  3885
           ||||||||||||||||||||||
Db     48  TTTTTTTTTTTTTTTTGCCTTTT    26
```

RESULT 36
US-09-925-065A-351757/c
; Sequence 351757, Application US/09925065A
; Publication No. US2004018104sA1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 351757
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-351757

Query Match   0.6%;   Score 23;   DB 6;   Length 451;
Best Local Similarity   100.0%;   Pred. No. 4.3e+02;
Matches 23;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy   3863  TTTTTTTTTTTTTTTTGCCTTTT  3885
           ||||||||||||||||||||||
Db    370  TTTTTTTTTTTTTTTTGCCTTTT   348
```

RESULT 37
US-10-689-742-18/c
; Sequence 18, Application US/10689742
; Publication No. US2005025018oA1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-689-742-18

Query Match   0.6%;   Score 23;   DB 8;   Length 481;
Best Local Similarity   100.0%;   Pred. No. 4.3e+02;

Matches 23;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy   3863  TTTTTTTTTTTTTTTTGCCTTTT  3885
           ||||||||||||||||||||||
Db    466  TTTTTTTTTTTTTTTTGCCTTTT   444
```

RESULT 38
US-11-136-527-1395/c
; Sequence 1395, Application US/11136527
; Publication No. US2005028757oA1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1395
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1395

Query Match   0.6%;   Score 23;   DB 12;   Length 491;
Best Local Similarity   100.0%;   Pred. No. 4.3e+02;
Matches 23;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy   3863  TTTTTTTTTTTTTTTTGCCTTTT  3885
           ||||||||||||||||||||||
Db      3  TTTTTTTTTTTTTTTTGCCTTTT    25
```

RESULT 39
US-11-136-527-5491/c
; Sequence 5491, Application US/11136527
; Publication No. US2005028757oA1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5491
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-5491

Query Match   0.6%;   Score 23;   DB 12;   Length 491;
Best Local Similarity   100.0%;   Pred. No. 4.3e+02;
Matches 23;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy   3863  TTTTTTTTTTTTTTTTGCCTTTT  3885
           ||||||||||||||||||||||
Db    489  TTTTTTTTTTTTTTTTGCCTTTT   467
```

RESULT 40
US-09-925-065A-98281
; Sequence 98281, Application US/09925065A
; Publication No. US2004018104sA1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98281
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-98281

Query Match   0.6%; Score 23; DB 6; Length 498;
Best Local Similarity   100.0%; Pred. No. 4.3e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3863 TTTTTTTTTTTTTTTTGCCTTTT 3885
          |||||||||||||||||||||||
Db   221 TTTTTTTTTTTTTTTTGCCTTTT 243

RESULT 41
US-09-925-065A-98282
; Sequence 98282, Application US/0992506SA
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98282
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-98282

Query Match   0.6%; Score 23; DB 6; Length 498;
Best Local Similarity   100.0%; Pred. No. 4.3e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3863 TTTTTTTTTTTTTTTTGCCTTTT 3885
          |||||||||||||||||||||||
Db   221 TTTTTTTTTTTTTTTTGCCTTTT 243

RESULT 42
US-09-925-065A-925330
; Sequence 925330, Application US/09925065A

; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 925330
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-925330

Query Match   0.6%; Score 23; DB 6; Length 503;
Best Local Similarity   100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3863 TTTTTTTTTTTTTTTTGCCTTTT 3885
          |||||||||||||||||||||||
Db   91 TTTTTTTTTTTTTTTTGCCTTTT 113

RESULT 43
US-09-925-065A-828324/c
; Sequence 828324, Application US2004018104SA
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 828324
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-828324

Query Match   0.6%; Score 23; DB 6; Length 522;
Best Local Similarity   100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3863 TTTTTTTTTTTTTTTTTGCCTTTT 3885
          ||||||||||||||||||||||||
Db   176 TTTTTTTTTTTTTTTTTGCCTTTT 154

RESULT 44
US-09-925-065A-819272
; Sequence 819272, Application US/09925065A1
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 819272
;   LENGTH: 523
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-819272

Query Match   0.6%; Score 23; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches   23; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3863 TTTTTTTTTTTTTTTTTGCCTTTT 3885
             |||||||||||||||||||||||
Db   348 TTTTTTTTTTTTTTTTTGCCTTTT 370

RESULT 45
US-09-925-065A-3410
; Sequence 3410, Application US/09925065A1
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3410
;   LENGTH: 556
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-3410

Query Match   0.6%; Score 23; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches   23; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3857 ACTAACTTTTTTTTTTTTTTTTG 3879
             |||||||||||||||||||||||

Db   444 ACTAACTTTTTTTTTTTTTTTTG 466

RESULT 46
US-09-925-065A-755600/c
; Sequence 755600, Application US/09925065A1
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 755600
;   LENGTH: 574
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-755600

Query Match   0.6%; Score 23; DB 6; Length 574;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches   23; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3864 TTTTTTTTTTTTTTTGCCTTTTT 3886
             |||||||||||||||||||||||
Db   127 TTTTTTTTTTTTTTTGCCTTTTT 105

RESULT 47
US-09-925-065A-278724
; Sequence 278724, Application US/09925065A1
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 278724
;   LENGTH: 575
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-278724

Query Match   0.6%; Score 23; DB 6; Length 575;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches   23; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 3865 TTTTTTTTTTTTTGCCTTTTT 3887
          |||||||||||||||||||||
Db   391 TTTTTTTTTTTTTTGCCTTTTT 413

RESULT 48
US-09-925-065A-561677
; Sequence 561677, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 561677
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-561677

Query Match   0.6%;   Score 23;   DB 6;   Length 576;
Best Local Similarity   100.0%;   Pred. No. 4.1e+02;
Matches   23;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 3863 TTTTTTTTTTTTTTTGCCTTTT 3885
          ||||||||||||||||||||
Db   27 TTTTTTTTTTTTTTTGCCTTTT 49

RESULT 49
US-11-136-527-5990/c
; Sequence 5990, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5990
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-5990

Query Match   0.6%;   Score 23;   DB 12;   Length 600;
Best Local Similarity   100.0%;   Pred. No. 4.1e+02;
Matches   23;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 3863 TTTTTTTTTTTTTTTTGCCTTTT 3885
          |||||||||||||||||||||
Db   600 TTTTTTTTTTTTTTTTGCCTTTT 578

RESULT 50
US-09-925-065A-478484/c
; Sequence 478484, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 478484
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-478484

Query Match   0.6%;   Score 23;   DB 6;   Length 601;
Best Local Similarity   100.0%;   Pred. No. 4.1e+02;
Matches   23;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 3856 GACTAACTTTTTTTTTTTTTTTT 3878
          ||||||||||||||||||||
Db   310 GACTAACTTTTTTTTTTTTTTTT 288

Search completed: March 7, 2006, 02:39:09
Job time : 1043 secs